OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: December 4, 2005, 20:37:26 ; Search time 5458.54 Seconds
(without alignments)
10242.778 Million cell updates/sec

Title: US-10-750-262-1
Perfect score: 1195
Sequence: 1 ccgagactcacggtcaagct..........ggaaaaaaaaaaaaaaaaa 1195
Scoring table: IDENTITY NUC
                Gapop 10.0, Gapext 1.0
Searched: 41078325 seqs, 2339541228 residues
Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
               1: gb_est1:*
               2: gb_est2:*
               3: gb_est3:*
               4: gb_htc:*
               5: gb_est4:*
               6: gb_est5:*
               7: gb_est6:*
               8: gb_est7:*
               9: gb_gss1:*
              10: gb_gss2:*
              11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1048.4	87.7	1050	10	AY403218	AY403218 Homo sapi
	2	931.6	78.0	1045	10	AY403219	AY403219 Pan trogl
	3	841	70.4	884	6	CA488012	CA488012 AGENCOURT
	4	806	67.4	1211	6	AK010437	AK010437 Mus muscu
	5	765.2	64.0	1050	10	AY403220	AY403220 Mus muscu
c	6	718.4	60.1	720	6	CA446381	CA446381 UI-H-ED1-
	7	692.8	58.0	881	2	BG565247	BG565247 602582917
c	8	683.2	57.2	961	2	BG762026	BG762026 602718984
	9	672.4	56.3	827	8	CV983083	CV983083 UMC-bmix
	10	672	56.2	710	2	BE875216	BE875216 601488516
	11	663	55.5	697	8	DN997716	DN997716 TC115356
	12	657.6	55.0	773	5	BU602279	BU602279 AGENCOURT
	13	656.2	54.9	742	8	CX757709	CX757709 AGENCOURT
	14	655	54.8	783	3	BI552907	BI552907 603197827
	15	654.6	54.8	825	8	CX753134	CX753134 AGENCOURT
	16	642.4	53.8	796	2	BG182296	BG182296
	17	640.8	53.6	788	7	CN153902	CN153902 RST1161.A
	18	640.4	53.6	661	3	BM995067	BM995067 941069 MA
	19	634.2	53.1	799	5	BU930271	BU930271 AGENCOURT
c	20	600	50.2	600	1	AI686139	AI686139 tt92e11.x
c	21	598	50.0	609	6	CD677954	CD677954 ho24h02.y
	22	597.8	50.0	920	2	BE881257	BE881257 601492338
	23	596.8	49.9	1003	3	BI551229	BI551229 601194629
	24	589	49.3	1071	3	BM920324	BM920324 AGENCOURT
	25	588	49.2	705	6	CB424830	CB424830 59943z MA
	26	587	49.1	684	2	BE439545	BE439545 HTM1-183F
	27	586.2	49.1	609	3	BX103101	BX103101 HTM1-183F
	28	577.8	48.4	584	3	BM675259	BM675259 UI-E-EJ0-
	29	576.2	48.2	636	6	CD690450	CD690450 EST6973 h
	30	573.4	48.0	581	2	BM714075	BM714075 UI-R-BJ0-
	31	559.4	46.8	891	2	BF965211	BF965211 602268114
c	32	554.4	46.4	581	2	BG577403	BG577403 N112 SH-
	33	553.8	46.3	773	2	BG104394	BG104394 602311010
	34	550.2	46.0	661	5	BU929991	BU929991 AGENCOURT
	35	534.6	44.7	600	5	BX506262	BX506262 DKFZp686E
	36	521.6	43.6	759	6	BI360480	BI360480 387409 MA
	37	504.8	42.2	600	3	CA509933	CA509933 UI-R-FS0-
	38	499.6	41.8	705	5	BY755449	BY755449 UI-R-FS0-
	39	497	41.6	1007	6	AI167942	AI167942 oo09b06.x
	40	494	41.3	497	1	CF596595	CF596595 AGENCOURT
c	41	484.2	40.5	729	3	BQ211210	BQ211210 UI-R-DY1-
	42	476.2	39.8	566	6	CB143042	CB143042 K-EST0196
c	43	475.6	39.8	654	7	CO594327	CO594327 DG2-93n7
c	44	474.4	39.7	696	3	BQ205543	BQ205543 UI-R-EP0-
	45	472.6	39.5	1020	3	BM811413	BM811413 AGENCOURT

ALIGNMENTS

RESULT 1
AY403218

LOCUS   AY403218   1050 bp   DNA   linear   GSS 15-DEC-2003
DEFINITION Homo sapiens STEAP gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY403218
VERSION   AY403218.1 GI:39759201
KEYWORDS   GSS.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 1050)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
JOURNAL   Science 302 (5652), 1960-1963 (2003)
PUBMED   14671302
REFERENCE   2 (bases 1 to 1050)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
TITLE   Direct Submission
JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES   Location/Qualifiers
     source   1..1050
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene   <1..>1050
                     /gene="STEAP"
                     /locus_tag="HCM1484"
ORIGIN

Query Match   87.7%; Score 1048.4; DB 10; Length 1050;
Best Local Similarity   99.9%;
Matches 1049; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

RESULT 2
AY403219

LOCUS   AY403219   1045 bp   DNA   linear   GSS 15-DEC-2003
DEFINITION Pan troglodytes STEAP gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY403219
VERSION   AY403219.1 GI:39759202
KEYWORDS   GSS.
SOURCE   Pan troglodytes (chimpanzee)
  ORGANISM Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1 (bases 1 to 1045)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
  PUBMED   14671302
REFERENCE   2 (bases 1 to 1045)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE   Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES   Location/Qualifiers
     source   1..1045
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
     gene   <1..>1045
                     /gene="STEAP"
                     /locus_tag="HCM1484"
ORIGIN

Query Match   78.0%; Score 931.6; DB 10; Length 1045;
Best Local Similarity   89.4%;
Matches 934; Conservative   0; Mismatches 111; Indels   0; Gaps   0;

Pred. No. 2.7e-205;

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LOCUS       CA488012                 884 bp    mRNA    linear   EST 14-NOV-2002
DEFINITION  AGENCOURT_10807821 MAPCL Homo sapiens cDNA clone IMAGE:6719746 5',
            mRNA sequence.
ACCESSION   CA488012
VERSION     CA488012.1  GI:24948800
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 884)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Kristi A. Egland, Ira Pastan
            cDNA Library Preparation: Invitrogen Corp
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
FEATURES             Location/Qualifiers
     source          1..884
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6719746"
                     /cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,
                     hTERT-HME1, LNCaP"
                     /clone_lib="MAPCL"
                     /lab_host="EMDH10B"
                     /note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
                     Subtracted with brain, liver, lung, kidney and muscle.
                     Directionally cloned. Priming method: oligo-dT. Average
                     insert size: 1800 bp. Library amplification: 26,000 fold.
                     Kristi A. Egland, James J. Vincent, Robert Strausberg,
                     Bungkook Lee & Ira Pastan: Discovery of new breast
                     cancer genes encoding membrane and secreted proteins.
                     Manuscript submitted."
ORIGIN
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Plate: LLAM1278 row: c column: 10
High quality sequence stop: 758.

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RESULT 3
CA488012
CA488012
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Query Match          70.4%;   Score 841; DB 6; Length 884;
Best Local Similarity 99.4%;   Pred. No. 2.9e-184;
Matches  844;  Conservative   0;  Mismatches   5;  Indels    0;  Gaps   0;
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Qy      1  CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTATAG   60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     17  CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTATAG   76

Qy     61  AATTAATTGGAAAGCAGAAAAGACATCACAAAACCAAGAGAAGAACTTTGGAAAATGAAGCCTA  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     77  AATTAATTGGAAAGCAGAAAAGACATCACAAAACCAAGAGAAGAACTTTGGAAAATGAAGCCTA  136

Qy    121  GGAGAAAATTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGGAGAGGACCAGCATGCTAA  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    137  GGAGAAAATTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGGAGAGGACCAGCATGCTAA  196

Qy    181  AAAGACCTGTGCTTTGGCATTTGCACCAAAACAGCCCATGCTGATGAATTGACTGCCCTT  240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    197  AAAGACCTGTGCTTTGGCATTTGCACCAAAACAGCCCATGCTGATGAATTGACTGCCCTT  256

Qy    241  CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    257  CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG  316

Qy    301  CTATTATAGCATCTCTGACTTTTCTTTACACTTCTGAGGGAGGGAAGTAATTCACCCTTTAG  360
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Db    317  CTATTATAGCATCTCTGACTTTTCTTTACACTTCTGAGGGAGGGAAGTAATTCACCCTTTAG  376

Qy    361  CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAGTCTGC  420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    377  CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAGTCTGC  436

Qy    421  CAATGGGTTTCCATCACTCTCTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGGCCATTG  480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    437  CAATGGGTTTCCATCACTCTCTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGGCCATTG  496

Qy    481  TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATTAAGTGGATGT  540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    497  TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATTAAGTGGATGT  556

Qy    541  TAACAAGAAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTGCTGTTACTGCAGGTCAAATTTATA  600
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Db    557  TAACAAGAAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTGCTGTTACTGCAGGTCAAATTTATA  616

Qy    601  GTCTGTGTCTTACCCAATGAGGCCGATCCCTACAGATACAAGTTGCTAAAACTGGGCAATTCAAC  660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    617  GTCTGTGTCTTACCCAATGAGGCCGATCCCTACAGATACAAGTTGCTAAAACTGGGCAATTCAAC  676

Qy    661  AGGTCCAACAAAATAAAGAAGAAGATGCCTGGAATTGAGCATGAATGTTTGAGAGAATGGAGATT  720
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Db    677  AGGTCCAACAAAATAAAGAAGAAGATGCCTGGAATTGAGCATGAATGTTTGAGAGAATGGAGATT  736
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(sequence alignment continues in the left column)

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Db    361  GGTCATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTCTGGCATTGGTTTACCTGCC  420

Qy    421  AGGTGTGATAGCAGCAGCAATTGTCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACA  480

Db    461  AGGTGTGATAGCAGCAGCAATTGTCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACA  520

Qy    521  TTGGTTGGATTAAGTGGATGTTAACAAGAAAACAGTTTGGGCTTCTCAGTTTCTTTTTGC  580

Db    481  TTGGTTGGATTAAGTGGATGTTAACAAGAAAAGCAGTTTGGGGCTTCTCAGTTTCTTTTTTGC  540

Qy    581  TGTTACTGCAGGTCAAATTTATAGTCTGTGTCTTACCCAATGAGGCCGATCCCTACAGATACAAGTT  640

Db    541  TGTACTGCAGGTCAAATTTATAGTCTTACCCAATGAGGCCGATCCCTACAGATACAAGTT  600

Qy    601  GCTAAACTGGGCAATATCAACAGGTCCAACAAAATAAAGAAGAANNNTGCCTGGATTTGAGCATGA  660

Db    601  GCTAAACTGGGCAATATCAACAGGTCCAACAAAATAAAGANNNNTGCCTGGATTGAGCATGA  660

Qy    661  CGTTTGGAATGGAGATTTATGTTGTCTCTGGGAATTGTGGGGAATTGGCAATACTGGCTCT  720

Db    701  TGTTTGGAATGGAGATTTATGTTGTGTCTCTGGGAATTGTGGGAATACTGGCTCT  760

Qy    721  GTTGGGCTGTGANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  780

Db    761  GTTGGGCTGTGACATCTATTCCATTCTGTGAGTGAGTCTTTGACATGGGAGGAATTTCACTA  820

Qy    781  NNNNNNNNAGCAAGCTAGGAATTGTTCCCTTCTCCTTCTACTGGGCACAATACACGCATTGATTT  840

Db    821  TATTCAGAGCAAGCTAGGAATTGTTCCCTTCTCCTTCTACTGGGCACAATACACGCATTGATTT  880

Qy    841  TGCCTGGAATAAGTGGATTGGATTAAAAACAATTTGTAATGGTATTGTTGGTATATAAAAACATTTT  900

Db    881  TGCCTGGAATAAGTGGATTAGATAAAAACAATTTGTAATGGTATTGTTGGTATACACCTTCCAACTTTTAT  940

Qy    901  GATAGCTGTGTTTTCCTTCCAACAATGTTGTGTCCTGATATATTTGTAATGGTATATACTAATACTAATTCCATG  960

Db    901  GATAGCTGTGTTTCCTTCCAATTGTTGTGTCCTGATATATTGTAATGGTATATACTAATACTAATTCCATG  960

Qy    961  CTTGAGGAAGAGAGATACTGAAGATTAGAAGAAGAGTCACCAGAAAAATTAACA  1020

Db    961  CTTGAGGAAGAGAGATACTGAAGATTAGAAGAAGAGTCACCAGAAAAATTAACA  1020

Qy   1001  CTTGAGGAAGAGAGTAGACACTGGTAGGGAGAGTCACCATACTATTTCCGCCATG  1060

Db   1021  AACTGAGATATCTTCCCAGTTGTAG  1045

Qy   1061  AACTGAGATATGTCTTCCCAGTTGTAG  1085
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Sequence numbering lines (left margin):
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Qy  361  GGTCATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTCTTCGGCATTGGTTTACCTGCC  420
Qy  461  AGGTGTGATAGCAGCAGCAATTGTCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACA  520
Qy  421  AGGTGTGATAGCAGCAGCAATTGTCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACA  480
Qy  521  TTGGTTGGATTAACTGGTAACTGGATGTTAACAAGAAAACAGTTTGGGCTTCTCAGTTTCTTTTTGC  580
Qy  481  TTGGTTGGATTAAGTGGATGTTAACAAGAAAAGCAGTTTGGGGCTTCTCAGTTTCTTTTTTGC  540
Qy  581  TCTACTGCAGGTCAAATTTATAGTCTGTGTCTTACCCAATGAGGCCGATCCCTACAGATACAAGTT  640
Qy  541  TCTACTGCAGGTCAAATTTATAGTCTTACCCAATGAGGCCGATCCCTACAGATACAAGTT  600
Qy  601  GCTAAACTGGGCATATCAACAGGTCCAACAAAAATAAAGAAGAATGCCTGGATTGAGCATGA  660
Qy  601  GCTAAACTGGGCATATCAACAGGTCCAACAAAATAAAGANNNNTGCCTGGATTGAGCATGA  660
Qy  701  TGTTTGGATGGAGGATTTATGTTGTGTCTCTGGGAATTGTGGGAATACTGGCTCT  760
Qy  661  CGTTTGGAATGGAGATTTATGTTGTGTCTCTGGGAATTGTGGGAATACTGGCTCT  720
Qy  721  GTTGGGCTGTGANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  780
Qy  761  GTTGGGCTGTGACATCTATTCCATTCTGTGAGTGAGTCTTTGACATGGGAGGAATTTCACTA  820
Qy  821  TATTCAGAGCAAGCTAGGAATTGTTCCCTTCTCCTTCTACTGGGCACAATACACGCATTGATTT  880
Qy  881  TGCCTGGAATAAGTGGATTGGATTAAAAACAATTTGTAATGGTATTGTTGGTATATAAAAACATTTT  940
Qy  841  TGCCTGGAATAAGTGGATTAGATAAAAACAATTTGTAATGGTATTGTTGGTATACACCTTCCAACTTTTAT  900
Qy  941  GATAGCTGTGTTTTCCTTCCAACAATGTTGTGTCCTGATATATTTCGTAATGGTATATACTAATACTAATTCCATG  1000
Qy  901  GATAGCTGTGTTTCCTTCCAATTGTTGTGTCCTGATATATTGTAATGGTATATACTAATACTAATTCCATG  960
Qy 1001  CTTGAGGAAGAGAGTAGACACTGGTAGGGAGAGTCACCATACTATTTCCGCCATG  1060
Qy 1061  AACTGAGATATGTCTTCCCAGTTGTAG  1085
Qy 1021  AACTGAGATATCTTCCCAGTTGTAG  1045
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Qy    721 ATGTGTCTCTCGGGAATTGTGGGAATTACTGGCTCTTGTGTCTGTGACATCTATTC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    737 ATGTGTCTCTCGGGAATTGTGGGAATTGGCAATTACTGGCTCTTGTGTCTGTGACATCTATTC 796

Qy    781 CATCTGTGAGTGAGTCTTTGACATGGAGAGGAATTCACATATATTCAGAGAGCAAGCTAGGAA 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    797 CATCTGTGAGTGAGTCTTTGACATGGAGAGGAATTCACTATATTCAGAGCAAGCTAGGA 856

Qy    841 TTGTTTCCC 849
          ||| |||
Db    857 ATTGTTTCC 865
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RESULT 4
AK010437
LOCUS   AK010437   1211 bp   mRNA   linear   HTC 03-APR-2004
DEFINITION   Mus musculus ES cells cDNA, RIKEN full-length enriched library,
             clone:2410007B19 product:six transmembrane epithelial antigen of
             the prostate, full insert sequence.
ACCESSION   AK010437
VERSION   AK010437.1 GI:12845880
KEYWORDS   HTC; CAP trapper.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
             Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
AUTHORS   Carninci,P. and Hayashizaki,Y.
TITLE   High-efficiency full-length cDNA cloning
JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
PUBMED   10349636
REFERENCE   2
AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
             Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE   Normalization and subtraction of cap-trapper-selected cDNAs to
             prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
PUBMED   11042159
REFERENCE   3
AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
             Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
             Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
             Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
             Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
             Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
             Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE   RIKEN integrated sequence analysis (RISA) system--384-format
             sequencing pipeline with 384 multicapillary sequencer
JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
PUBMED   11076861
REFERENCE   4
AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
             FANTOM Consortium.
TITLE   Functional annotation of a full-length mouse cDNA collection
JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
             Group Phase I & II Team.
TITLE   Analysis of the mouse transcriptome based on functional annotation
             of 60,770 full-length cDNAs
JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6 (bases 1 to 1211)
AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
             Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
             Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,
             Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,
             Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,
             Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,Y., Nishi,K.,
             Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,
             Saito,H., Saito,R., Sakai,K., Sano,H., Sasaki,D.,
             Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,
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Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,
Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,
Yoshino,M., Muramatsu,M. and Hayashizaki,Y.

TITLE        Direct Submission
JOURNAL      Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
             Physical and Chemical Research (RIKEN), Laboratory for Genome
             Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
             RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
             Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
             URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
             Fax:81-45-503-9216)
COMMENT      Please visit our web site (http://genome.gsc.riken.jp/) for further
             details.
             cDNA library was prepared and sequenced in Mouse Genome
             Encyclopedia Project of Genome Exploration Research Group in Riken
             Genomic Sciences Center and Genome Science Laboratory in RIKEN.
             Division of Experimental Animal Research in Riken contributed to
             prepare mouse tissues. First strand cDNA was primed with a primer
             [5' GAGGAGAGAAGAGATCCAAGAGAGTCTCTTTTTTTTTTTTTTTTTTVN 3'], CDNA was
             prepared by using trehalose thermo-activated reverse transcriptase.
             Second strand cDNA was prepared with the primer adapter of sequence [5'
             and subsequently enriched for full-length by cap-trapper. Second
             GAGAGAGAGATTCGAGTTAATTAAATTAAATCCCCCCCCCCCC 3'], cDNA was cleaved
             with XhoI and SstI. Cloning sites; 5' end: XhoI; 3' end: SstI.
             Host: SOLR.
FEATURES             Location/Qualifiers
     source          1..1211
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="FANTOM_DB:2410007B19"
                     /db_xref="taxon:10090"
                     /clone="2410007B19"
                     /cell_type="ES cells"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
     CDS             98..1117
                     /note="unnamed protein product; putative
                     six transmembrane epithelial antigen of the prostate
                     (MGD|MGI:1917608, GB|AK010437, evidence: BLASTN, 100%,
                     match=1211)"
                     /codon_start=1
                     /protein_id="BAB26938.1"
                     /db_xref="GI:12845881"
                     /translation="MEISDDVTNPEQLWKMKPKGNLEDDSYSTKDSGETSMLKRPGLS
                     HLQHAVHVDAFFCGPSELQHTQFPFNNWRLPVKVAAIISSLTFLYTLREIIYLPVTSR
                     EQYFYKPILVINKVLPNAVAITILLAVLVLPGELAAVVQLRNGTNKYKKKPPWLDRWMLA
                     KKQFGLLSFFFAVLHAVYSLSYPMRRSYRYKLLNWAYKQVQQNKEDANVEHDVWRMEI
                     YVSLGIVGLALALLAVTSIPSVSDSLTWREFHYIQSKLGIVSLLLGTVHALVFAWNK
                     WVDVSQFWYWPPTFMIAVFLPTLVLICKHIAIGLPLCRKKILKIRCGWEDVSKINRTE
                     MASRL"
     polyA_signal    1186..1191
                     /note="putative"
     polyA_site      1211
                     /note="putative"
ORIGIN
Query Match         67.4%;  Score 806;  DB 4;  Length 1211;
Best Local Similarity   81.0%;
Matches 952;  Conservative    0;  Mismatches 220;  Indels    4;  Gaps    1;

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Qy      3 GAGACTCACGGTCAAGCTAAGGCGAAGAGAGTGGGTGGCGTGAAGCCATACTATTTTATAGAA  62
          ||| ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     35 GCGCCTTCGCCGTCCGGTCCCACGGAGAGAGGCCGGTGGCGTGGCTGAAGCCGTACTATTTTATAGCA  94

Qy     63 TTAATGGAAAGCAGAAAAAGCACATCACAACCAAGAAGACTTTGGAAAAATGAAGCCTAGG 122
          ||| |||||||| ||||||||||| ||| ||||||||||||||||||||||||||||||||
Db     95 GTCATGGAGATCAGTGACGATGTTACAAACCCAGAACAACTTTGGAAAAATGAAGCCAAAG 154

Qy    123 AGAAATTTAGAAGAAGACCAGCATTATTTTGCATAAGACACGGGAGAGACCAGCATCCTAAAA 182
          ||||| ||||||||| |||||||||||| ||||| |||||||||||||||||||||||||
Db    155 GGAAACCTGAAGAAGACACGTTACTCGACTAAGGACTCCGGAGAGACGAGCATCGTGAAA 214

Qy    183 AGACCTGTGCTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCA 242
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RESULT 5
LOCUS       AY403220                1050 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  Mus musculus STEAP gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY403220
VERSION     AY403220.1  GI:39759203
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1050)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 1050)
  AUTHORS   Todd,M.A., Clark,A.G., Glanowski,S., Nielson,R., Thomas,P.,
            Kejariwal,A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1..1050
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
     gene            <1..>1050
                     /gene="STEAP"
                     /locus_tag="HCM1484"
ORIGIN

Query Match  64.0%;  Score 765.2;  DB 10;  Length 1050;
Best Local Similarity  83.0%;
Matches  872;  Conservative   0;  Mismatches 178;  Indels   0;  Gaps   0;

Qy     36 TGGCTGAAGCCATACTACTTATTTTTATAGAATTAATGGAAAGCAGAAAAGACATCACAAACCAA 95
          |||||||||      |||| |||||||||||     | ||||| | |  ||| || ||||||| |
Db      1 TGGCTGAAGCGGTACTATTTTTATAGACAGTCATGGAGATCAGTGACGATGTTACAAACCCA 60

Qy     96 GAAGAACTTTGGAAAATGAAAGCCTAGGAGAGAAATTTAGAGAGAAGAGCGATTATTTGCATAAG 155
          || ||||||||||||||||| |||    |  |||| || ||||||||| ||| | | |||||| |
Db     61 GAACAACTTTGGAAAATGAAGCCAAAGGGAAACCTGGAAGATGACAGTTACTCGACTAAG 120

Qy    156 GACACAGGAGGAGAACGACCAGCCATGCTAAAAAGACCCTGCTTTTGCATTTGCACCAAAACAGCC 215
          ||| | |  |||||  ||| |||||||||| |||||||||          ||||||| | | |||
Db    121 GACTCGGGGGAGAGGACGAGCCATGCTGAAAAGACCGGGGGGCTCTCGCACTTGCACCGGGTC 180

Qy    216 CATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACAGGAGAGAACTCTTTCCACAG 275
          || | || ||| ||||||||||| || || ||||||||| ||| | ||| |||||| | ||
Db    181 CACGTCGGATGCTTTGACTGCCCCTCCGAGCTTCAGCACGCACACGCGGAATTCTTTCAAAC 240

Qy    276 TGGCACTTGCCAATTAAAATAGCCTGCTATTATAGACTCTGACTTTCTTTACTCTTT 335
          ||||  |||||| | ||| |  || ||||| ||| | ||||||||||  | ||| ||
Db    241 TGGCCGCTTGCCAGTGAAAGTGCCGCCATCATAATCCCTGACTTTCCTGTACACACTT 300

Qy    336 CTGAGGGAGTAATTCACCCTTTAGCAACTTCCCATCAACAATATTTTTATAAAATTCCA 395
          |||||||| | |||||| | |||| |||||||| ||||||||||||||||||||||||
Db    301 CTGAGGGAAATCACTACCCGTTAGTAACTTCCCGTGAACAATATTTTTATAAAATTCCA 360

Qy    396 ATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTCTTGGCATTGTTTAC 455
          |||||  | || |||||||||||||||||||| | ||| || |||||||||  | ||||
Db    361 ATCCTCGGTTATTAACAAAGTCTTGCCAATGGTCGCCATTACCCTCTTGGCACTGGTTAC 420

Qy    456 CTGCCAGGTGTGATAGCACAACAATTGCCAAACTTCATAATGGTTGGAACCAAGTATAAGAAGTT 515
          |||||||| | | ||||  || ||||| || | ||||  ||||  || |||||| || |||||| |
Db    421 TTGCCAGGAGGAGTTAGCGGCAGTTGTACAGCTTGCAATGGAACCAAGTTACAAGAAGTTC 480

Qy    215 AGACCGCGGGCGTCTGCGAACTTCGCACGCACGGTCCAGCGTCGANGCCCTTGACTGCCCCTCC 274
          | ||||  ||| |||| ||||||| |||||||  |||||||  |  ||| |||||||||| |
Db    243 GAACTTCAGCACACAGGAGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCT 302

Qy    275 GAGCTTCAGCACGCACAGGCGGAATTCTTTCAAACTGGCCGCTTGCCAGTGAAAGTGCCGCC 334
          |||||||||||||||||| |||||||||||||| ||||| ||||||||| ||| |||||||
Db    303 ATTATAGACTCTGACTTTCTTTACTCTTTCTGAGGGAGTAATTCACCCTTTAGCA 362

Qy    335 ATCATAATCCCTGACTTTCCTGTACACACTTCTGAGGGAAATCACTACCCGTTAGTA 394
          || |||| ||||||||||| | || ||| ||||||||| |  || || | |||| |
Db    363 ACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCA 422

Qy    395 ACTTCCCGTGAACAATATTTTTATAAAATTCCAATCCTCGGTTATTAACAAAGTCTTGCCA 454
          |||||||  |||||||||||||||||||||||||||| ||| || ||||||||||||||||
Db    423 ATGGTTTCCATCACTCTCTTGGCATTGTTTACCTGCCAGGTGTGATAGCAGCAACAATTGTC 482

Qy    455 ATGGTCGCCATTACCCTCTTGGCACTGGTTACTTGCCAGGAGGAGTTAGCGGCAGTTGTA 514
          ||||| | ||| || ||||||||| || |||| |||||||  || ||||  || |||| |
Db    483 CAACTTGCAATGGAACCAAGTATAAGAAGTTCCACATTCGGTTGGATGAAGTTGGATGGTTA 542

Qy    515 CAGCTTGCAATGGAACCAAGTTACAAGAAGTTCCCACCTCGGTTAGATAAGNTGGATGGCTG 574
          ||| |||||||||||||||||||| |||||||| | ||| ||||||| || | ||||| |
Db    543 ACAAGAAAGCAGTTTGGGCCTTCTCAGTTTCTTTTTTTTGTACTGCCATGCAAATTTATAGT 602

Qy    575 GCCAAGAAGCAGTTGGTGTCCTCCAGCTTCTTTTTGCTGGTCTGCAGCGCTGTTTACAGT 634
          |||| | | ||||| | ||||| ||| ||||||||| || | ||| ||| ||||| ||||
Db    603 CTGTCTTACCCAATGAGGGCGATCCTACAGATACAAGTTGCTAAAACTGGGCGCATATCAAACAG 662

Qy    635 CTCTCAATACCCAATGGAGGAGGAATTCAACTATATTGCTAACTGGGCTTAAAACAG 694
          || || || ||||||| |||  | ||||| ||| |||||| |  |||| | ||||||
Db    663 GTCCAACAAAATAAAGAGGAAGATGCCTGGATTGAGCAGTGTTGAGGAATTTAT 722

Qy    695 GTTCAACAAAAACAAAAGAGGAGGAATGCCTGGGTAGAGCAAGATGGAGAGAGATTTAT 754
          || ||||||||  ||| ||||| | | |||||| | |||| ||| ||||| | |||||
Db    723 GTGTTCTTCTGGGAATTGTGGGAGGCTGGCCAATACTGGCTCTGTTGGCTGTGTGTGACATCTATTCCA 782

Qy    755 GTGTCCTCTGGGGATTGTGGGGCTGCCATCTTGGCTCTCTGCTGTGTGACAGTTCCA 814
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Db    783 TCTGTGAGTGACTCTTTGACATGGCATGAGCAAGCTAGGAATT 842

Qy    815 TCTGTGAGGGGACTCTTTAACCTGGAGAATTCACTATATTCAGTGACAAGCTAGGAATT 874
          |||||||| | |||||| |||||||||| ||| |||| ||||| || |||||||||||
Db    815 TCTGTGAGTGACTCTTTGACATGGCATGAGCAAGCTAGGAATT 842

Qy    843 GTTTCCCTTCTTACTGGGCACACGCTACGCACGCATTGATTTTGGTTGGAATAAGTGATGATGAT 902
          || ||||| ||  | || |||| || | || | || |||||| ||  |||||| | |||||| |
Db    875 GTCCTCTCTTCTTGGTTTTTTGCCTGAATAAATAAAAGTGGGTAGAT 934

Qy    903 ATAAAACAATTGTATAGGTATACACCTCCAACTTTATGATAGTGTGTTTTCCTTCCTTCCAATT 962
          || ||||| ||||  |||  | ||||||||||||| | || |  | ||||||||||||| ||||
Db    935 GTCAGTCAATTTGTATAGGTTGCATGCCTCGGACTTTTATGTAGAGCTGGTTTTCCTTCCAACT 994

Qy    963 GTTGTCCTGATATTTAAAAGCACTACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAG 1022
          || |||| |||| || ||  ||| || |||| ||| || |||||||||||||| |||||||
Db    995 CTTGTCCTGATAGTGTAAAAATCGCCCCTGTCCGCCATGCTTGAGGAAGAAGATACTTGAAG 1054

Qy   1023 ATTAGACAATGGTTGGGACGTCACCAAAATTAACACAAACTGAGATATGCTTCCCAGTTG 1082
          ||||| ||| ||| ||||| |||||||||||| |||| ||||| |  || | ||||| ||
Db   1055 ATTAGATGTGGTTGGGAAGAGTGCAAAAATTAACAGGACTGAGATGGCCTTCCAGGGTTG 1114

Qy   1083 TAGAAATTACTGTTTTACACACATTTTGTTCAAATATGATATATTTATACCACACATTC 1142
          ||||| ||| || ||| ||||| ||||| | || | |  |   || ||||||||| |||
Db   1115 TAGAACTACTGTTTTGCACAATATTTGCTTGTTTAT---TGATGTCCTATCATAAGCATTTC 1170

Qy   1143 AAGTTTGTATTTGTTTAATAAAAATGATTAATTCAAGGA 1178
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Db   1171 AAATTTGTGTTGTTGTTAATAAAAATGAATAATACTTTGGGA 1206
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FEATURES             Location/Qualifiers
     source          1..720
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-EDI-axr-o-23-0-UI"
                     /tissue_type="Chondrosarcoma"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_ED1"
                     /note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
                     (Pharmacia) with a modified polylinker; Site 1: EcoR I;
                     Site 2: Not I; NCI_CGAP_ED1 is a normalized cDNA library
                     containing the following tissue(s): Chondrosarcoma cell
                     line CS5. The library was constructed according to
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. First strand cDNA synthesis was primed with an
                     oligo-dT primer containing a Not I site. Double stranded
                     cDNA was ligated to an EcoR I adaptor, digested with Not
                     I, and cloned directionally into pT7T3-Pac vector. The
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tag for this library is GCTCAAGCCT.
                     TAG_TISSUE=chondrosarcoma
                     TAG_LIB=UI-H-ED1
                     TAG_SEQ=CGTCAAGCCT"
ORIGIN
```

```
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jose Mercuende
            cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
            Seq primer: M13 FORWARD
            POLYA=Yes.
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RESULT 6
CA446381/c
LOCUS       CA446381                 720 bp    mRNA    linear   EST 08-NOV-2002
DEFINITION  UI-H-EDI-axr-o-23-0-UI.s1 NCI_CGAP_ED1 Homo sapiens cDNA clone
            UI-H-EDI-axr-o-23-0-UI 3', mRNA sequence.
ACCESSION   CA446381
VERSION     CA446381.1  GI:24810801
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 720)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
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Query Match          60.1%;   Score 718.4;   DB 6;   Length 720;
Best Local Similarity 99.9%;              Pred. No. 8e-156;
Matches 719;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;
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Qy    516 CCACATTGGTTGGATAAGTGGATGGTAGTTAACAAGAGAAAGCAGTTTGGGCTTCTCAGTTTCTT 575
          |||| |  ||||| ||| | |   ||   | |   ||  ||||||||| |  |   ||||||| ||
Db    481 CCACCCTGGTTAGATAGANTGGCNGGCCAGGAAGCAGTTTGGTCTTCCTACAGTTCTTT 540

Qy    576 TTTGCTCTACTGCATGCAANTTTATAGNTCTGTTCTTACCCANTGAGGCGATCCTACAGATAC 635
          ||||||||  |  | |      | |    |||||||||||| |||||| | ||| ||||||||
Db    541 TTTGCTCTGCACGCTGTTTACAGTCTCTCATACCCAATGAGGAGTCGACAGATAC 600

Qy    636 AAGTTGCTAAACTGGGCCATATCACAGGTCCACAAANAATATAAAGAAAGAATGGATCCAACAGATAC 695
Db    601 AAGCTACTCAACTGGGCTTACAACAGGTTCAACAAAAACAAGGAGGATGCCCTGGGTAGAG 660

Qy    696 CATGAGATGTTTGGAGAAGATTATGTCTCTCGGGAATTGTTGGGCAATTGGCAATACTG 755
Db    661 CATGAGATGTTTGGAGAAGATTATGTTGGGAATTGCTGGGCAATTGGCCATCTTG 720

Qy    756 GCTCGTGTTGGGCTGTGACATCTATTCCATCTGTGTGAGTGACTCTTTGACATGGAGGAATTT 815
Db    721 GCTTCTTGGCCTGTGACATCTATTCCATCTGTAGAGCGACTCTTTACCTGGGCATCCTTG 780

Qy    816 CACTATATTCAGAGCAACAGCTAGGAATTTGTTTCCCTTTCTACTGGGCACAATACACGGCATTG 875
Db    781 CACTATATTCAGAGCAACAGCTAGGAATTTGTCTCTCTTTCTTCTCTCGGGCACAGTACACGCTTG 840

Qy    876 ATTTTTGCCTGGAATAAGTGGATTAGATAATAAAACAAATTTGTTATGGTATACACCTTCCAACT 935
Db    841 GTTTTTTGCCTGAAATAAATGGGTTAGAGTCTCAGTGCATCAATTTGTATACGTTACATGCTCCGACT 900

Qy    936 TTTATGATAGCTGTTTTCCTTCCCAATTGTTGTCTGATGATATTTAAAAGCAATACTTATTCCTG 995
Db    901 TTTATGAATAGCTGTTTCCTTCGTCCCTGATGATATGTAAAAATCGCCCTGTGCCTG 960

Qy    996 CCATGCTTGAGGAAGGAAGAGAGGATACTGAGAAGAAGTACATTGCAAAAATT 1055
Db    961 CCCTGTCTGAGGAAGGAAGAGATACTCAGAAGAAGATTAGAGATGGTGTTGGGGAAGAGTCAGCAAAAATT 1020

Qy   1056 AACAAAACTGAGAATATGTTCCCAGTTGTGTAG 1085
          |||||||||||||||||||| ||||||||||||
Db   1021 AACAGGACTGAGATGGCCTTCCCAGTTGTTAG 1050
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Qy    476 AATTGTCCAACTTCATATAATGGAACCAAGTATAATAAGAAGTTTCCACATTGGTTGGATAAGTG 535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    540 AATTGTCCAACTTCATATAATGGAACCAAGTATAATAAGAAGTTTCCACATTGGTTGGATAAGTG 481

Qy    536 GATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTCTTTTTTGCTGTACTGCATGCCAAT 595
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    480 GATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTCTTTTTTGCTGTACTGCATGCAAT 421

Qy    596 TTATAGTCTGTTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCCATA 655
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    420 TATTCCATCTGTGAGTGACTTTGACATGGAGGAGAAGAATTTCACTATATTCAGAGCAAGCT 361

Qy    656 TCAACAGGTCCACAAAAATAAAGAAGAGATGCCTGGAGTTGAGCGATGAGTGTTGGGAGAATGGA 715
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    360 AGGAATTGTTTCCCTTCTACTGGGCCAATGACAATACACGCCATTGATTTTTGCCTGGAATAAGTG 301

Qy    716 GATTTTATGTGTCTCTGGGAATTGTGGGGCCACAATACTGGCACATTGGTTGGATCATC 775
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    300 GATTAGATAATAAAACAAATTTGTTATGGTATACACCTTCCGACTTTTATGATAGCTGTTTT 241

Qy    776 TATTCCATCTGTGAGTGACTCTTTGACATGGAGGAGAAGAATTTCACTATATTCAGAGCAAGCT 835
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    240 TCCAATTGTGTCCTGATGATATGTAAAAATCGCCCTGTGCCTGCCCTGTCTGAGGAAGGAAGAGAT 181

Qy    836 AGGAATTGTTTCCCTTCTACTGGGCCAATGACAATACACGCCATTGATTTTTGCCTGGAATAAGTG 895
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    180 ACTGAAGAGATTAGACATGGTTGGGGAAGAGTCAGCAAAAATTAACAAAACTGAGAATATGTTC 121

Qy    896 GATTAGATAATAAAACAAATTTGTTATGGTATACACCTTCCGACTTTTATGATAGCTGTTTT 955
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    120 CCAGTTGTAGAATTACATGGTTGGGGAAGAGACGTCACCAAAAATTAACAAAACTGAGATATGTTC 61

Qy    956 TCCAATTGTTGTCTGATGATATTTAAAAGCACATTTTGTTGTTCAATATGATTATTTATCACCA 1015
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    240 TCCAATTGTTGTCCTGATGATATTTAAAAGCATCATTTTGTTGTTCAATATTGATATATTTATCACCA 181

Qy   1016 ACTGAAGAATTAGACATGGTTGGGGAAGAGCGTCACCAAAAATTAACACTGAGATATGTTC 1075
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1075 ACTGAAGAGATTAGACATGGTTGGGGAAGAGACGTCACCAAAAATTAACAAAACTGAGATATGTTC 1075

Qy   1076 CCAGTTGTAGAATTACACACATTTTGTTACACATTTTGTTCAATATTGATATATTTATCACCA 1135
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    120 CCAGTTGTAGAATTACTGTTTACACACATTTTGTTCAATATTGATATATTTATCACCA 61
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Qy   1136 ACATTTCAAGTTTGTTATTGTTAATAAATGATTATTCAAGGATAAAATCAAGGAAAAAAAAAAAA 1195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     60 ACATTTCAAGTTTGTTATTGTTAATAAATGATTATTCAAGGATAAAATCAAGGAAAAAAAAAAAA 1.
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RESULT 7

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LOCUS       BG565247                  881 bp    mRNA    linear   EST 10-APR-2001
DEFINITION  602582917F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4710436 5',
            mRNA sequence.
ACCESSION   BG565247
VERSION     BG565247.1  GI:13572900
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 881)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONETECH Laboratories, Inc.
            cDNA Library Preparation: CLONETECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1549 row: b  column: 05
            High quality sequence stop: 704.
FEATURES             Location/Qualifiers
     source          1..881
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4710436"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_76"
                     /note="Organ: liver; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence: 5'-CACGGCCATTATGGCC-3', and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C, G, or T). Average insert size 1.85
                     kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN
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Query Match   58.0%; Score 692.8; DB 2; Length 881;
Best Local Similarity 92.0%; Pred. No. 7.2e-150;
Matches 786; Conservative 0; Mismatches 62; Indels 6; Gaps 5;

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Qy    251 GCAGCACAGGAACTCTTTCCACAGTGGCCGCA 281
          |||||||||||||||||||||||||||||||
Db      1 GCACACAGGAACTCTTTCCACAGTGGCCGCA 60

Qy    311 ATCTCTGACTTTTCTTTACACTCTTCTCTGAGGGAAGGAAGTAATTCACCCTTTAGCAACTTCCCA 370
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ATCTCTGACTTTTCTTTACACTCTTCTCTGAGGGAAGGAAGTAATTCACCCTTTAGCAACTTCCCA 120

Qy    371 TCAACAATATTTTTATAAAAATTCCAATCCTGGTCGTCATCAACAAAGTCTTCGCCAATGGTTTC 430
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TCAACAATATTTTTATAAAAATTCCAATCCTGGTCGTCATCAACAAAGTCTTCGCCAATGGTTTC 180

Qy    431 CATCACTCTCTTGGCATTGGTTTACCTGCCCAGGTGTGATAGCAGCAGCAAATTGTCAAACTTCA 490
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CATCACTCTCTTGGCATTGGTTTACCTGCCCAGGTGTGATAGCAGCAGCAAATTGTCAAACTTCA 240
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Qy    491 TAATGGAACCAAGTATATAAGAAGAGTTTCCACACAATTGGGTTGGGATAAGTGGATAGTTAACAGAAA 550
          ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db    241 TAATGGAACCAAGTATAAGAAGAGTTTCCACAGTGGTTGGGATAAGTGGATAGTTAACAGAAA 300

Qy    551 GCAGTTTGGGCTTCTCAGTTTCTTTTTTTGCTGGTACTGGCATGCCAATTATAGTCTGTCTTA 610
          |||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db    301 GCAGTTTGGGCTTCTCAGTTTCTTTTTTTGCTGGTACTGGCATGCCAATTATAGTCTGTCTTA 360

Qy    611 CCCAATGAGGCCGATCCTTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTCCAACA 670
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CCCAATGAGGCCGATCCTTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTCCAACA 420

Qy    671 AAATAAAGAAGACGATGCCTGGATTGAGCATGAGTGTTGGAGAATGGGAGGATTTATGTGTCTCT 730
          |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db    421 AAATAAAGAAGATGCCCTGGATTGAGCATGAGTGTTGGAGAATGGGAGGATTTATGTGTCTCT 480

Qy    731 GGGGAATTGTCGGGATTGGCAATACTCGGCGTCTCGTGTTGGCTGTGACAACATCTATTCCATCTGTGAG 790
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GGGGAATTGTCGGGATTGGG-AATACTCGGCGTCTCGTGTTGGCTGTGACAACATCTATTCCATCTGTGAG 539

Qy    791 TGACTCTTTGACATGGGAGAATTTCACTATATATTCAGAGAGCAAGCTAGGAATTGTTTCCCT 850
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    540 TGACTCTTTGACATGGGAGAATTTCACTATATATTCAGAGAGCAAGCTAGGAATTGTTTCCCT 599
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RESULT 8

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LOCUS       BG762026                  961 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602719984F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4858820 5',
            mRNA sequence.
ACCESSION   BG762026
VERSION     BG762026.1  GI:14072679
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 961)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1713 row: h  column: 21
            High quality sequence stop: 750.
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Qy    851 TCTACTGGGGCACATACACCCATTCGATTTTGTGCCCGGAATAAGTGG--ATAGATTATAAAA 908
          |||||||||||||||||||||||||||||||||||||||||||||||    |||||||||||
Db    600 TCTACTGGGGCACAATACACCGCATTCGATTTTGGCCTCCGGAATAAGTGGGATAGATCATAAAC 659

Qy    909 CAATTTGTATGGTATACACCTCCAACTTTTTATGATAGCTGCGTTTCCTTCCAATTGTTGTGTC 968
          ||| ||||||||||||||||||||||||||||||||||||||||| |||| |||||||||||
Db    660 ACAATTGTATGGTATACACCTCCAACTTTTTATGATAGCGTGTTTCCTTCCAATTGTTGTGTCC 719

Qy    969 CTGATATTT-AAAAGCATACTATT-CCTGCCATGCTTGAGGAAGAAGAAGATAGT-GAAGATT 1025
          |||||||   ||||||||||||||  |||||||||||||||||||||||||||||  || ||||
Db    720 CTGATATTTCAAAACGCATACTATTACTTGCCATGCTTGAGCAGAAGAAGATACTGGGACGATT 779

Qy   1026 AGACATGGTTGGGGAAGACGTCACCAAAAATTAACAAAAACTGAGAATAGTTTCCAGTTGTTAG 1085
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    780 AGACTTGGTTGGGGAAGAACGTCACCAAAAATCAAAAAACTGAGAATTTGTCCAGTGGAATAA 839

Qy   1086 AATTACTGTTTACA 1099
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Db    840 ACCTGGTTACCACA 853
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FEATURES　　　　　Location/Qualifiers
　　source　　　　1..961
　　　　　　　　　/organism="Homo sapiens"
　　　　　　　　　/mol_type="mRNA"
　　　　　　　　　/db_xref="taxon:9606"
　　　　　　　　　/clone="IMAGE:4858820"
　　　　　　　　　/tissue_type="melanotic melanoma, high MDR (cell line)"
　　　　　　　　　/clone_lib="NIH_MGC_49"
　　　　　　　　　/lab_host="DH10B (phage-resistant)"
　　　　　　　　　/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
　　　　　　　　　EcoRI; cDNA made by oligo-dT priming. Directionally cloned
　　　　　　　　　into EcoRI/XhoI sites using the following 5' adaptor:
　　　　　　　　　GGCACGAG(G). Size-selected >500bp for average insert size
　　　　　　　　　1.8kb. Library constructed by Ling Hong in the laboratory
　　　　　　　　　of Gerald M. Rubin (University of California, Berkeley)
　　　　　　　　　using ZAP-cDNA synthesis kit (Stratagene) and Superscript
　　　　　　　　　II RT (Life Technologies). Note: this is a NIH_MGC
　　　　　　　　　Library. |"

ORIGIN
Query Match　　　57.2%;　　Score 683.2; DB 2;　　Length 961;
Best Local Similarity　　93.2%;　　Pred. No. 1.2e-147;
Matches 772;　Conservative　0; Mismatches　43; Indels　13; Gaps　5;

Qy　　　1 CCGAGACTTCACGGTCACCTAAGGCGAAGAGAGTGGGTGGCTGAAGCCACTACTATTTATAG 60
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　 57 CTGAGACTTCACGGTCACCTACGGCGAGGAGAGTGGGTGGCTGAAGCCACTACTATTTATAG 116

Qy　　 61 AATTAATGGAAAAGCAGAAAAGACAGAANCACACAAAACAAGAGAGAACTTTGGAAAATGAAAGCCTA 120
　　　　　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　117 AATTAATGGAAAAACCAGAAAAGACATCACAAAACCAAGAGAGAAATTTGGAAAATGAAGCCTA 176

Qy　　121 GGAGAAAATTAGAAGAAGAAGACGATATTATTTGCATTAAGGACCACGGGAGAGACCAGCATGCTAA 180
　　　　　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　177 GGAGAAAATTTAGAAGACAAACGATTATTTGCATTAAGGACACGGGAGGAGACCAGCATGCTAA 236

Qy　　181 AAAGACCTGTGCTTTTGCACCAAAACAGCCCATGCTGATGAATTGACTGCCCTT 240
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　237 AAAGACCTGTTGCTTTTGCAATTGCAGCCCATGCTGATGAATTTGACTGCCCTT 296

Qy　　241 CAGAACTTCAGCACACACAGGGACTCTTCTTTCCACAGTGGCCACTTGCCAATTAAAATAGCTG 300
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　297 CAGAACTTCAGCACGACACAGGAGACTCTTTCCACAGTGGCCACTTGCCAATTAAAATAGCTG 356

Qy　　301 CTATTAATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
　　　　　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　357 CTCGTTAATGGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 416

Qy　　361 CAACTTCCCATCAACAAATATTTTTATAAAAATTCCAATACTCCTGGTCATCAACAAAGTCTTGC 420
　　　　　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　417 CAACTTCCCATCAACAATATTTTTATAAAAATTCCAATACTCCTGGTCATCAACAAAGTCTTGC 476

Qy　　421 CAATGGTTTCCATCACTCTCTTGCATTGGTTTACCTCCAGGTGTGATTAGCAGCCAATTG 480
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　477 CAATGGTTTCCATCACTCTCTTGCATTGGTTTACCTCCAGGTGTGATTAGCAGCCAATTG 536

Qy　　481 TCCAACTTCATAATGGAACCAAGTAATATAAGAAGTTTCCACATTGGTTGGATAAGTGGGATGT 540
　　　　　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　537 TCCAAGTTCATAATGGAACCAAGTAATAAGAAGTTTCCACATTGGTTGGATAAGTGGGATGT 596

Qy　　541 TAACAAGAAAAGCAGTTTGGGCCTTCTCTCAGTTT-GGTTTGCGTGTGTACTGCCATATCAAC 597
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　597 TAACAAGAAAAGCAGTTTGGGCCTTCTCTCAGTTTT-GGTTTGCGTGTACTGCCATATCAAC 655

Qy　　601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACCAAGTTGCTAAACTGGGCATATCAAC 660
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　656 CTCTGTCTTACGCAATGAGGCGATCCTACAGATACCAAGTTGCTAAACTGGGCATATCAAC 715

Qy　　661 AGGTCCACAAAATAAAGAAGATGCGCTGGATTGAGCATGATGTTTGGAGAAT--GGAGAT 718
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Db　　716 AGGTCCACAAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTCGGAGAATGGCCCACT 775

Qy　　719 TTAGTGTGTCTCTGGGAATTGTGGGGATTGGC------------AATACTGGCTCTGTTGGC--TGT 769
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　776 TCATGTGTCCCCGGGGACTTTGTGGCGACAGGGGCAACACTGGTGCTCTGTTGGCCTGTT 835

RESULT 9
LOCUS　　　　CV983083　　　　　827 bp　　　mRNA　　　linear　　EST 30-NOV-2004
DEFINITION　UMC-bmix_0B02.007-e08 Conceptus-Corpus Luteum (mixed) bmix Bos
　　　　　　　taurus cDNA 3', mRNA sequence.
ACCESSION　　CV983083
VERSION　　　CV983083.1　　GI:56143804
KEYWORDS　　　EST.
SOURCE　　　　Bos taurus (cow)
　ORGANISM　　Bos taurus
　　　　　　　　Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
　　　　　　　　Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
　　　　　　　　Pecora; Bovidae; Bovinae; Bos.
REFERENCE　　1 (bases 1 to 827)
　AUTHORS　　Prather,R.S., Antoniou,E., Garverick,H.A., Green,J.A., Lucy,M.C.,
　　　　　　　Roberts,R.M., Smith,M.F. and Youngquist,R.S.
　TITLE　　　USDA Grant NRI-2002-03476: Bovine ESTs: Focus on Female
　　　　　　　Reproduction
　JOURNAL　　Unpublished (2002)
COMMENT　　Contact: DNA Core Facility (Bovine Project)
　　　　　　　Animal Science -- RS Prather
　　　　　　　University of Missouri-Columbia
　　　　　　　M616 Medical Sciences Bldg., Columbia, MO 65212, USA
　　　　　　　Tel: (573)882-0428
　　　　　　　Fax: (573)884-5552
　　　　　　　Email: bovine@rnet.missouri.edu
　　　　　　　POLYA=No.
FEATURES　　　　Location/Qualifiers
　　source　　　　1..827
　　　　　　　　　/organism="Bos taurus"
　　　　　　　　　/mol_type="mRNA"
　　　　　　　　　/db_xref="taxon:9913"
　　　　　　　　　/clone="Conceptus-Corpus Luteum (mixed)"
　　　　　　　　　/dev_stage="bmix"
　　　　　　　　　/note="Vector: pSportI; Funding: The production of ESTs
　　　　　　　　　submitted in this project was funded by USDA Grant
　　　　　　　　　NRI-2002-03476 entitled 'Bovine ESTs: Focus on Female
　　　　　　　　　Reproduction' to RS Prather (Primary Investigator), E
　　　　　　　　　Antoniou, HA Garverick, JA Green, MC Lucy, RM Roberts, MF
　　　　　　　　　Smith and RS Youngquist. Genetic Source: Heifers for the
　　　　　　　　　project were purchased from Circle A Ranch, Iberia, MO
　　　　　　　　　(http://www.circlearanch.com/home.html). These heifers,
　　　　　　　　　while not registered have known Angus pedigrees going back
　　　　　　　　　at least 4 generations. Samples collected: The samples
　　　　　　　　　consisted of the following: germinal vesicle-stage
　　　　　　　　　oocytes; in vitro derived embryos (2-cell, morula,
　　　　　　　　　blastocyst and nuclear transfer blastocyst); in vivo
　　　　　　　　　blastocysts and conceptuses (days 8, 14, 16 and 18);
　　　　　　　　　corpora lutea (days 3, 5, 8, 14, 16, 18 and 35); ovarian
　　　　　　　　　follicles (days 0, non-recruited, recruited, early
　　　　　　　　　selected and preovulatory); oviduct (days 0, 3 and 5);
　　　　　　　　　endometrium (days 5, 8, 14, 16, 18 and 35); and
　　　　　　　　　placenta/embryo from day 35 conceptuses. Expanded
　　　　　　　　　descriptions of how the tissues were collected can be
　　　　　　　　　found at the following URL:
　　　　　　　　　http://genome.rnet.missouri.edu/Bovine/Methods.html.
　　　　　　　　　Library construction (Standard Protocol): All procedures
　　　　　　　　　have been described in detail elsewhere (Soares et al.,
　　　　　　　　　1994; Bonaldo et al., 1996; Jiang et al., 2001). Total
　　　　　　　　　cellular RNA from each sample was isolated by using
　　　　　　　　　STAT-60 reagent (Tel-Test, Friendswood, TX) and the
　　　　　　　　　poly(A)+ RNA was obtained by two rounds of purification
　　　　　　　　　with the Oligotex mRNA isolation kit (Qiagen) according to
　　　　　　　　　the manufacturer's instructions. The libraries were
　　　　　　　　　constructed essentially as described by the manufacturer's

Db　　776 TCATGTGTCCCCGGGGACTTTGTGGCGACAGGGGCAACACTGGTGCTCTGTTGGCCTGTT 835
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　　770 GACATCTATTCCATCTGTGA-GTGACTCTTTGACATGGAGAGAATTTC 816
　　　　　|||||||||||||||||||||||||||||||||||||||||||||||
Db　　836 GACATCTATTCCATCTGTGACGTGACCTTTGACCTGGCGAGAATTCC 883

RESULT 10

BE875216
LOCUS   BE875216   710 bp   mRNA   linear   EST 20-OCT-2000
DEFINITION   601488516F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3890930 5',
             mRNA sequence.
ACCESSION   BE875216
VERSION   BE875216.1 GI:10323992
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE   1 (bases 1 to 710)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLAM9674 row: p column: 03
             High quality sequence stop: 701.

FEATURES   Location/Qualifiers
     source   1..710

ORIGIN

Query Match   56.3%; Score 672.4; DB 8; Length 827;
Best Local Similarity 89.3%; Pred. No. 3.9e-145;
Matches 735; Conservative 0; Mismatches 87; Indels 1; Gaps 1;

Qy   1 CCGAGACTCACGGTCAAGCTAAGGCCGAAGAGTGGGTGGGCTGAAGCCATACTATTTATAG 60
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Db   5 CCCGAACTTACCGTCAGGTCACGACAAGAAGCCGGGTGGGCTGAACGCCATACTATTTATAG 64

Qy   61 AATT-AATGGAAAACGAGAAAAAGACATCACAAACCAAAGAAGAACTTTGGAAAATGAAGCCT 119
            |||| |||||||||||||||| |||||||||||||| |||||||||||||| |||||||||
Db   65 AATTAAATGGAAGAGCGAGAAATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCT 124

Qy   120 AGGAGAAATTAGAAGAAGACGAGTTATTTGCATAAGGACACGGAGAGACCAGCATGCTA 179
            ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db   125 AGGAGAAAATCTAGAAGAAGATGATATATTTGAATAAAGACTCAGAGAGATCGGCATGCTG 184

Qy   180 AAAAGACCTGTGCTTTTGCACAATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCT 239
            |||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   239 ...

Db   185 AAAAGACCATGTGCTTTTGCACTTGCACCAAACAACCCCATTTTGATGAAATTTGATTGCCCC 244
Qy   240 TCAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGGCACTTGCCACTTATTTAAAATAG 299
            ||||||||||||||| |||| |||||||||||||||||||||||||||||||||| |||||||
Db   245 CCAGAGCTTCAGGAAAACAGAAACTCTTTCCAAAGTGCGGCCTTGGCGGAGAGCC 304

Qy   300 GCTATTATAGCATCCTCGACTTTTCTTACACTCTTCTGACGGGAGTAATTCACCCTTTA 359
            |||| |||||||||||||||||||||||||
Db   305 GCTATTGTATCATCTCTGACTTTTCTCTACACTTCCTGTGTGTGACGGGGAAAAATTCAACAGT 364

Qy   360 GCAACTTCCCATCACACAATATTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTG 419
            |||||||||||||||||||||||||||||||||||||||||||||
Db   365 GTGACTTCCCATCACACAGTATTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTG 424

Qy   420 CCAATGGTTTCCATCACTCTTCTTGGCATTGGTTACCTGCCAGGTGTGATAGCAGGCAATT 479
            ||||| |||||||||||| |||||||||||||||||||| ||||||||||||||||
Db   425 CCAATGGTTTCCATCACTCTTCGGCACTGGTTGATTGCCAGGGTGTGAATAGCAGCAGTT 484

Qy   480 GTCCAACTTCATAATGGAACCAAGTATATAAGAGTTTCCACATTGGTTGTTGGATAAGTGGATG 539
            |||||||||||||| ||||||||||||||||||||||||||| || ||||||||||||
Db   485 GTGCAGCTTCAATAATGGAACTAAGTATAAAGAAATTTCCGGCACTGGTTGGATAGGTGGATG 544

Qy   540 TTAACAAGAAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTTTTGCTGTTGTTGGATAGCATTTTAT 599
            |||||||||||||||||||||||||||||||||||||||| ||||| |||||||||||
Db   545 GTAACAAGAAAAGCAGTTTGGTCTTCTCACGTTTCTTTTTCCTGTTACTACATGCATCACAATTTAC 604

Qy   600 AGTCTGTCTTACCCAATGAGGCGATCCTACAGATACAGAGGTGCATGCCATGCAATTTAT 659
            |||||||||||||||||||||||||||||||||||||||||
Db   605 AGTTATTCCTATCCCGATGAGGGCGATCCTACAGATACAGAGTGCTAAACTGGGCATATCAA 664

Qy   660 CAGGTCCAACAAAAATAAAGAAGAATGCCTGGATTGAGCATCATGATTGTTGGGAGAATGGAGAGATT 719
            ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   665 CAGGTCCAACAAAAATAACCTGGATTGAACATCAGTAGATGGTTGCTGAACTGGGCAAAATT 724

Qy   720 TATGTGTCTCTGGGGAATTGTGGGATTGGGCAATACTGGCCTCTGTTGGCTGTGACATCTATT 779
            ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db   725 TATGTATCACTGGGGAATCGTTGGCACTTGCAATATACTAGCTCTATTGGGCTGTGACATCTATT 784

Qy   780 CCATCTGTGAGTGTGACTCCTTTGACATGGAGGAGAAATTTCACTATA 822
            |||||||||||||||||||||||||||||||||||||||||||||||
Db   785 CCATCTGTGAGTGATTCTCTCGACACATGGAGGAGAAATTTCACTATA 827

Db   The following is the narrative COMMENT block (library construction):

instructions provided with the SuperScript Plasmid System
(Invitrogen, cat. no. 18248-013). Briefly, 1mcg of
poly(A)+ RNA was annealed at c37 degrees with 10mcg of
NotI-tag-dT18 oligonucleotide (GCTGTCGGCGGCGC-tag-T18)
and reverse transcribed at c37 degrees with SuperScript II
(Invitrogen) reverse transcriptase (Jiang et al., 2001).
The 'tag' represents a tissue/stage-specific ten-base
sequence identifier
(http://genome.uiowa.edu/pubsoft/software.html) present in
the oligonucleotide used to prime first-strand synthesis.
Second strand synthesis was performed with T4 DNA
polymerase in the presence of DNA ligase and RNase H.
After second strand synthesis, the double-stranded cDNAs
were ligated to SalI adapters (Invitrogen-Life
Technologies) and digested with NotI. The cDNAs were size
selected by passage through cDNA size fractionation
columns (Invitrogen-Life technologies). The cDNAs derived
from each developmental stage of a particular tissue were
mixed on an equimolar basis and ligated directionally into
the NotI and SalI sites of the pCMV-SPORT6 vector
(Invitrogen). After ligation of the inserts, the plasmids
were electroporated into DH10B bacteria. Preliminary
library Characterization: Randomly chosen clones from each
library were analyzed by restriction digestion to
determine average insert size (96 clones) and by
sequencing (~4 96-well plates) to confirm library quality
(e.g. the presence of short polyA+ tails, genomic DNA
contamination (must be <1%), ribosomal RNA clones (must be
<1%, etc.) and to provide a sequence database
representing the predominant clones in each library. The
clones were sequenced at the University of
Missouri-Columbia DNA Core Facility. After production of
the libraries, equal numbers of recombinants from each
library were pooled to produce a single mixed library
(mega-library) for more extensive sequencing.
Bioinformatics work was performed by GK Springer's
bioinformatics group in Computer Science at the University
of Missouri-Columbia. Clone Requests: Requests for clones
should be made to the Director of the University of
Missouri DNA Core facility at: bovine@rnet.missouri.edu.
Citations: Bonaldo MF, Lennon G, Soares MB. Normalization
and Subtraction: Two approaches to facilitate gene
discovery. Genome Res, 1996; 6:791-806. Jiang H, Bivens
NJ, Ries JE, Whitworth KM, Green JA, Forrester LJ,
Springer GK, Didion BA, Mathialagan N, Prather RS, Lucy MC
(2001) Constructing cDNA libraries with fewer clones that
contain long poly(dA) tails. Biotechniques 31:38-42.
Soares MB, MF Bonaldo, P Jelene, L Su, L Lawton, A
Estrantialis. 1994. Construction and characterization of
a normalized cDNA library. Proc Natl Acad Sci,
91.9228-9232.
TAG_TISUB=Conceptus-Corpus Luteum (mixed)
TAG_SEQ=Not found"

RESULT 11

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LOCUS       DN997716                 697 bp    mRNA    linear   EST 17-MAY-2005
DEFINITION  TC115356 Human breast cancer tissue, large insert, pCMV expression
            library Homo sapiens cDNA clone TC115356 5' similar to Homo sapiens
            six transmembrane epithelial antigen of the prostate 1 (STEAP1),
            mRNA sequence.
ACCESSION   DN997716
VERSION     DN997716.1  GI:66257543
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 697)
  AUTHORS   Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L.,
            Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M.,
            Zhang,X., Jay,G. and He,W.
  TITLE     High-throughput cloning of full-length human cDNAs directly from
            cDNA libraries optimized for large and rare transcripts
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Kovacs, KF
            High Throughput cDNA Cloning
            OriGene Technologies, Inc. ( www.origene.com )
            6 Taft Court, Suite 100, Rockville, MD 20850, USA
            Tel: 301 340 3188
            Fax: 301 340 8606
            Email: cDNA@origene.com
            This EST submission is part of an on-going human full-length
            cloning project at OriGene Technologies, Inc.
            Please contact OriGene for access.
            OriGene Technologies, Inc.
            6 Taft Ct. Suite 100
            Rockville, MD 20850
            Tel: (301) 340-3188
            http://www.origene.com
            Seq primer: pCMV6 5prime forward vector primer, OriGene
            Technologies Inc.
FEATURES             Location/Qualifiers
     source          1..697
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="TC115356"
                     /tissue_type="Breast cancer"
                     /clone_lib="Human breast cancer tissue, large insert, pCMV
                     expression library"
                     /note="Organ: Mammary gland (cancer tissue); Vector:
                     pCMV6-XL5; Site_1: EcoRI; Site_2: XhoI/SalI compatible end
                     ligatio; Oligo-dT primed reverse transcription optimized
                     for large and GC rich mRNA transcripts, cDNA size
                     selection, optimized ligation for large inserts into
                     mammalian expression vector, random clones selected for
                     end sequence verification of full-length genes"
ORIGIN
```

Query Match 55.5%; Score 663; DB 8; Length 697;
Best Local Similarity 100.0%; Pred. No. 5.8e-143;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     1 CCGAGACTCACGGTCAAGCTAAGCGAAGAGTGGGTGGGTGGCTGAAGCCATACTATTTATAG 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    35 CCGAGACTCACGGTCAAGCTAAGCGAAGAGTGGGTGGGTGGCTGAAGCCATACTATTTATAG 94

Qy    61 AATTAATGGAAAAGCAGAAAAAGACATCACAAACCAAGAAGAAACTTTGGGAAAATGAAGCCTA 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    95 AATTAATGGAAAAGCAGAAAAAGACATCACAAACCAAGAAGAAACTTTGGGAAAATGAAGCCTA 154

Qy   121 GGAGAAAATTTAGAAGAAGACGAATTATTTGCATAAGGACACACGGGAGAGACCAGCACATGCTAA 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   155 GGAGAAAATTTAGAAGAAGACGAATTATTTGCATAAGGACACACGGGAGAGACCAGCACATGCTAA 214

Qy   181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   215 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 274

Qy   241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   275 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 334
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Query Match 56.2%; Score 672; DB 2; Length 710;
Best Local Similarity 99.0%; Pred. No. 4.7e-145;
Matches 697; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

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Qy    45 CCATACTATTTTATAGAATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTT 104
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 CCATACTATTTTATAGAATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAAC-T 59

Qy   105 TGGAAAAATGAAGCCTAGGAGAGAAAATTTAGAAGAAGACGAATTATTTGCATAAGGACACGGGA 164
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    60 TGGAAAAATGAAGCCTAGGAGAGAAAATTTAGAAGAAGACGAATTATTTGCATAAGGACACGGGA 119

Qy   165 GAGACCAGCACATGCTAAAAAAGACCTGTGCTTTTGCCATTTGCACCAAACAGCCCATGCTGAT 224
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   120 GAGACCAGCACATGCTAAAGAGACCTTGTGCTTTTGCACCATTTGCACCAAACAGCCCATGCTGAT 179

Qy   225 GAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTG 284
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   180 GAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTG 239

Qy   285 CCAATTAAAATAGCTGCTATTATATAGCATCTCTGACTTTTCTTTCTTTTACACTCTTTTTACACTCTTTCTGAGGAA 344
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   240 CCAATTAAAATAGCTGCTATTATATAGCATCTCTGACTTTTCTTTTACACTCTTTCTGAGGAA 299

Qy   345 GTAATTCACCCTTTAGCCAACTTCCCATCAACAATATATTTATAAAATTCCAATCCTGGTC 404
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   300 GTAATTCACCCTTTAGCAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGTC 359

Qy   405 ATCAACAAAGTCTTGCCAATGGTTCATCACTCTCTTGGCATTGGTTTACCTGCCCAGGT 464
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   360 ATCAACAAAGTCTTGCCAATGGTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGT 419

Qy   465 GTAATAGCAGCAATTGTCCAACTTCATAATGGAACCAACGTATAAGAAGTTTCCACATTGG 524
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   420 GTGATAGCAGCAATTGTCCAACTTCATAATGGAACCAACGTATAAGAAGTTTCCACATTGG 479

Qy   525 TTGGATAAGTGGATGGTAGTTAACAAGAAAAGCAGTTTGGGCCTTCTCAGTTTCTTTTTTTGCTGTA 584
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   480 TTGGATAAGTGGAGTGTAACAAGAAAAGCAGTTTGGGCTTCTCTCAGTTTCTTTTTTGCTGTA 539

Qy   585 CTGCATGCAAATTTATAGTCTGTCTTACCCCAATGAGCGGCGATCCTACAGATACAAGTTGCTA 644
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   540 CTGCATGCAAATTTATAGTCTGTCTTACCCCAATGAGCGGCGATCCTACAGATACAAGTTGCTA 599

Qy   645 AACTGGGGCATATCACACAGTCCAACAAAATAAACAAGAGACGCCTCGGACATGCATGATGTT 704
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   600 AACTGGGCATATCAACAGGTCCAACAAAATAAACAAGAGATGCCTGGATTGAGCATGATGTT 659

Qy   705 TGGAGAAATCGG-AGATTTAAGTGTGTCTCTGGGAAATGTGTGGGGATTGG 747
         |||||||||||||||||||||||||||||||||||||||||||||
Db   660 TGGAGAAATGGCAGATTTAAGTGTGTCTCTGGGAAATCGTGTGGGGATTG 703
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RESULT 12
BU602279
LOCUS       BU602279                773 bp    mRNA    linear    EST 20-SEP-2002
DEFINITION  AGENCOURT 10016846 NIH_MGC_142 Homo sapiens cDNA clone
            IMAGE:6496341 5', mRNA sequence.
ACCESSION   BU602279
VERSION     BU602279.1  GI:23254038
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 773)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: NCI
            cDNA Library Preparation: Michael Brownstein Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2675 row: j column: 22
            High quality sequence stop: 604.
FEATURES             Location/Qualifiers
     source          1..773
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6496341"
                     /clone_lib="NIH_MGC_142"
                     /note="Vector: pDNR-LIB; Site_1: SfiI (ggccattatggcc);
                     Site_2: SfiI (ggccgcctcggcc); Double-stranded cDNA was
                     prepared from a pool of 40 cell line polyA+ RNAs (bladder
                     - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
                     4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
                     kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%,
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                     ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary
                     gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were
                     used in cloning as follow:
                     5'-AAGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGG-3' and
                     5'-ATTCTAGAGGCCGAGGCGGCCGACANTG-dT(30)NN-3'. Full-length
                     enriched library was constructed using the Clontech
                     Creator SMART kit and size-selected to contain the >0.5 kb
                     size fraction (other fractions present in NIH_MGC_141)
                     library created in the laboratory of M. Brownstein (NIH).
                     NIH. Note: this is a NIH_MGC Library."
ORIGIN
Query Match          55.0%;    Score 657.6;    DB 5;   Length 773;
Best Local Similarity   99.1%;    Pred. No. 1e-141;
Matches  682;    Conservative   0;    Mismatches   4;    Indels   2;    Gaps   2;

Qy      1 CCGAGACTCACGGTCAAGCTCAAGGCGGAGAGAGTGGGGTGGGCTGAAGCCATACTATTTTATAG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     80 CCGAGACTCACGGTCAAGCTAAGGCGGAGAGAGTGGGGTGGGCTGAAGCCATACTATTTTATAG 139

Qy     61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAGAAGAACTTTGGAAAATGAAGGCTA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    140 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAGAAGAACTTTGGAAAATGAAGGCTA 199

Qy    121 GGAGAAATTTAGAAGAAGAACGATTATTTATTTGCATTAAGGACCACCGGGAGACACCAGCCATGCTAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    200 GGAGAAATTTAGAAGAAGAACGATTATTTGCATTAAGGACCACCGGGAGAGACCAGCCATGCTAA 259

Qy    181 AAAGACCTGTGCCTTTTGCATTTGCACCAAACAGCCCCATGCTGATGAATTTGACTGCCCTT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    260 AAAGACCTGTGCCTTTTGCATTTGCACCAAACAGCCCCATGCTGATGAATTTGACTGCCCTT 319

Qy    241 CAGAACTTCAGCACACACAGGAGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    320 CAGAACTTCAGCACACACAGGAGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 379

Qy    301 CTATTATAGCATCTCTGACTTTTTCTTTACACTTCTTCTGAGGGAAGTAAATTCACCCTTTAG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    380 CTATTATAGCATCTCTGACTTTTTCTTTACACTTCTTCTGAGGGAAGTAAATTCACCCTTTAG 439

Qy    361 CAACTTCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    440 CAACTTCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 499

Qy    421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAAGTGAGT 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    500 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAAGTGAGT 559

Qy    481 TCCAACTTCATAATGGAACCAAGTATAAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    560 TCCAACTTCATAATGGAACCAAGTATAAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 619

Qy    541 TAACAAGAAAGCAGTTTGGGGCTTCTCAGTTTCTTTTTGCTGTGTACTGCATGCAATTTATA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    620 TAACAAGAAAGCAGTTTGGGGCTTCTCAGTTTCTTTTTGCTGTGTACTGCATGCAATTTATA 679

Qy    601 GTCTGTCTTACCCAATGAGGCGGATCCTACAGATACAAGTTGCTAAACT-GGGCATATCAA 659
          |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db    680 GTCTGTCTTACCCAATGAGGCGGATCCTACAGATACAAGTTGCTAAACTGGGGCATATCAA 739

Qy    660 CA-GGTCCCAACAAAAATTAAGAAGATGCC 686
          || |||||||||||||||||||||||||||
Db    740 CAGGGGTCCCACCAAATTAAGAAGATGCC 767
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```
RESULT 13
CX757709
LOCUS       CX757709                742 bp    mRNA    linear    EST 24-JAN-2005
DEFINITION  AGENCOURT 41384224 NIH_MGC_278 Homo sapiens cDNA clone
            IMAGE:7772991 3', mRNA sequence.
ACCESSION   CX757709
VERSION     CX757709.1  GI:58054365
KEYWORDS    EST.
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SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 742)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Contact: Meri Firpo
            Tissue Procurement: Express Genomics
            cDNA Library Preparation: Express Genomics
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM15916 row: h column: 13
            High quality sequence start: 6
            High quality sequence stop: 726.
FEATURES   Location/Qualifiers
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                     /clone="IMAGE:7772991"
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                     /db_xref="taxon:9606"
                     /lab_host="DH10B TonA"
                     /clone_lib="NIH MGC 278"
                     /note="Organ: Blastocyst; Vector: pExpress-1; Site_1:
                     EcoRV; Site_2: NotI; RNA obtained from pluripotent cell
                     line derived from blastocyst inner cell mass (cell line
                     HSF-1.14, NIH Registry designation UC01. Positive for OCT4
                     expression by rtPCR, Positive for SSEA-3, SSEA-4,
                     Tra-1-81, Tra-1-60 by immunofluorescence. Negative for
                     SSEA-1 by immunofluorescence. Passage 35. This line is a
                     subclone of the parental line; the parental line was
                     subcloned to remove aneuploid cells). cDNA was primed
                     using oligo-dT primer;
                     5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)25-3' and cloned into
                     the EcoRV/NotI sites of pExpress-1. Size-selection >1.25
                     kb resulted in an average insert size of 1.9 kb. This
                     primary library is non-normalized (normalized primary
                     library is NIH_MGC_279) and was constructed by Express
                     Genomics (Frederick, MD). Note: this is a Mammalian Gene
                     collection library."

ORIGIN

Query Match   54.9%; Score 656.2; DB 8; Length 742;
Best Local Similarity   97.4%;
Matches 667; Conservative   0; Mismatches   18; Indels   0; Gaps   0;

Qy   1 CCGAGACTCACGGTCAAGCTAAGGCGAGGAAGAGAGTGGGTGGGTGTGGCTGAGGCCCATCTATATTTTATAG 60
              | ||||||||||||||||||| | ||||| ||||||||||||||||||||||||||| ||||||||||||||
Db   58 CTGAGACTCACGGTCAAGCTACCGCGAGGAGAGTGGGTGGGTGTGGCTGAGGCCCATACTATATTTTATAG 117

Qy   61 AATTAAATGAAAAGCAGAAAAAGACATCACAAAACCAAGAAGAGAACTTTGGAAAATGAAGAAGCCTA 120
              ||||||||| ||||||||||||||| | |||||||||||| ||| | ||||||||||||||||| |||||
Db   118 AATTAAATGGAAAAGCAGAAAAAGAGAGTCACAAAACCAAGAGAGAAATTTGGAAAATGAAGAGCCTA 177

Qy   121 GGAGAAAATTTAGAAGAAGACGGATTATTTTGCATTAAGGACACGGGAGACCAGCCATGCATGCTAA 180
              |||||||||||||| || ||| ||||||||||||| |||||||||||||||||||||||||||||||||
Db   178 GGAGAAAATTTAGAGAACAACGATTATTTTGCATAAGGACACGGGAGAGACCAGCCATGCATGCTAA 237

Qy   181 AAAGACCTGTGCTTTGCATTTGCACCAAAACACCCATGCTGTGATGAGTGAAATTTGACTGCCCCCTT 240
              ||||||||||||||||||||||||| |||| || ||||||| || |||| |||||||||| ||||||
Db   238 AAAGACCTGTGCTTTGCATTTGCACGGAACAGCCCCATGCTGATGAATTTGACTCGCCCCTT 297

RESULT 14
BI552907
BI552907

LOCUS   BI552907   783 bp   mRNA   linear   EST 05-SEP-2001
DEFINITION 603197827F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5277295 5',
            mRNA sequence.
ACCESSION   BI552907
VERSION   BI552907.1 GI:15440219
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 783)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11700 row: e column: 08
            High quality sequence stop: 769.
FEATURES   Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5277295"
                     /tissue_type="hippocampus"
                     /clone_lib="NIH MGC 95"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI

Qy   241 CAGAACTTCAGCACACACAGGAAACTCTTTCCACAGTGGCGCACTTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||| ||||| |||||||||||||||||
Db   298 CAGAACTTCAGCACACACAGGAAACTCTTTCCACAGTGGCCACTTGCCAATTAAAATAGCTG 357

Qy   301 CTATTATATAGCATCTCTGGACTTTTCTTTACACTCTTCTGAGGAGGGAGTAATTCACCCTTTAG 360
              || || ||| ||| |||| ||||||||||||||||||||||||||||||||||||||||||||||
Db   358 CTGTTARGGCARCTCTCGACTTTTCTTTACACTCTTCTGAGGAGGGAGTAATTCACCCTTTAG 417

Qy   361 CAACTTCCCATCAACACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAAGTCTTGC 420
              ||||||||| |||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db   418 CAACTTCCCGTCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAAGTCTTGC 477

Qy   421 CAGTGGTTTCCATCACTCCTCTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   478 CAGTGGTTTCCATCACTCCTCTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 537

Qy   481 TCCAACTTCATAATGGAACCAAGTAATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   538 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 597

Qy   541 TAACAAGAAAGCAGGTTTGGGCTTCCAGTTTCTTTTTTGCGTTACTGCCATGCAATTTATA 600
              |||||||||||||| |||||||||||||||||||||||| |||||||| |||||||||||||
Db   598 TAACAAGAAAGCAGTTTGGGCTTCCAGTTTCTTTTTTGCTGTTACTGCATGCAATTTATA 657

Qy   601 GTCTGTCTTACCCAATGAGGCGGATCCTACAGAGATACAAGTTGCTAAAACTGGGGCATATCAAC 660
              | ||||||||| |||||| |||||||||||||| ||||||||||||||||| ||||||||||||||
Db   658 CTCTGTCTTACCGCAATGATGCGGATCCTACAGATACAAGTTGCTAAAACGGGGCATATCAAC 717

Qy   661 AGGTCCAACAAAAATGAAGAAGAGATGC 685
              ||||||||||||||||||||||||||||
Db   718 AGGTCCAACAAAAATGAAGAAGAGATGC 742

RESULT 15

```
LOCUS       CX753134       825 bp    mRNA    linear   EST 24-JAN-2005
DEFINITION  AGENCOURT 40991781 NIH_MGC_281 Homo sapiens cDNA clone
            IMAGE:7780881 3', mRNA sequence.
ACCESSION   CX753134
VERSION     CX753134.1  GI:58049789
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

```
REFERENCE   1  (bases 1 to 825)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Meri Firpo
            cDNA Library Preparation: Express Genomics
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM15937 row: a  column: 07
            High quality sequence stop: 538.
FEATURES             Location/Qualifiers
     source          1..825
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:7780881"
                     /tissue_type="pluripotent cell line derived from
                     blastocyst inner cell mass"
                     /clone_lib="NIH_MGC_281"
                     /lab_host="DH10B TonA"
                     /note="Organ: Blastocyst; Vector: pExpress-1; Site_1:
                     EcoRV; Site 2: NotI; RNA obtained from pluripotent cell
                     line derived from blastocyst inner cell mass (cell line
                     HSF-6, NIH Registry designation UC06. Positive for OCT4
                     expression by rtPCR, positive for SSEA-3, SSEA-4,
                     Tra-1-81, Tra-1-60 by immunofluorescence. Negative for
                     SSEA-1 by immunofluorescence Passage 62. cDNA was primed
                     using oligo-dT primer:
                     5'-pGACTAGTTGTAGATCGGCGAGCGGCCGCC(T)25-3', and cloned into
                     the EcoRV/NotI sites of pExpress-1. Size-selection >1.25
                     kb resulted in an average insert size of 2.0 kb. This
                     primary library is normalized (non-normalized primary
                     library is NIH_MGC_280) and was constructed by Express
                     Genomics (Frederick, MD). Note: this is a Mammalian Gene
                     Collection library."
```

ORIGIN

Query Match 54.8%; Score 654.6; DB 8; Length 825;
Best Local Similarity 98.5%;
Matches 671; Conservative 0; Pred. No. 5.2e-141; Mismatches 9; Indels 1; Gaps 1;

```
Qy     1 CCGAGACTCACGGTCAAGCTAAGGCCAAGAGACTGGGGTGGCTGAAGCCATACTATTTTATAG  60
         |||||||||||||||||||||||||| ||||| |||||||||||||||||||||||||||||
Db    65 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGGTGGCTGAAGCCATACTATTTTTATAG 124

Qy    61 AATTAATGGAAAGCAGAAAAAGACATCACAAACCAAGAGAAGAACTTTGGAAAATGAAGCCTA 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   125 AATTAATGGAAAGCAGAAAAAGACATCACAAACCAAGAGAAGAACTTTGGAAAATGAAGCCTA 184

Qy   121 GGAGAAAATTTAGAAGAAGACGATTATTTTGCATAAGGACACACGGGAGGAGACCAGCCATGCTAA 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   185 GGAGAAAATTTAGAAGAAGACGATTATTTTGCATAAGGACACACGGGAGGAGACCAGCCATGCTAA 244

Qy   181 AAAGACCTGTGCTTTTGCATTTGACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   245 AAAGACCTGTGCTTTTGCATTTGACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTT 304

Qy   241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   305 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 364

Qy   301 CTATTATAGCCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   365 ...
```

ORIGIN

(gtcgag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.5 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: this
is a NIH_MGC Library."

Query Match 54.8%; Score 655; DB 3; Length 783;
Best Local Similarity 99.0%;
Matches 680; Conservative 0; Pred. No. 4.2e-141; Mismatches 5; Indels 2; Gaps 2;

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Qy     1 CCGAGACTCACGGTCAAGCTAAGGCCAAGAGACTGGGGTGGCTGAAGCCATACTATTTTATAG  60
         |||||||||||||||||||||||||| ||||| |||||||||||||||||||||||||||||
Db    97 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGGTGGCTGAAGCCATACTATTTTTATAG 156

Qy    61 AATTAATGGAAAGCAGAAAAAGACATCACAAACCAAGAGAAGAACTTTGGAAAATGAAGCCTA 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   157 AATTAATGGAAAGCAGAAAAAGACATCACAAACCAAGAGAAGAACTTTGGAAAATGAAGCCTA 216

Qy   121 GGAGAAAATTTAGAAGAAGACGATTATTTTGCATAAGGACACACGGGAGGAGACCAGCCATGCTAA 180
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Db   217 GGAGAAAATTTAGAAGAAGACGATTATTTTGCATAAGGACACACGGGAGGAGACCAGCCATGCTAA 276

Qy   181 AAAGACCTGTGCTTTTGCATTTGACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   277 AAAGACCTGTGCTTTTGCATTTGACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTT 336

Qy   241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   337 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 396

Qy   301 CTATTATAGCCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   397 CTATTATAGCCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 456

Qy   361 CAACTCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   457 CAACTCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 516

Qy   421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCCAACAATTG 480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   517 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCCAACAATTG 576

Qy   481 TCCAACTTCATAATGGAACCAAGTAATAAGAAGAGTTCCACATTGGTTGGATAAGTGGATGT 540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   577 TCCAACTTCATAATGGAACCAAGTAATAAGAAGAGTTCCACATTGGTTGGATAAGTGGATGT 636

Qy   541 TAACAAGAAAGCAGTTTGGGCCTTCTCAGTTTCTTTTTTGCGTGTTACTGCA-TGCAATTTAT 599
         ||||||||||||||||||||| ||||||||||||| |||||||||||||||| |||||||||
Db   637 TAACAAGAAAGCAGTTTGGGCTTTCTCAGTTTCTTTTTCTGCGTGTTACTGCATTGCAATTTAT 696

Qy   600 AGTCTGTCTTACCCAATGAGGGGCCATCCTACAGATACAAGTTGTTGCTAAACT-GGGCATATCA 658
         |||||||||||||||||||||| |||||||||||||||||| ||||||||||| |||||||||
Db   697 AGTCTGTCTTACCCAATGAGGGCGATCCTACAGATACAAGTTGCTAAACTGGGGCATATCA 756

Qy   659 ACAGGTCCAACAAAATAAGAAGAAGGATGC 685
         |||||||||||||||| |||||||||||
Db   757 CCAGGTCCAACAAAACTACCGAAGATGC 783
```

```
Db   365  CTATTAATAGCAATCTCTGACTTTTCTTTTACACTTCTTCTGAGGGGAAGTAATTCACCCTTTAG 424
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   361  CAAACTTCCCATCAACAATATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   425  CAACTTCCCATCAACAATATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 484

Qy   421  CAATGGTTTCCATCACTCTCTTGGCATTGGTTTTACCTGCCAGGTGTGATAGCAGCAAATTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   485  CAATGGTTTCCATCACTCTCTTGGCATTGGTTTTACCTGCCAGGTGTGATAGCAGCAAATTG 544

Qy   481  TCCAACTTCATAAATGGAACCAAGTAATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   545  TCCAACTTCATAAATGGAACCAAGTAATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 604

Qy   541  TAACAAGAAAGCAGTTTGGGGCTTCTCAGTTTCTTTTTTGCTGTACTGGCATGCAAATTTATA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   605  TAACAAGAAAGCAGTTTGGGGCTTCTCAGTTTCTTTTTTGCTGTACTGGCATGCAAATTTATA 664

Qy   601  GTCTGTGTCTTACCCAATGAGGGCGATCCTACACGATTACAAGTTGCTAAAACTGGGGCATATCAAC 660
          ||||||||| ||||||||| | ||||||||||||  |||||||||||||||||||||||||||
Db   665  GTCTGTGTCCTACCCAATGAAGCGGATCCTACACGA-ACCAGTTGCTAAAACTGGGGCATATCAAC 723

Qy   661  AGGTCCAACAAAATAAAGAAG 681
          ||||| |||||||||| ||
Db   724  AGGTCAACAAAATAAAAGATG 744
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GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: December 4, 2005, 20:13:31 ; Search time 802.249 Seconds
(without alignments)
9927.475 Million cell updates/sec

Post-processing: Minimum Match 0%
Listing first 45 summaries

Maximum Match 100%

Maximum DB seq length: 200000000
Minimum DB seq length: 0

Total number of hits satisfying chosen parameters: 9993994

Searched: 4996997 seqs, 333246308 residues

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Sequence: 1 ccgagactcacggtcaagct.........ggaaaaaaaaaaaaaaaaaaa 1195

Title: US-10-750-262-1
Perfect score: 1195

Database : N_Geneseq_21:

1:	geneseqn1980s:*
2:	geneseqn1990s:*
3:	geneseqn2000s:*
4:	geneseqn2001as:*
5:	geneseqn2001bs:*
6:	geneseqn2002as:*
7:	geneseqn2002bs:*
8:	geneseqn2003as:*
9:	geneseqn2003bs:*
10:	geneseqn2003cs:*
11:	geneseqn2003ds:*
12:	geneseqn2004as:*
13:	geneseqn2004bs:*
14:	geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1195	100.0	1195	4	AAH93924	Aah93924 P789P ful
2	1195	100.0	1195	4	AAS64160	Aas64160 Human pro
3	1195	100.0	1195	5	ACA59968	Aca59968 Prostate
4	1195	100.0	1195	5	ABL95531	Abl95531 Human P78
5	1195	100.0	1195	6	ABK92128	Abk92128 Prostate
6	1195	100.0	1195	8	ACC95695	Acc95695 Prostate
7	1195	100.0	1195	10	ADB75572	Adb75572 Prostate
8	1195	100.0	1195	10	ADB14328	Adb14328 Human pro
9	1195	100.0	1195	10	AAD63162	Aad63162 Human STE
10	1195	100.0	1195	10	AAD62763	Aad62763 Human STE
11	1195	100.0	1195	10	ADG26744	Adg26744 Human pro
12	1195	100.0	1195	11	ADN39812	Adn39812 Cancer/an
13	1195	100.0	1195	11	ADN33395	Adn33395 Cancer/an
14	1195	100.0	1195	11	ADP88258	Adp88258 Prostate
15	1195	100.0	1195	12	ADL06462	Adl06462 Human tum
16	1195	100.0	1195	12	ADL06436	Adl06436 Human tum
17	1195	100.0	1195	12	ADJ75176	Adj75176 Marker ge
18	1195	100.0	1330	13	ADR14190	Adr14190 Human NF-
19	1195	100.0	1330	13	ADU06030	Adu06030 Novel bro

ALIGNMENTS

RESULT 1
AAH93924

ID   AAH93924 standard; cDNA; 1195 BP.
XX
AC   AAH93924;
XX
DT   04-OCT-2001 (first entry)
XX
DE   P789P full length cDNA sequence.
XX
KW   Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW   cytostatic; gene therapy; metastasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200151633-A2.
XX
PD   19-JUL-2001.
XX
PF   16-JAN-2001; 2001WO-US001574.
XX
PR   14-JAN-2000; 2000US-00483672.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI   Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI   Wang A, Meagher MJ;
XX
DR   WPI; 2001-425873/45.
XX
PT   New polynucleotide encoding a prostate-specific protein, for diagnosing,
PT   monitoring and treating prostate cancer in a patient and for use in
PT   vaccines.
XX
PS   Claim 1; Page 510; 543pp; English.
XX
CC   The present invention describes polynucleotide sequences (I) which encode
CC   prostate-specific proteins (II), (I) and (II) have cytostatic activity,
CC   and can be used in vaccine production and gene therapy, (I), (II),
CC   antibodies to (II), fusion proteins comprising (III), and isolated T cells
CC   prepared using (I) or (II) are used treat cancer in a patient. (I) and

20	1195	100.0	1330	14	ADY15575	Ady15575 DNA encod
21	1195	100.0	1330	14	ADY19959	Ady19959 DNA encod
22	1193	99.8	1193	3	AAZ49395	Aaz49395 Human STR
23	1193	99.8	1193	5	AAD70067	Aad70067 Human six
24	1193	99.8	1193	14	ADY92698	Ady92698 Human STE
25	1190	99.6	1294	4	AAK51978	Aak51978 Human pol
26	1182	99.0	1198	8	ACD02628	Acd02628 STEAP-1 v
27	1181.8	98.9	1193	8	ACD02597	Acd02597 cDNA enco
28	1181.8	98.9	1193	8	ACD02629	Acd02629 STEAP-1 v
29	1180.4	98.8	1198	8	ADL46020	Adl46020 Human ova
30	1178	98.5	1277	5	ADV73174	Adv73174 Human col
31	1177	98.5	1177	14	ADX33625	Adx33625 Plant ful
32	1177	98.3	1201	13	AAK52962	Aak52962 Human pol
33	1174.4	98.3	1229	4	ADG22300	Adg22300 Human sof
34	1166	97.6	1354	12	ACD02599	Acd02599 cDNA enco
35	1048	87.7	1365	8	ACD02630	Acd02630 STEAP-1 v
36	1048	87.7	1365	8	ACD02632	Acd02632 STEAP-1 v
37	1044	87.4	1369	8	ACD02631	Acd02631 STEAP-1 v
38	1042.4	87.2	1369	8	ACD02601	Acd02601 cDNA enco
39	827.2	69.2	3627	3	AAZ49396	Aaz49396 Human STR
40	825.6	69.1	3627	5	AAD70071	Aad70071 Human six
41	825.6	69.1	3627	8	ACD02613	Acd02613 cDNA enco
42	825.6	69.1	3627	8	ACD02605	Acd02605 cDNA enco
43	825.6	69.1	3627	8	ACD02606	Acd02606 cDNA enco
44	825.6	69.1	3627	8	ACD02598	Acd02598 cDNA enco
45	825.6	69.1	3627	8	ACD02612	Acd02612 cDNA enco

CC   the antibodies are also used in the detection of cancer in a patient. The
CC   cancer that is diagnosed or treated is particularly prostate cancer. (I)
CC   and (II) can be used in vaccines. The antibodies or (I) and (II) can also
CC   be used to improve diagnostic and therapeutic methods for prostate
CC   cancer. They can indicate the level of metastasis as well as the prostate
CC   volume. AAH93357 to AAH93944 and AAM01115 to AAM01318 represent
CC   polynucleotide and amino acid sequences used in the exemplification of
CC   the present invention

XX

SQ   Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

Query Match   100.0%;   Score 1195;   DB 4;   Length 1195;
Best Local Similarity   100.0%;   Pred. No. 4.4e-276;
Matches 1195;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGAGAGGTGGGCTGGGCCCATACTATTTTATAG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGAGAGGTGGGCTGGGCCCATACTATTTTATAG 60

Qy   61 AATTAAATGAAAACGAGAAAAAGACATCACAAAACCAAGAAGAACTTTGGGAAAATGAAGCCTA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AATTAAATGAAAACGAGAAAAAGACATCACAAAACCAAGAAGAACTTTGGGAAAATGAAGCCTA 120

Qy   121 GGAGAAATTTAGGAAGAAGACGATTATTTGCATAAGGACACGGGGAGGAGGACCAGCATGCTAA 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGAGAAATTTAGGAAGAAGACGATTATTTGCATAAGGACACGGGGAGGAGGACCAGCATGCTAA 180

Qy   181 AAAGACCCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAAATTGACTGCCCTT 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AAAGACCCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAAATTGACTGCCCTT 240

Qy   241 CAGAAACTTCAGCACACAGGAACTCTTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CAGAAACTTCAGCACACAGGAACTCTTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy   301 CTATTATAGCATCTCTGACTTTTCTTACACTCTTCTCGAGGGAAGTAATTCACCCTTTAG 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTATTATAGCATCTCTGACTTTTCTTACACTCTTCTCGAGGGAAGTAATTCACCCTTTAG 360

Qy   361 CAACTTCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CAACTTCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy   421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAAATTG 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAAATTG 480

Qy   481 TCCAACTTCATAATGGAACCAAGTATATAAGAGAAGTTCCACATTGGTTGGATAAGTGGATGT 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TCCAACTTCATAATGGAACCAAGTATATAAGAGAAGTTCCACATTGGTTGGATAAGTGGATGT 540

Qy   541 TAACAAGAAAGCAGTTTGGGCCTTCTCAGTTTCTTTTTTGCTGTACTGCAATGCAATTTATA 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TAACAAGAAAGCAGTTTGGGCCTTCTCAGTTTCTTTTTTGCTGTACTGCAATGCAATTTATA 600

Qy   601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGCATATCAAC 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGCATATCAAC 660

Qy   661 AGGTCCAACAAAAATAAAGAAGATGCCCTGGATTGAGCATGAGTGTTGGAGAAATGGAGATT 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 AGGTCCAACAAAAATAAAGAAGATGCCCTGGATTGAGCATGAGTGTTGGAGAAATGGAGATT 720

Qy   721 ATGTGTCTCTGGGAATTGTGGGCAATACTGGCTCTGTGTTGGCTGTGACATCTATTC 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATGTGTCTCTGGGAATTGTGGGCAATACTGGCTCTGTGTTGGCTGTGACATCTATTC 780

Qy   781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGACCAAGCTAGGAA 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGACCAAGCTAGGAA 840

Qy   841 TTGTTTCCCTTCTACTGGGCACAATACACGGCCAATTGATTTTTGCCTGGAATAAGTGGATAG 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TTGTTTCCCTTCTACTGGGCACAATACACGGCCAATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy   901 ATATAAAACAAATTGTATGGTATACACACCTCCAAAATTACACGGCATTGATTTTTGTCGTTTTCCTTCCAA 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 ATATAAAACAAATTGTATGGTATACACACCTCCAAAATTACACGGCATTGATTTTTGTCGTTTTCCTTCCAA 960

Qy 1021 AGATTAGACACATGGTTGGGAAGACGTCACCCAAAATTAACAAAACTGAGAATATGTTCCCAGT 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 AGATTAGACACATGGTTGGGAAGACGTCACCCAAAATTAACAAAACTGAGAATATGTTCCCAGT 1080

Qy 1081 TGTAGAATTACTGTTTACACACATTTTGTTCAATATTGATTATATTTTATCACCAACATT 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 TGTAGAATTACTGTTTACACACATTTTGTTCAATATTGATTATATTTTATCACCAACATT 1140

Qy 1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAAA 1195
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAAA 1195

RESULT 2
AAS64160
ID   AAS64160 standard; cDNA; 1195 BP.
XX
AC   AAS64160;
XX
DT   29-JAN-2002   (first entry)
XX
DE   Human prostate cDNA sequence #590.
XX
KW   Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
XX
OS   Homo sapiens.
XX
PN   WO200173032-A2.
XX
PD   04-OCT-2001.
XX
PF   27-MAR-2001; 2001WO-US009919.
XX
PR   27-MAR-2000; 2000US-00336857.
PR   09-MAY-2000; 2000US-00568100.
PR   12-MAY-2000; 2000US-00570737.
PR   13-JUN-2000; 2000US-00593793.
PR   27-JUN-2000; 2000US-00605783.
PR   09-AUG-2000; 2000US-00636215.
PR   29-AUG-2000; 2000US-00651236.
PR   06-SEP-2000; 2000US-00657279.
PR   02-OCT-2000; 2000US-00679426.
PR   10-OCT-2000; 2000US-00685166.
PR   09-NOV-2000; 2000US-0070972.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI   Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI   Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
DR   WPI; 2001-632232/73.
DR   P-PSDB; AAU69927.
XX
PT   New human prostate-specific polypeptides and polynucleotides useful for
PT   the diagnosis and treatment of cancer, especially prostate cancer.
XX
PS   Claim 1; Page 548; 579pp; English.
XX
CC   The invention relates to isolated prostate-specific polypeptides,
CC   polypeptides, fusion proteins of the polypeptides, antibodies raised
CC   against the polypeptides (or antigenic epitopes derived from them) and

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CC   antigen-presenting cells expressing the polypeptides. The antibodies are
CC   useful for detecting the presence of cancer, especially prostate cancer.
CC   The polypeptides, polynucleotides and the antigen-presenting cells are
CC   useful for stimulating and/or expanding T cells specific for a tumour
CC   protein, and for inhibiting the development of cancer especially prostate
CC   cancer. Compositions comprising the polynucleotide and/or polypeptide are
CC   useful for stimulating an immune response, and for treating cancer. The
CC   oligonucleotide is useful for detecting cancer. The present sequence is a
CC   prostate specific polynucleotide of the invention
XX
SQ   Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

Query Match             100.0%;  Score 1195;  DB 4;  Length 1195;
Best Local Similarity   100.0%;  Pred. No. 4.4e-276;
Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTGAAGGCGAAGAGCTGGGGTTCGGCTGAAGCCATACTATTTTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTGAAGGCGAAGAGCTGGGGTTCGGCTGAAGCCATACTATTTTATTTTATAG 60

Qy         61 AATTAAATGGAAAGCAGAAAAAGACATCACAAAACCAAGAAGAAGAACTTTGGAAAATGAAGCCTA 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAAATGGAAAGCAGAAAAAGACATCACAAAACCAAGAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACACGGGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACACGGGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACAGCAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACAGCAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCAATGGTTTACCTGCCAGGTGTGATGTAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCAATGGTTTACCTGCCAGGTGTGATGTAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAAGTATAAGAAGTTTCCACATTGTTTTGGTTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAAGTATAAGAAGTTTCCACATTGTTTTGGTTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCCTTCTCTCAGTTTCTTTTTGCTGTACTGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCCTTCTCTCAGTTTCTTTTTGCTGTACTGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCCATATCAAC 660

Qy        661 AGGTCCAACAAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTGGAGAAATGAGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTGGAGAAATGAGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGTGGAATTGGCAATACTGGCTCTCGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGTGGAATTGGCAATACTGGCTCTCGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACAATGGAGAATTTCACTATATTCAGAGCAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACAATGGAGAATTTCACTATATTCAGAGCAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCCAATACACGCCATTGATTTTTGCCTGGAATAAGTGGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCCAATACACGCCATTGATTTTTGCCTGGAATAAGTGGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGGTATACACCTCCAAACTTTTTATATGATAGAGCTGTTTTTCCTTCCAA 960
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGGTATACACCTCCAAACTTTTTATATGATAGAGCTGTTTTTCCTTCCAA 960

Qy        961 TTGGTTGTCCTGATATTTAAAAGCATACTACTTATTCCTTGCCATGTGCTTGAGGAAGAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGGTTGTCCTGATATTTAAAAGCATACTACTTATTCCTTGCCATGTGCTTGAGGAAGAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGGAAGAGGTCACCAAAATTAACAAAAACTGAGATATGTTCCCAGT 1080
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGGAAGAGGTCACCAAAATTAACAAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATATTTTATCACCAACATT 1140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAAATGATTATTCAAGAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAAATGATTATTCAAGAAAAAAAAAAAAAAAAAA 1195
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RESULT 3
ACA59968

```
ID   ACA59968 standard; cDNA; 1195 BP.
XX
AC   ACA59968;
XX
DT   10-JUN-2003  (first entry)
XX
DE   Prostate cancer therapy associated cDNA #655.
XX
KW   Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
KW   immunogen; cancer; prostate specific antigen; PSA;
KW   prostatic acid phosphatase; PAP; prostate specific membrane antigen;
KW   PSMA; gene; ss.
XX
OS   Homo sapiens.
XX
PN   US200219276 3-A1.
XX
PD   19-DEC-2002.
XX
PF   29-JUN-2001; 2001US-0895793.
XX
PR   04-OCT-1999; 99US-0157455P.
PR   04-OCT-2000; 2000US-0067 9272.
PR   28-MAR-2001; 2001US-00822827.
XX
PA   (XUJJ/)  XU J.
PA   (DILL/)  DILLON D C.
PA   (MITC/)  MITCHAM J L.
PA   (HARL/)  HARLOCKER S L.
PA   (JIAN/)  JIANG Y.
PA   (KALO/)  KALOS M D.
PA   (FANG/)  FANGER G R.
PA   (RETT/)  RETTER M W.
PA   (STOL/)  STOLK J A.
PA   (DAYC/)  DAY C H.
PA   (VEDV/)  VEDVICK T S.
PA   (CART/)  CARTER D.
PA   (LISX/)  LI S X.
PA   (WANG/)  WANG A.
PA   (SKEI/)  SKEIKY Y A W.
PA   (HEPL/)  HEPLER W T.
PA   (HEND/)  HENDERSON R A.
PA   (HURA/)  HURAL J.
PA   (MCNE/)  MCNEILL P D.
PA   (HOUG/)  HOUGHTON R L.
PA   (DBAS/)  Y DE BASSOLS C V.
PA   (FOYT/)  FOY T M.
```

XX

PI   Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI   Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI   Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;
PI   Mcneill PD, Houghton RL, Y De BassolSCV, Foy TM;
XX

DR   WPI; 2001-2450062/25.
DR   P-PSDB; ABU71821.
XX

PT   Prostate specific protein and its encoding polynucleotide, useful for the
PT   treatment and diagnosis of prostate cancer.
XX

PS   Example 5; SEQ ID NO 878; 85pp; English.
XX

CC   The invention describes a fusion protein comprising at least one amino
CC   acid sequence of immunogenic portions of any of the 3 sequences not
CC   defined in the specification, or sequences having at least 70 or 90 %
CC   sequence identity to any one of the 35 sequences defined in the USPTO web
CC   site, which is encoded by any of the 4 nucleotide sequences not defined
CC   in the specification. The fusion protein, composition and methods are
CC   useful for diagnosing, preventing and/or treating cancer, particularly
CC   prostate cancer. The proteins are useful as markers to indicate the
CC   presence or absence of cancer. This sequence represents a prostate cancer
CC   therapy associated cDNA. Note: The sequence data for this patent did not
CC   form part of the printed specification, but was obtained in electronic
CC   format directly from the US patent office at
CC   seqdata.uspto.gov/sequence.html?DocID=US2002019Z763

SQ   Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

Query Match   100.0%; Score 1195; DB 5;   Length 1195;
Best Local Similarity 100.0%; Pred. No. 4.4e-276;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 CCGAGACTTCACGGTCAAGCTAAGGCGAGAGTGGGTGGCTGGCTGAAGCCATACTATTTATAG 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CCGAGACTTCACGGTCAAGCTAAGGCGAGAGTGGGTGGCTGGCTGAAGCCATACTATTTATAG 60

Qy   61 AATTAATGGAAAGCAGAAAAGACATCACAAAACCAAGAGAAACTTTGGAAAAATGAAGCCTA 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AATTAATGGAAAGCAGAAAAGACATCACAAAACCAAGAGAAACTTTGGAAAAATGAAGCCTA 120

Qy   121 GGAGAAATTAGAGAAGAACGATTATTTGCATAAGGACACACGGGAGACCAGCATGCTAA 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGAGAAATTAGAGAAGAACGATTATTTGCATAAGGACACACGGGAGACCAGCATGCTAA 180

Qy   181 AAAGACCCTGTGCTTTTGCACCAAAACAGCCCATCGTGATGAAATTGACTGCCCTT 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AAAGACCCTGTGCTTTTGCACCAAAACAGCCCATCGTGATGAAATTGACTGCCCTT 240

Qy   241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy   301 CTATTAATAGCATCTCTGACTTTTTCTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTATTAATAGCATCTCTGACTTTTTCTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy   361 CAACTTCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAGTCTTGC 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CAACTTCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAGTCTTGC 420

Qy   421 CAATGGTTTCCATCACTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCACGCAATTG 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CAATGGTTTCCATCACTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCACGCAATTG 480

Qy   481 TCCAAACTTCATATAATGGAACCAAGTATAAGAGAAGTTTCCACATTGGTTGGATAAGTGGGATGT 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TCCAAACTTCATATAATGGAACCAAGTATAAGAGAAGTTTCCACATTGGTTGGATAAGTGGGATGT 540

Qy   541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTGTACTGCATGCAATTTATA 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTGTACTGCATGCAATTTATA 600

Qy   601 GTCTGTCTTACCCAATGAGGCGGATCCTACAGATACAAGTTGCTAAAACTGGGCATATCAAC 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTCTGTCTTACCCAATGAGGCGGATCCTACAGATACAAGTTGCTAAAACTGGGCATATCAAC 660

Qy   661 AGGGTCCAACAAAAATAAAGAAGATGCCTGGATTGAGCATTGGGCATGATGTTTGGAGAATGAGAGATTT 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 AGGGTCCAACAAAAATAAAGAAGATGCCTGGATTGAGCATTGGGCATGATGTTTGGAGAATGAGAGATTT 720

Qy   721 ATGTGTCTCTGGGAATTGTGGGATTGGGCAATACTGGGCTTCGTTGGCTGTTGGACATCTATTC 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATGTGTCTCTGGGAATTGTGGGATTGGGCAATACTGGGCTTCGTTGGCTGTTGGACATCTATTC 780

Qy   781 CATCTGTGAGTGACTCTTTGACATGGAAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 CATCTGTGAGTGACTCTTTGACATGGAAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy   841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTTGCCTGGGAATAAGGGATAG 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTTGCCTGGGAATAAGGGATAG 900

Qy   901 ATATAAAACAAATTTGTATGGTATACACCTCCAACTTTATGATACGTGTTTTCCTTCCAA 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 ATATAAAACAAATTTGTATGGTATACACCTCCAACTTTATGATACGTGTTTTCCTTCCAA 960

Qy   961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATCCTTGAGGAGAAGAGATACTGA 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATCCTTGAGGAGAAGAGATACTGA 1020

Qy   1021 AGATTAGACATGGTTGGGAAGGACTCACCAAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 AGATTAGACATGGTTGGGAAGGACTCACCAAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy   1081 TGTAGAATTACTGTTTACACACATTTGTTCAATATTGTTCAATATTTTATCACCAACATT 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TGTAGAATTACTGTTTACACACATTTGTTCAATATTGTTCAATATTTTATCACCAACATT 1140

Qy   1141 TCAAGTTTGTATTTGTTAATTAAAATGAATTATTCAAGGAAAAAAAAAAAAAAA 1195
             ||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TCAAGTTTGTATTTGTTAATTAAAATGAATTATTCAAGGAAAAAAAAAAAAAAA 1195

RESULT 4
ABL95531

ID   ABL95531 standard; cDNA; 1195 BP.
XX

AC   ABL95531;
XX

DT   19-JUL-2002 (first entry)
XX

DE   Human P789P cDNA sequence SEQ ID NO 878.
XX

KW   Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW   gene therapy; gene; SS.
XX

OS   Homo sapiens.
XX

PN   US2002022248-A1.
XX

PD   21-FEB-2002.
XX

PF   12-JAN-2001; 2001US-00759143.
XX

PR   25-FEB-1997; 97US-00806099.
PR   01-AUG-1997; 97US-00904804.
PR   10-FEB-1998; 98US-00020956.
PR   25-FEB-1998; 98US-00030607.
PR   14-JUL-1998; 98US-00115453.
PR   23-SEP-1998; 98US-00159812.
PR   15-JAN-1999; 99US-00232149.
PR   09-APR-1999; 99US-00288946.
PR   13-JUL-1999; 99US-00352616.
PR   12-NOV-1999; 99US-00439313.

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PR   18-NOV-1999;        99US-00443686.
PR   14-JAN-2000;    200US-00483672.
PR   27-MAR-2000;    200US-00536857.
PR   09-MAY-2000;    200US-00568100.
PR   12-MAY-2000;    200US-00570737.
PR   13-JUN-2000;    200US-00593793.
PR   27-JUN-2000;    200US-00605783.
PR   10-AUG-2000;    200US-00636215.
PR   29-AUG-2000;    200US-00651236.
PR   06-SEP-2000;    200US-00657279.
PR   02-OCT-2000;    200US-00679426.
PR   10-OCT-2000;    200US-00685166.
XX
PA   (XUJU/)  XU J.
PA   (DILL/)  DILLON D C.
PA   (MITC/)  MITCHAM J L.
PA   (HARL/)  HARLOCKER S L.
PA   (JIAN/)  JIANG Y.
PA   (KALO/)  KALOS M D.
PA   (FANG/)  FANGER G R.
PA   (RETT/)  RETTER M W.
PA   (STOL/)  STOLK J A.
PA   (DAYC/)  DAY C H.
PA   (VEDV/)  VEDVICK T S.
PA   (CART/)  CARTER D.
PA   (LISX/)  LI S X.
PA   (WANG/)  WANG A.
PA   (SKEI/)  SKEIKY Y A W.
PA   (HEPL/)  HEPLER W T.
PA   (HEND/)  HENDERSON R A.
XX
DR   WPI; 2002-255649/30.
XX
PI   Xu J., Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI   Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI   Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
PT   New prostate-specific polynucleotides for diagnosing and treating
PT   diseases, in particular prostate cancer, and as markers for the
PT   progression of cancer.
XX
PS   Claim 1; SEQ ID NO 878; 87pp; English.
XX
CC   The present invention provides prostate-specific coding sequences and
CC   their encoded proteins. These can be used in the diagnosis and treatment
CC   of cancers, particularly prostate cancer. The present sequence is a cDNA
CC   described in the invention
XX
SQ   Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

Query Match        100.0%;  Score 1195;  DB 6;  Length 1195;
Best Local Similarity   100.0%;  Pred. No. 4.4e-276;
Matches 1195;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 CCGAGACTCACGGTCAACGGCGGAGAGAGTGGGTGGCTGAGCCATACTATTTTATG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAACGGCGGAGAGAGTGGGTGGCTGAGCCATACTATTTTATG 60

Qy         61 AATTAATCGAAAAGCAGAAAAAGACATCACAAAACCAAGAGAGTGGGTGAAAAATGAAGCCTA 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATCGAAAAGCAGAAAAAGACATCACAAAACCAAGAGAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGGACGATATATTTGCATAAGGACACGGGAGAGAGACCAGCAGCATGCTAA 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGGACGATATATTTGCATAAGGACACGGGAGAGAGACCAGCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAAATTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAAATTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCCACTTGCCCAATTAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCCACTTGCCCAATTAAATAGCTG 300

Qy        301 CTATTATAGCAATCTCTGACTTTTCTTCTTTCTTTACACTCTTCTTCTCTGAGGGAAGTAAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCAATCTCTGACTTTTCTTCTTTCTTTACACTCTTCTTCTCTGAGGGAAGTAAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAAATATTTTATAAAAATTCCAATCCTCGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAAATATTTTATAAAAATTCCAATCCTCGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCCTTTGGGCATTGGTTTACCTGCCAGGTGTGATAGCGCAAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCCTTTGGGCATTGGTTTACCTGCCAGGTGTGATAGCGCAAATTG 480

Qy        481 TCCAACTTCATTAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATTAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGGCTTCTCAGTTTCTTTTTTTGCTGTACTGCATGCAATTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGGCTTCTCAGTTTCTTTTTTTGCTGTACTGCATGCAATTATA 600

Qy        601 GTCTCGTTCTTACCCAATGAGCGCGATCCTACAGATACAAAGTTGCTAAACTGGGCCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTTCTTACCCAATGAGCGCGATCCTACAGATACAAAGTTGCTAAACTGGGCCATATCAAC 660

Qy        661 AGGTCCAACAAAAATAAAGAAGAAGATGCCTGGAATTGAGGCATGATGTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAAATAAAGAAGAAGATGCCTGGAATTGACGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATGTGGGATGGCAATACTGGCCTCGTGTTGGCTGTGCGATCTATTC 780
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATGTGGGATGGCAATACTGGCCTCGTGTTGGCTGTGCGATCATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGCAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGCAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCCACAATACAGGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCCACAATACAGGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAAATTGTATGGTATACACCTCCAACTTTTATGATAAGCTGTTTCCTTCCAA 960
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAAATTGTATGGTATACACCTCCAACTTTTATGATAAGCTGTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACAATACCTGACGAGGAAGAGGATACTGA 1020
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACAATACCTGACGAGGAAGAGGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACAATTTTGTTCAATATTTGATATTTTATCACCAACACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACAATTTTGTTCAATATTTGATATTTTATCACCAACACATT 1140

Qy       1141 TCAAGTTGTTGTATTTGTTTAATTAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAAA 1195
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTTGTATTTGTTTAATTAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAAA 1195
```

```
RESULT 5
ABK92128
ID   ABK92128 standard; DNA; 1195 BP.
XX
AC   ABK92128;
XX
DT   15-AUG-2002 (first entry)
XX
DE   Prostate cancer-associated DNA sequence #14.
XX
KW   Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
```

KW   gene therapy; gene; ds.
XX
OS   Mammalia.
XX
PN   WO020230268-A2.
XX
PD   18-APR-2002.
XX

PF   12-OCT-2001; 2001WO-US032045.
XX
PR   13-OCT-2000; 2000US-0687576.
PR   08-DEC-2000; 2000US-00733288.
PR   08-DEC-2000; 2000US-00733742.
PR   24-JAN-2001; 2001US-0269557P.
PR   16-MAR-2001; 2001US-0276791P.
PR   16-MAR-2001; 2001US-0276888P.
PR   06-APR-2001; 2001US-0281922P.
PR   24-APR-2001; 2001US-0286214P.
PR   30-APR-2001; 2001US-00847046.
PR   04-MAY-2001; 2001US-0288589P.
XX

PA   (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI   Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
XX
DR   WPI; 2002-471335/50.
DR   P-PSDB; ABG61813.
XX
PS   Claim 22; Page 311-312; 436pp; English.
XX

PT   The present invention relates to methods of detecting a prostate cancer-
PT   associated transcript in a cell from a patient. The method comprises
PT   contacting a biological sample from the patient with prostate cancer-
PT   associated polynucleotides (designated PC genes) that selectively
PT   hybridise to a sequence that is at least 80% identical to them. The

CC   Detecting a prostate cancer-associated polynucleotide sequences are differentially
CC   expressed in prostate cancer and are derived
CC   from the tissues of various organisms such as humans or other mammals
CC   (e.g. mice, sheep and dogs). The methods of the invention are useful for
CC   diagnosing and treating prostate cancer in mammals. The prostate cancer-
CC   associated genes are useful for diagnosing or treating prostate cancer,
CC   as well as for identifying modulators of prostate cancer or agents that
CC   inhibit prostate cancer. The nucleic acid sequences are particularly
CC   useful in gene therapy, as a vaccine or in antisense applications.
XX
CC   ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
CC   sequences
XX

SQ   Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

Query Match   100.0%; Score 1195; DB 6; Length 1195;
Best Local Similarity 100.0%; Pred. No. 4.4e-276;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 CCGAGACTCACGGTCAACGGTCAAGGCGGAGAGAGTGGGTGGCTGAAGCCATACTATTTATAG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CCGAGACTCACGGTCAACGGTCAAGGCGGAGAGAGTGGGTGGCTGAAGCCATACTATTTATAG 60

Qy   61 AATTAATGGAAAGCAGAAAAGACATCACAAAACCAAGAAGAGAACTTTGGAAAATGAAGCCTA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AATTAATGGAAAGCAGAAAAGACATCACAAAACCAAGAAGAGAACTTTGGAAAATGAAGCCTA 120

Qy   121 GGAGAAATTAGAAGAAGACGAGCGATTATTTGCATTAGGACACACGGAGAGACCAGCACATGCTAA 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGAGAAATTAGAAGAAGACGAGCGATTATTTGCATTAGGACACACGGAGAGACCAGCACATGCTAA 180

Qy   181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCCATGCTGCTGATGAATTGACTGCCCTT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCCATGCTGCTGATGAATTGACTGCCCTT 240

Qy   241 CAGAACTTCAGCACACACAGCAGGAACTCTTTCCACAGTGCACTTGCCAATTAAAATAGCTG 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CAGAACTTCAGCACACACAGCAGGAACTCTTTCCACAGTGCACTTGCCAATTAAAATAGCTG 300

Qy   301 CTATTATTAGCATCTGACTTTTCTTTACACTCTTCTGAGGGAGGGAAGTAATTCACCCTTTAG 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTATTATTAGCATCTGACTTTTCTTTACACTCTTCTGAGGGAGGGAAGTAATTCACCCTTTAG 360

Qy   361 CAACTTCCCATCAACAATATTTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CAACTTCCCATCAACAATATTTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy   421 CAATGGTTTCCATCACTCTTCTTGGCATTGGTTTACCTGCCCAGGTGTGTGATAGCAGCAATTG 480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CAATGGTTTCCATCACTCTTCTTGGCATTGGTTTACCTGCCCAGGTGTGTGATAGCAGCAATTG 480

Qy   481 TCCAACTTCATAATGGAACCAAGTAATAAGAAGAGTTTCCACACATTGGTTGGATAAGTGGATGT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TCCAACTTCATAATGGAACCAAGTAATAAGAAGAGTTTCCACACATTGGTTGGATAAGTGGATGT 540

Qy   541 TAACAAGAAAAGCAGTTTGGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCCATGCAATCAAC 600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TAACAAGAAAAGCAGTTTGGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCCATGCAATCAAC 600

Qy   601 GTCTGTCTTACCCAATGAGGCGGATCCTACAGATACAACAACTTGCTAAACTGGGCATATCAAC 660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTCTGTCTTACCCAATGAGGCGGATCCTACAGATACAACAACTTGCTAAACTGGGCATATCAAC 660

Qy   661 AGGTCCAACAAAATAAAGAGAAGATGCGTCGGATTGACAATGGACAATGAGCATGAGTAAGTTAGGTA 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 AGGTCCAACAAAATAAAGAGAAGATGCGTCGGATTGACAATGGACAATGAGCATGAGTAAGTTAGGTA 720

Qy   721 ATGTGTCTCCTGGGAATTGTGGGATTGGGCAATACTGGGCTCCTGTTGGGCCGTGACATCTATTC 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATGTGTCTCCTGGGAATTGTGGGATTGGGCAATACTGGGCTCCTGTTGGGCCGTGACATCTATTC 780

Qy   781 CATCTGTGAGTGGACTCTTTGACATGGACAGAGAAATTCACTATATCAGAGCAAGCCTAGGAA 840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 CATCTGTGAGTGGACTCTTTGACATGGACAGAGAAATTCACTATATCAGAGCAAGCCTAGGAA 840

Qy   841 TTGTTTCCCTTCTACTGGGCACAATACACGGCATTGATGATTTGCCTGGAATAAGTGGATAG 900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TTGTTTCCCTTCTACTGGGCACAATACACGGCATTGATGATTTGCCTGGAATAAGTGGATAG 900

Qy   901 ATATAAAAACAAATTTGTATGGTATAACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 ATATAAAAACAAATTTGTATGGTATAACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy   961 TTGTTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTCAGGGAGGAAGGATACTGA 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TTGTTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTCAGGGAGGAAGGATACTGA 1020

Qy   1021 AGATTAGACATGGTTGGGGAAGACGTCACCCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 AGATTAGACATGGTTGGGGAAGACGTCACCCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy   1081 TGTAGAATTACTGTTTACACACATTTTGTTCAATATGATATATTTATCACCAACATT 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TGTAGAATTACTGTTTACACACATTTTGTTCAATATGATATATTTATCACCAACATT 1140

Qy   1141 TCAAGTTTGTATTTGTTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAA 1195
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TCAAGTTTGTATTTGTTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAA 1195

RESULT 6
ACC95695
ID   ACC95695 standard; cDNA; 1195 BP.
XX
AC   ACC95695;
XX
DT   28-AUG-2003 (first entry)

XX
DE Prostate tumour specific cDNA sequence SEQ ID 878.
XX
KW Cytostatic; gene therapy; prostate-specific protein; PSP; human;
KW immune response; prostate cancer; ss.
XX
PD 14-NOV-2002.
XX
OS Homo sapiens.
XX
PN WO020289747-A2.
XX
PD 09-MAY-2002; 2002WO-US014753.
XX
PF 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
XX
PA (CORI-) CORIXA CORP.
XX
DR WPI: 2003-167130/16.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
PI McneilI PD, Houghton RL, Vinals Y De BassolsC, Foy TM, Watanabe Y;
PI Deng T;
XX
PT New prostate-specific proteins and genes, useful in gene therapy,
PT particularly for stimulating an immune response in a patient, or treating
PT prostate cancer in a patient, as well as for diagnosing prostate cancer
PT in a patient.
XX
PS Example 5; Page 617-618; 691pp; English.
XX
CC The present invention relates to novel prostate-specific proteins (PSP)
CC and their coding sequences. The PSPs and their coding sequences are
CC useful for stimulating an immune response in a patient, or for treating
CC prostate cancer in a patient and for determining, detecting or diagnosing
CC the presence of a cancer in a patient. The present sequence was used to
CC illustrate the invention
XX
SQ Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

```
Query Match             100.0%;  Score 1195;  DB 8;  Length 1195;
Best Local Similarity   100.0%;  Pred. No. 4.4e-276;
Matches 1195;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     1 CCGAGACTCACGGTCAAGCTGAAGGCGAGAAGTGGGTGGCGCCATACTATTTTTATAG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 CCGAGACTCACGGTCAAGCTGAAGGCGAGAAGTGGGTGGCGCCATACTATTTTTATAG 60

Qy    61 AATTAAATGGAAAGCAGAAAAAGACATCACAAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 AATTAAATGGAAAGCAGAAAAAGACATCACAAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy   121 GGAGAAATTTAGAAGAAGACGATTATTTTGGCATAAGGACAACGGGAGACCAGCCATGCTAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGAGAAATTTAGAAGAAGACGATTATTTTGGCATAAGGACAACGGGAGACCAGCCATGCTAA 180

Qy   181 AAAGACCTGTCGTCTTTGCATTGACCAAAACAGCCCATGCTGCTGTGATGAATTTGACTGCCCCTT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AAAGACCTGTCGTCTTTGCATTGACCAAAACAGCCCATGCTGCTGTGATGAATTTGACTGCCCCTT 240

Qy   241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy   301 CTATTATAGGCATCTCTGACTTTTTCTTTACACTCTTCTGAGGGAGTAATTCACCCTTTAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTATTATAGGCATCTCTGACTTTTTCTTTACACTCTTCTGAGGGAGTAATTCACCCTTTAG 360

Qy   361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy   421 CAATGGTTTCCATCACTCACTTCTTTGGCATTGGTTTACCTTGCCCAGGTGGTGTGATAGGCGAATTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CAATGGTTTCCATCACTCACTTCTTTGGCATTGGTTTACCTTGCCCAGGTGGTGTGATAGGCGAATTG 480

Qy   481 TCCAACTTCATAATGAACCAAGTATTAGAAGAGTTTCCACATTGGTTTGGATAAGTGGATGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TCCAACTTCATAATGAACCAAGTATTAGAAGAGTTTCCACATTGGTTTGGATAAGTGGATGT 540

Qy   541 TAACAAGAAAAGCAGTTTGGGCTTCTCCAGTTTCTTTTTTTGCTGTACTGCATCTCATTATA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TAACAAGAAAAGCAGTTTGGGCTTCTCCAGTTTCTTTTTTTGCTGTACTGCATCTCATTATA 600

Qy   601 GTCTGTCTTACCCAATGAGGCGGATCCTTACAGATACAAGTTGCTAAACTGGGGCATATCAAC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTCTGTCTTACCCAATGAGGCGGATCCTTACAGATACAAGTTGCTAAACTGGGGCATATCAAC 660

Qy   661 AGGTCCAACAAAATAAGAAGAAGATGCCTGGATTGAGCAGTGTTTGTGAGAATGGAGATTT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 AGGTCCAACAAAATAAGAAGAAGATGCCTGGATTGAGCAGTGTTTGTGAGAATGGAGATTT 720

Qy   721 ATGTGTCTTCTCGGGAATTGTGGGGATTGGCAATTACTGCCTCTCGTTGGCTGTGCATCTCATTC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATGTGTCTTCTCGGGAATTGTGGGGATTGGCAATTACTGCCTCTCGTTGGCTGTGCATCTCATTC 780

Qy   781 CATCTGTGAGTGACTCTTTGACATGGAAGGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 CATCTGTGAGTGACTCTTTGACATGGAAGGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy   841 TTGTTTCCCTTCTACTGGGGCACAAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TTGTTTCCCTTCTACTGGGGCACAAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy   901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTTCCTTCCAA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTTCCTTCCAA 960

Qy   961 TTGTTGTCCTGATATTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TTGTTGTCCTGATATTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy  1021 AGATTAGACATGGTTGGGAGACGTCACCAAAATTAACAAAAACTGAGATATGTTCCCAGT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 AGATTAGACATGGTTGGGAGACGTCACCAAAATTAACAAAAACTGAGATATGTTCCCAGT 1080

Qy  1081 TGTAGAATTACTGTTTCACACATTTTGTTCAATATTGATATATTTATCACCAACATT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 TGTAGAATTACTGTTTCACACATTTTGTTCAATATTGATATATTTATCACCAACATT 1140

Qy  1141 TCAAGTTTGTATTTGTTAATAAAATGAATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 TCAAGTTTGTATTTGTTAATAAAATGAATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195
```

RESULT 7
ADB75572
ID ADB75572 standard; cDNA; 1195 BP.
XX
AC ADB75572;
XX
DT 04-DEC-2003 (first entry)
XX
DE Prostate cancer marker cDNA.
XX
KW Prostate; cancer; cytostatic; gene therapy; marker; ss.
XX
OS Homo sapiens.
XX
PN WO200309814-A2.
XX
PD 06-FEB-2003.

XX
PF   25-JUL-2002; 2002WO-US023911.
XX
PR   25-JUL-2001; 2001US-0307982P.
PR   22-AUG-2001; 2001US-0314356P.
PR   25-SEP-2001; 2001US-0325020P.
PR   12-DEC-2001; 2001US-0341746P.
PR   05-MAR-2002; 2002US-0362158P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbatcheva B;
PI   Hoersh S, Kamatkar S, Wonsey AM, Glatt K, Zhao X, Anderson D;
XX
DR   WPI; 2003-248033/24.
XX
PS   Disclosure; SEQ ID NO 396; 99pp; English.
XX
PT   New nucleic acid molecule, useful for diagnosing or treating prostate
PT   cancer.
XX
CC   The invention relates to newly discovered cancer markers associated with
CC   the cancerous state of prostate cells. Also disclosed is a method of
CC   assessing whether a patient is afflicted with prostate cancer. The method
CC   of the invention involves assessing whether a patient is afflicted with
CC   prostate cancer by comparing the level of expression of a marker in a
CC   patient sample and the normal level of expression of the marker in a
CC   control non-prostate cancer sample, where a significant increase in the
CC   level of expression of the marker in the patient sample and the normal
CC   level indicates that the patient is afflicted with prostate cancer.
CC   Nucleic acids of the invention are useful for diagnosing or treating
CC   prostate cancer, and may be useful in gene therapy. Sequences given in
CC   ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

Query Match   100.0%; Score 1195; DB 10; Length 1195;
Best Local Similarity   100.0%; Pred. No. 4.4e-276;
Matches 1195; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy          1 CCGAGACTCACGGTCAAGCTAAGCGGAGAGAGTGGGGTGGGGTGAAGCCATACTATTTATAG 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGCGGAGAGAGTGGGGTGGGGTGAAGCCATACTATTTATAG 60

Qy         61 AATTAATGGAAAACCAGAAAAAGACATCACAAAACCAAGAAGAGAACTTTGGAAAATGAAGCCTA 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAACCAGAAAAAGACATCACAAAACCAAGAAGAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAAATTTAGAAGAAGAACGATTATTTGCATTAAGGACAACGGGAGAGAGAACCAGAATGCTAA 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAAATTTAGAAGAAGAACGATTATTTGCATTAAGGACAACGGGAGAGAGAACCAGAATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTGGACCAAAACAGCCCATGCTGATGAATTTGACTGCCCCTT 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTGGACCAAAACAGCCCATGCTGATGAATTTGACTGCCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGACACTCTTTCCCAATTAAAATAGCTG 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGACACTCTTTCCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACTCTTCGAGGGAAGTAATTCACCCTTTAG 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACTCTTCGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTTGGTCATCAACAAAGTCTTGC 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGCATTGGTTTACCTGCAGGGTGTGATAGCACCAATTG 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGCATTGGTTTACCTGCAGGGTGTGATAGCACCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTCCACATTGGTTGGATAAGTGGGATGT 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTCCACATTGGTTGGATAAGTGGGATGT 540

Qy        541 TAACAAGAAAAGCAAGTTTGGGCCTTCTCAGTTTCTTTTTTGCTGTGACGAATTTATA 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAAGCAAGTTTGGGCCTTCTCAGTTTCTTTTTTGCTGTGACGAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGGATCCTACGAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGGATCCTACGAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGAATGCCTGGATTGAGCATGAGTTGGGAGAATGGAGATTT 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGAATGCCTGGATTGAGCATGAGTTGGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGGATTGCAATACTGGCCTCTGTTGGCTGTGACATCTATTC 780
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGGATTGCAATACTGGCCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAATTCACTATATCAGAGACGACAAGCTAGGAA 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAATTCACTATATCAGAGACGACAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAAATTTGTATGGTATACACCTCCACACTTTTATGAATAGCTGTGTTTCTTCCAA 960
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAAATTTGTATGGTATACACCTCCACACTTTTATGAATAGCTGTGTTTCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGGAAGACGTCACCAAAATTAACAAAAACTGAGATATGTTCCCAGT 1080
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGGAAGACGTCACCAAAATTAACAAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAAATTACTGTTTTACACACATTTTTGTTCAATATTTGATATTTATTCACCCAACATT 1140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAAATTACTGTTTTACACACATTTTTGTTCAATATTTGATATTTATTCACCCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTAATTCAAGGAAAAAAAAAAAAAAAAA 1195
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTAATTCAAGGAAAAAAAAAAAAAAAAA 1195
```

RESULT 8
ADB14328
ID   ADB14328 standard; cDNA; 1195 BP.
XX
AC   ADB14328;
XX
DT   18-DEC-2003 (first entry)
XX
DE   Human prostate specific full length cDNA P789P.
XX
KW   prostate specific cDNA; cytostatic; immunostimulant;
KW   gene therapy; cell therapy; vaccine; T-cell epitope;
KW   class I major histocompatibility complex allele; MHC; prostate cancer;
KW   tumour; antigen presenting cell.
OS   Homo sapiens.
XX
PN   US2003185830-A1.
XX
PD   02-OCT-2003.
XX
PF   12-NOV-2002; 2002US-00294025.

XX
PR   25-FEB-1997;
PR   01-AUG-1997;   97US-0080604.
PR   09-FEB-1998;   97US-0094804.
PR   25-FEB-1998;   98US-0009056.
PR   14-JUL-1998;   98US-00030607.
PR   23-SEP-1998;   98US-0115453.
PR   15-JAN-1999;   98US-0159812.
PR   09-APR-1999;   99US-0232149.
PR   12-NOV-1999;   99US-0288946.
PR   13-JUL-1999;   99US-0352616.
PR   18-NOV-1999;   99US-0439313.
PR   14-JAN-2000;   2000US-0443686.
PR   27-MAR-2000;   2000US-00383672.
PR   09-MAY-2000;   2000US-00536857.
PR   12-MAY-2000;   2000US-00568100.
PR   13-JUN-2000;   2000US-00570737.
PR   27-JUN-2000;   2000US-00593793.
PR   09-AUG-2000;   2000US-00605783.
PR   29-AUG-2000;   2000US-00636215.
PR   06-SEP-2000;   2000US-00651236.
PR   02-OCT-2000;   2000US-00657279.
PR   10-OCT-2000;   2000US-00679426.
PR   09-NOV-2000;   2000US-00885166.
PR   12-JAN-2001;   2000US-00709729.
PR   09-FEB-2001;   2001US-00759143.
PR   09-MAY-2001;   2001US-00780669.
PR   29-JUN-2001;   2001US-00852911.
PR   10-DEC-2001;   2001US-0095814.
PR   09-MAY-2002;   2001US-00012896.
PR   2002US-00144678.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Xu J, Stolk JA, Kalos MD;
XX
DR   WPI: 2003-756193/71.
DR   P-PSDB; ADB14329.
XX
PT   New isolated polypeptide for use in a vaccine for stimulating an immune
PT   response, or for diagnosis cancer, preferably prostate
PT   cancer.
XX
PS   Example 5; Page; 101pp; English.
XX
CC   The invention relates to an isolated polypeptide comprising no more than
CC   11-542 amino acids of ADB13563 comprising a sequence ADB14487. The
CC   peptides comprise a fragment ADB13563 of that contain naturally processed
CC   T-cell epitopes for 3 class I major histocompatibility complex (MHC)
CC   alleles. ADB13563 is a polypeptide encoded by a human prostate specific
CC   cDNA, one of 648 disclosed as new. Also included are nucleic acids
CC   encoding the proteins and peptides, expression vectors, a host cell
CC   transformed with the vector, an isolated antibody (or antigen binding
CC   fragment) that specifically binds to the protein or peptide, detecting
CC   the presence of a cancer in a patient (comprising contacting a patient
CC   sample with a binding agent that binds to the peptides or a polypeptide
CC   appearing as ADB13558, detecting the amount of polypeptide that binds to
CC   the agent and comparing the amount of polypeptide to a predetermined cut-
CC   off value to determine the presence of cancer), a fusion protein
CC   comprising the peptides or proteins, stimulating or expanding T cells
CC   specific for a tumour protein comprising contacting T cells with the
CC   peptides or the isolated T cell population, treating prostate cancer in a
CC   patient comprising administering a composition comprising the peptides,
CC   nucleic acids, antibodies or compounds, determining the presence of a
CC   cancer in a patient and treating prostate cancer in a patient comprising
CC   incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated
CC   from a patient with the peptides or antigen presenting cells that express
CC   encoding the proteins so that the T cells proliferate, and administering the
CC   proliferated T cells to the patient. The peptides (or an oligonucleotide
CC   that hybridies to nucleic acid encoding them), is used to detect the
CC   presence of cancer in a patient. The peptides, nucleic acids encoding, or
CC   antigen-presenting cells expressing the nucleic acid, are used to
CC   stimulate or expand T cells specific for a tumour protein. The peptides,
CC   nucleic acids, antibodies, fusion proteins, T cell populations or antigen

presenting cells are used to stimulate an immune response or treat
prostate cancer in a patient. The present sequence is a known cDNA
showing sequence similarity to one of the disclosed human prostate
specific cDNAs. Note: Except where otherwise indicated, the sequence data
for this patent did not form part of the printed specification, but was
obtained in electronic format directly from USPTO at
seqdata.uspto.gov/sequence.html?DocID=2003018S830.
XX
SQ   Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

Query Match   100.0%; Score 1195; DB 10; Length 1195;
Best Local Similarity   100.0%; Pred. No. 4.4e-276;
Matches 1195; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CCGAGACTCACGGTCAAGCTAAGGCGGAAGAGTGGGTGGCTGAAGCCATACTACTTTTATAG   60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CCGAGACTCACGGTCAAGCTAAGGCGGAAGAGTGGGTGGCTGAAGCCATACTACTTTTATAG   60

Qy   61 AATTAATGGAAAAGCAGAAAAAGACATCACAAAACCAAGAAGAGAAGACTTTGGAAAATGAAGCCTA   120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AATTAATGGAAAAGCAGAAAAAGACATCACAAAACCAAGAAGAGAAGACTTTGGAAAATGAAGCCTA   120

Qy   121 GGAGAAAATTTAGAGAAGAGACGATTATTTGCATTAAGGACACAGGGAGAGACCAGCATGCTAA   180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGAGAAAATTTAGAGAAGAGACGATTATTTGCATTAAGGACACAGGGAGAGACCAGCATGCTAA   180

Qy   181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT   240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT   240

Qy   241 CAGAACTTCAGCACACACAGGAACTCTTCCACAGTGGCACTTGCCAATTAAAATAGCTG   300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CAGAACTTCAGCACACACAGGAACTCTTCCACAGTGGCACTTGCCAATTAAAATAGCTG   300

Qy   301 CTATTATTAGCATCTCTGACTTTTCTTTTACACTCTTCTGAGGGAGAAGTAAATTCACCCTTTAG   360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTATTATTAGCATCTCTGACTTTTCTTTTACACTCTTCTGAGGGAGAAGTAAATTCACCCTTTAG   360

Qy   361 CAACTTCCCATCACACAATATTTTTATAAAAATTCCAATCCTGGTCATCACAAAGTCTTGC   420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CAACTTCCCATCACACAATATTTTTATAAAAATTCCAATCCTGGTCATCACAAAGTCTTGC   420

Qy   421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGATAGCACGCAANTTG   480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGATAGCACGCAANTTG   480

Qy   481 TCCAACTTCATTAATGGAACCAAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT   540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TCCAACTTCATTAATGGAACCAAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT   540

Qy   541 TAACAAGAAAAGCAGTTTGGGGCTTCTCAGTTTCTTTTTTGGCTGCTACTGCATGCAAATTATA   600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TAACAAGAAAAGCAGTTTGGGGCTTCTCAGTTTCTTTTTTGGCTGCTACTGCATGCAAATTATA   600

Qy   601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAAACTGGGCAATATCAAC   660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAAACTGGGCAATATCAAC   660

Qy   661 AGGTCCAACAAAATAAAGAAGAATGCCCTGGATTGAGCATGATGAGTTTGGAGAATGAGATTT   720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 AGGTCCAACAAAATAAAGAAGAATGCCCTGGATTGAGCATGATGAGTTTGGAGAATGAGATTT   720

Qy   721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC   780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC   780

Qy   781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCACGAGCAAGCTAGGAA   840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCACGAGCAAGCTAGGAA   840

Qy   841 TTGTTTCCCTTCTACTGGGCCACAATACACGCAATGATTTTTGCCTGGAATAAGTGGATAG   900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TTGTTTCCCTTCTACTGGGCCACAATACACGCAATGATTTTTGCCTGGAATAAGTGGATAG   900

```
Qy    901 ATATAAAACAAATTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTCCTTCCAA  960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ATATAAAACAAATTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTCCTTCCAA  960

Qy    961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGTACTGA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGTACTGA 1020

Qy   1021 AGATTAGACATGGTTGGGAAGGACGTCACCAAAAATTAACAAAACTGAGATAGTTCCCAGT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 AGATTAGACATGGTTGGGAAGGACGTCACCAAAAATTAACAAAACTGAGATAGTTCCCAGT 1080

Qy   1081 TGTAGAATTACTGTTTACACACATTTTGTTCAATATTGATATATTTTATCACCAACACATT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TGTAGAATTACTGTTTACACACATTTTGTTCAATATTGATATATTTTATCACCAACACATT 1140

Qy   1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195
```

RESULT 9

AAD63162

ID   AAD63162 standard; DNA; 1195 BP.
XX
AC   AAD63162;
XX
DT   12-FEB-2004 (first entry)
XX
DE   Human STEAP (six transmembrane epithelial antigen of the prostate) DNA.
XX
KW   Human; breast cancer; metastasis; differential modulation; therapy;
KW   STEAP; six transmembrane epithelial antigen of the prostate; ds.
XX
OS   Homo sapiens.
XX
PN   US2003190656-A1.
XX
PD   09-OCT-2003.
XX
PF   21-MAR-2003; 2003US-00393590.
XX
PR   29-MAR-2002; 2002US-0368789P.
XX
PA   (WANG/) WANG Y.
XX
PI   Wang Y;
XX
DR   WPI; 2003-831621/77.
XX
PT   The present invention relates to a method of prognosticating metastasis
PT   in a breast cancer patient comprises identifying differential modulation
PT   of expression of the same genes in a normal population in combination of
PT   genes.
XX
PS   Example 2; Page 54-55; 0pp; English.
XX
CC   The present invention relates to a method of prognosticating metastasis
CC   in a breast cancer patient involves identifying differential modulation
CC   of each gene relative to the expression of the same genes in a normal
CC   population of genes. The invention is useful for
CC   prognosticating breast cancer in a patient. The present sequence is human
CC   STEAP (six transmembrane epithelial antigen of the prostate) DNA used to
CC   illustrate the method of the invention
XX
SQ   Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

Query Match   100.0%; Score 1195; DB 10; Length 1195;
Best Local Similarity   100.0%; Pred. No. 4.4e-276;
Matches 1195; Conservative   0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 CCGAGACTCACGGTCAAGCTAAGGCGGAAGAGTGGGTGGCTGAAGGCATACTATTTTATAG  60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 CCGAGACTCACGGTCAAGCTAAGGCGGAAGAGTGGGTGGCTGAAGGCATACTATTTTATAG  60

Qy   61 AATTAATGGAAAAGCAGAAAAAGACATCACAACAACCAAGAAGAAGAACTTTGGAAAATGA 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AATTAATGGAAAAGCAGAAAAAGACATCACAACAACCAAGAAGAAGAACTTTGGAAAATGA 120

Qy  121 GGAGAAAATTTAGAAGCAGAAGACGATTATTTGCATGAAGACGAAGAGGACCAGCATGCTA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GGAGAAAATTTAGAAGCAGAAGACGATTATTTGCATGAAGACGAAGAGGACCAGCATGCTA 180

Qy  181 AAAGACCTGTGCTTTTGCATTTGCACCAAAACAGCCCCATGCTGATGAATTTGACTGCCTT 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 AAAGACCTGTGCTTTTGCATTTGCACCAAAACAGCCCCATGCTGATGAATTTGACTGCCTT 240

Qy  241 CAGAACTTCAGCACACACAGGAACTCTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 CAGAACTTCAGCACACACAGGAACTCTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy  301 CTATTATAGCATCTTCTGACTTTTCTTTACACTCTTCTGAGGGGAAGTAATTCACCCTTTAG 360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 CTATTATAGCATCTTCTGACTTTTCTTTACACTCTTCTGAGGGGAAGTAATTCACCCTTTAG 360

Qy  361 CAACTTCCCATCAACAATATTTTTATAAAAATTCCAAATCCTGGTCATCAACAAAGTCTTGC 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 CAACTTCCCATCAACAATATTTTTATAAAAATTCCAAATCCTGGTCATCAACAAAGTCTTGC 420

Qy  421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGTGTGATAGCAGCAATTG 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGTGTGATAGCAGCAATTG 480

Qy  481 TCCAAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 TCCAAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy  541 TAACAAGAAAAGCAGTTTGGGGCTTCTCAGTTTCTTTTTGCTGTACTGCATGCAAATTTATA 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 TAACAAGAAAAGCAGTTTGGGGCTTCTCAGTTTCTTTTTGCTGTACTGCATGCAAATTTATA 600

Qy  601 GTCTGTCTTACCCAAATGAGGCGGATCCTACAGATACAAGTGGTCTAAACTGGGCATATCAAC 660
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 GTCTGTCTTACCCAAATGAGGCGGATCCTACAGATACAAGTGGTCTAAACTGGGCATATCAAC 660

Qy  661 AGGTCCAACAAAAATAAAAGAAGATCCCTGGATTGAGCATGAATGGTTGGAGAAATGGAGATTT 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 AGGTCCAACAAAAATAAAAGAAGATCCCTGGATTGAGCATGAATGGTTGGAGAAATGGAGATTT 720

Qy  721 ATGTCTCTGGGAATTGTGGGGGATTGGCAATGACTGGCTCGTTGGCTCGTTGGCTGACATCTATTC 780
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 ATGTCTCTGGGAATTGTGGGGGATTGGCAATGACTGGCTCGTTGGCTCGTTGGCTGACATCTATTC 780

Qy  781 CATCTGTGAGTGACTCTTTGACATGGAGGAATTCACTATTATTCAGAGCCAAGCTAGGAA 840
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 CATCTGTGAGTGACTCTTTGACATGGAGGAATTCACTATTATTCAGAGCCAAGCTAGGAA 840

Qy  841 TTGTTTCCCTTCTACTGGGCACAATACACGCCATTGATTTTTTGCCTGGGAATAAGTGGATAG 900
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 TTGTTTCCCTTCTACTGGGCACAATACACGCCATTGATTTTTTGCCTGGGAATAAGTGGATAG 900

Qy  901 ATATAAAACAAATTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTCCTTCCAA 960
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 ATATAAAACAAATTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTCCTTCCAA 960

Qy  961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGTACTGA 1020
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGTACTGA 1020

Qy 1021 AGATTAGACATGGTTGGGAAGGACGTCACCAAAAATTAACAAAACTGAGATAGTTCCCAGT 1080
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 AGATTAGACATGGTTGGGAAGGACGTCACCAAAAATTAACAAAACTGAGATAGTTCCCAGT 1080

Qy 1081 TGTAGAATTACTGTTTACACACATTTTGTTCAATATTGATATATTTTATCACCAACACATT 1140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 TGTAGAATTACTGTTTACACACATTTTGTTCAATATTGATATATTTTATCACCAACACATT 1140
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Db   1081  TGTAGAATTACTGTTTACACACATTTTTGTTCAATTATATATTTATCACCAACATT 1140

Qy   1141  TCAAGTTTGTATTTGTTAATAAAATGATTAATTCAAGGAAAAAAAAAAAAAAAAAA 1195
           ||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  TCAAGTTTGTATTTGTTAATAAAATGATTAATTCAAGGAAAAAAAAAAA 1195
```

RESULT 10
AAD62763
ID   AAD62763 standard; DNA; 1195 BP.
XX
AC   AAD62763;
XX
DT   12-FEB-2004 (first entry)
XX
DE   Human STEAP (six transmembrane epithelial antigen of the prostate) DNA.
XX
KW   Human; cancer; differential modulation; gene expression profile; STEAP;
KW   six transmembrane epithelial antigen of the prostate; ds.
XX
OS   Homo sapiens.
XX
PN   US20031947331-A1.
XX
PD   16-OCT-2003.
XX
PF   21-MAR-2003; 2003US-00393567.
XX
PR   29-MAR-2002; 2002US-0368667P.
XX
PA   (WANG/) WANG Y.
XX
PI   Wang Y;
XX
DR   WPI; 2003-844450/78.
XX
PT   Diagnosing cancer comprises identifying differential modulation of each
PT   gene (relative to the expression of the same genes in a normal
PT   population) in a combination of genes.
XX
PS   Claim 4; Page 54-55; 0pp; English.
XX
CC   The invention relates to a method for diagnosing cancer. The method
CC   comprising identifying differential modulation of each gene (relative to
CC   the expression of the same genes in a normal population) in a combination
CC   of genes. The method, diagnostic portfolio and the kit are useful in
CC   diagnosing cancer. The present sequence is human STEAP (six
CC   transmembrane epithelial antigen of the prostate) DNA used to illustrate
CC   the method of the invention
XX
SQ   Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

Query Match   100.0%; Score 1195; DB 10; Length 1195;
Best Local Similarity   100.0%; Pred. No. 4.4e-276;
Matches 1195; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAACCCACTACTTTTATAG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAACCCACTACTTTTATAG 60

Qy   61 AATTAATGGAAAACAGAGAAAAGACATCACAAAACCAAGAGAGTGGGTGGCTGAACCCA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AATTAATGGAAAACAGAGAAAAGACATCACAAAACCAAGAGAGAACTTTGGAAAATGAAGCCTA 120

Qy   121 GGAGAAATTTAGAAGAGAAGAGATATATTTTGCATAAGGACACACGGGAGAGACCAGCAGCATGCTAA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGAGAAATTTAGAAGAAGAGATATTTTTGCATAAGGACACACGGGAGAGACCAGCATGCTAA 180

Qy   181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGCTGATGAATTTGACTGCCCCTT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGCTGATGAATTTGACTGCCCCTT 240
```

```
Qy    241  CAGAACTTCAGCACACACAGAGAAACTCTTTCCACAGTGCACTTGCCAATTAAAATAGCTG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  CAGAACTTCAGCACACACAGAGAAACTCTTTCCACAGTGCACTTGCCAATTAAAATAGCTG 300

Qy    301  CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAAATTCACCCTTTAG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAAGTCTTGC 360

Qy    361  CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAAGTCTTGC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAAGTCTTGC 420

Qy    421  CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy    481  TCCAACTTCATAATGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  TCCAACTTCATAATGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy    541  TAACAAGAAAAGCAGTTTGGGGCTTCTCAGTTTCTTTTTGGTACTGCAATTTATA 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  TAACAAGAAAAGCAGTTTGGGGCTTCTCAGTTTCTTTTTGGTACTGCAATTTATA 600

Qy    601  GTCTGTCTTACCCAATGAGGGGATCCTTACAGATACAAGTGCCATATCAAC 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  GTCTGTCTTACCCAATGAGGGGATCCTTACAGATACAAGTGCCATATCAAC 660

Qy    661  AGGTCCAACAAAATAAAGAAGAATGCCTGGATTGAGCGATGAGATGGAGATTT 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  AGGTCCAACAAAATAAAGAAGAATGCCTGGATTGAGCGATGAGATGGAGATTT 720

Qy    721  ATGTGTCTCTGGGAATTGTGGGGATTGGCAATACTGGCGCTCTTGGTGCATCTATTC 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  ATGTGTCTCTGGGAATTGTGGGGATTGGCAATACTGGCGCTCTTGGTGCATCTATTC 780

Qy    781  CATCTGTCTTACCCAATGAGGGGATCCTTACAGATACAAGTGCCATATCAAC 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  CATCTGTCTTACCCAATGAGGGGATCCTTACAGATACAAGTGCCATATCAAC 840

Qy    841  TTGTTTCCCTTCTACTGGGGCACAATACACCGCCATTGATGTTTTTGCCTGGAATAAGTGGATAG 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  TTGTTTCCCTTCTACTGGGGCACAATACACCGCCATTGATGTTTTTGCCTGGAATAAGTGGATAG 900

Qy    901  ATATAAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  ATATAAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy    961  TTGTTTGTCCTCGATATATTAAAGCATACTATTCCTCGCCATGCTTGAGGACGAGATACTGA 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  TTGTTTGTCCTCGATATATTAAAGCATACTATTCCTCGCCATGCTTGAGGACGAGATACTGA 1020

Qy   1021  AGATTAGACATGGTTGGGAAGACGTCACCAAAAATTACAAAAACTGAGATATGTTCCCAGT 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  AGATTAGACATGGTTGGGAAGACGTCACCAAAAATTAACAAAAACTGAGATATGTTCCCAGT 1080

Qy   1081  TGTAGAATTACTGTTTACACACATTTTTGTTCAATTATATATTTATCACCAACATT 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  TGTAGAATTACTGTTTACACACATTTTTGTTCAATTATATATTTATCACCAACATT 1140

Qy   1141  TCAAGTTTGTATTTGTTAATAAAATGATTAATTCAAGGAAAAAAAAAAAAAAAAAA 1195
           ||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  TCAAGTTTGTATTTGTTAATAAAATGATTAATTCAAGGAAAAAAAAAAA 1195
```

RESULT 11
ADG26744
ID   ADG26744 standard; cDNA; 1195 BP.
XX
AC   ADG26744;
XX
DT   26-FEB-2004 (first entry)
XX

```
DE   Human prostate-specific cDNA #678.
XX
XX
KW   Human; prostate-specific polypeptide; gene; ss; prostate cancer;
KW   cytostatic.
XX
XX
OS   Homo sapiens.
XX
XX
PN   US20031S7089-A1.
XX
PD   21-AUG-2003.
XX
PF   09-MAY-2002; 2002US-0014678.
XX
PR   25-FEB-1997; 97US-0080609.
PR   01-AUG-1997; 97US-0090480.
PR   09-FEB-1998; 98US-0020095.
PR   25-FEB-1998; 98US-0003060.
PR   14-JUL-1998; 98US-0011545.
PR   23-SEP-1998; 98US-0015981.
PR   15-JAN-1999; 99US-0023214.
PR   09-APR-1999; 99US-0028894.
PR   13-JUL-1999; 99US-0035261.
PR   12-NOV-1999; 99US-0043931.
PR   18-NOV-1999; 99US-0044538.
PR   14-JAN-2000; 2000US-0048367.
PR   27-MAR-2000; 2000US-0053685.
PR   09-MAY-2000; 2000US-0056810.
PR   12-MAY-2000; 2000US-0057073.
PR   13-JUN-2000; 2000US-0059379.
PR   27-JUN-2000; 2000US-0060578.
PR   09-AUG-2000; 2000US-0063621.
PR   29-AUG-2000; 2000US-0065123.
PR   06-SEP-2000; 2000US-0065727.
PR   02-OCT-2000; 2000US-0067942.
PR   10-OCT-2000; 2000US-0068516.
PR   09-NOV-2000; 2000US-0070972.
PR   12-JAN-2001; 2001US-0075914.
PR   09-FEB-2001; 2001US-0078066.
PR   09-MAY-2001; 2001US-0085291.
PR   29-JUN-2001; 2001US-0089581.
PR   10-DEC-2001; 2001US-0012896.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
PI   Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
PI   Carter D, Li SX, Wang A, Skelky YAW, Hepler WT, Hural J;
PI   Mcneill PD, Houghton RL, Vinals Y De Bassolsc, Foy TM, Watanabe Y;
PI   Meagher MJ, Deng T;
XX
DR   WPI; 2003-777973/73.
DR   P-PSDB; ADG26745.
XX
PT   New polynucleotides encoding prostate specific polypeptides isolated from
PT   a human prostate tumor cDNA library are useful to diagnose and treat
PT   cancer particularly prostate cancer.
XX
PS   Example 5; SEQ ID NO 878; 99pp; English.
XX
CC   The invention relates to human prostate-specific polypeptides and the
CC   polynucleotides encoding them. The invention also relates to an isolated
CC   antibody or its antigen-binding fragment that specifically binds a
CC   polypeptide of the invention, a method of detecting cancer in a patient
CC   comprising contacting a biological sample of the patient with an agent
CC   that binds a prostate-specific polypeptide and comparing the amount of
CC   bound polypeptide compared to a predetermined cut-off value and a fusion
CC   protein comprising a prostate-specific polypeptide. The sequences of the
CC   invention are used to diagnose and treat cancer, particularly prostate
CC   cancer. This sequence represents a human prostate-specific
CC   polypeptide of the invention. Note: The sequence data for this patent did
CC   not form part of the printed specification but was obtained in electronic
CC   format directly from USPTO at seqdata.uspto.gov/sequence.html.
```

```
SQ   Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

Query Match            100.0%;  Score 1195;  DB 10;  Length 1195;
Best Local Similarity  100.0%;  Pred. No. 4.4e-276;
Matches 1195;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy     1 CCGAGACTCACCGGTCAAGGTCAAGCTAAGGCGGAGAGAGTGGTTGGGCTGAAGGCCATACTATTTTATAG 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 CCGAGACTCACCGGTCAAGGTCAAGCTAAGGCGGAGAGAGTGGTTGGGCTGAAGGCCATACTATTTTATAG 60

Qy    61 AATTAATGGAAAAGCAGAAAAAGCATCACAAAACCAAGAAGAACTTTGAAAATGAAGCCTA 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 AATTAATGGAAAAGCAGAAAAAGCATCACAAAACCAAGAAGAACTTTGAAAATGAAGCCTA 120

Qy   121 GGAGAAATTTAGAAGAAGACGAGATTAATTTGCATAAGGACACGGGAAGACCAGCATGCTAA 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGAGAAATTTAGAAGAAGACGAGATTAATTTGCATAAGGACACGGGAAGACCAGCATGCTAA 180

Qy   181 AAAGACCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGTGATGAATTTGACTGGCCCTT 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AAAGACCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGTGATGAATTTGACTGGCCCTT 240

Qy   241 CAGAACTTCAGCACACACACAGGAACTCTTTCCACAGTGGCCACTTGCCAATTAAAATAGTG 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CAGAACTTCAGCACACACACAGGAACTCTTTCCACAGTGGCCACTTGCCAATTAAAATAGTG 300

Qy   301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGGAAGTAATTCACCCTTTAG 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGGAAGTAATTCACCCTTTAG 360

Qy   361 CAACTTCCCATCAACAATAATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CAACTTCCCATCAACAATAATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy   421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy   481 TCCAACTTCATAATGGAACCCAAGTATAAGAAGAGTTTCCACATTGGTTGGATAAGTCTTGC 540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TCCAACTTCATAATGGAACCCAAGTATAAGAAGAGTTTCCACATTGGTTGGATAAGTGATGT 540

Qy   541 TAACAAGAAAAGCAAGTTTGGGGCTTCTCAGTTTCTTTTTTGCGTACTGCATGCAATTTATA 600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TAACAAGAAAAGCAAGTTTGGGGCTTCTCAGTTTCTTTTTTGCGTACTGCATGCAATTTATA 600

Qy   601 GTCTGTGTTCTTACCCAATGAGCGGATCCTACAGAATACAAGTTGCTAAACTGGGCATATCAAC 660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTCTGTGTTCTTACCCAATGAGCGGATCCTACAGAATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy   661 AGGTCCAACAAAAATAAAAGAAGATGCCCTGGATTGAGCATGCATGAGAATGGGAAGATTT 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 AGGTCCAACAAAAATAAAAGAAGATGCCCTGGATTGAGCATGCATGAGAATGGGAAGATTT 720

Qy   721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCCTCGTTGGCTGGCATCTATTC 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCCTCGTTGGCTGGCATCTATTC 780

Qy   781 CATCTCTGTGAGTGACTCTTTGACACATGGAGAGAGCAGCTAGGAA 840
         |||||||||||||||||||||||||||||||||||||||||||||
Db   781 CATCTCTGTGAGTGACTCTTTGACACATGGAGAGAGCAGCTAGGAA 840

Qy   841 TTGTTTCCCTTCTACTGGGGCACAATACAGGCATTGATATTTGCCTGGATTAAGTGGATAG 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TTGTTTCCCTTCTACTGGGGCACAATACAGGCATTGATATTTGCCTGGATTAAGTGGATAG 900

Qy   901 ATATAAAAACAAATTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 ATATAAAAACAAATTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy   961 TTGTTGTCCTGATATTTAAAAGCATAATTCTCCCATGCTTGAGGAAGAGATACTGA 1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TTGTTGTCCTGATATTTAAAAGCATAATTCTCCCATGCTTGAGGAAGAGATACTGA 1020
```

RESULT 12
ADN39812

```
ID   ADN39812 standard; cDNA; 1195 BP.
XX
AC   ADN39812;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:C184.
XX
KW   Human; differential expression; cancer; angiogenic disorder;
KW   fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW   inflammatory disease; autoimmune disease;
KW   retinal neovascularisation syndrome; scarring; uterine fibroid;
KW   detection; diagnosis; prognosis; drug screening; drug targeting;
KW   wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW   vulnerary; gene therapy; vaccine; gene; ss.
XX
OS   Homo sapiens.
XX
XX
PN   WO2003042661-A2.
XX
PD   22-MAY-2003.
XX
PF   13-NOV-2002; 2002WO-US036810.
XX
PR   13-NOV-2001; 2001US-0350666P.
PR   21-NOV-2001; 2001US-0332464P.
PR   29-NOV-2001; 2001US-0343393P.
PR   03-DEC-2001; 2001US-0335394P.
PR   14-DEC-2001; 2001US-0340376P.
PR   08-JAN-2002; 2002US-0347211P.
PR   10-JAN-2002; 2002US-0347349P.
PR   08-FEB-2002; 2002US-0355250P.
PR   13-FEB-2002; 2002US-0356714P.
PR   20-FEB-2002; 2002US-0359077P.
PR   29-MAR-2002; 2002US-0368809P.
PR   04-APR-2002; 2002US-0370110P.
PR   12-APR-2002; 2002US-0372246P.
PR   05-JUN-2002; 2002US-0386614P.
PR   16-JUL-2002; 2002US-0396839P.
PR   22-JUL-2002; 2002US-0397775P.
PR   22-JUL-2002; 2002US-0397845P.
PR   09-SEP-2002; 2002US-0409450P.
XX
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI   Afar D, Aziz N, Ginsburg WM, Gish KC, Glynne R, Hevezi PA;
PI   Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX
DR   WPI; 2003-468649/44.
DR   P-PSDB; ADN40029.
XX
PT   Determining the presence or absence of a pathological cell in a patient,
PT   useful for diagnosing, prognosing or treating cancer, comprises detecting
PT   a nucleic acid in a biological sample.
XX
PS   Claim 8; SEQ ID NO C184; 1385pp; English.
XX
```

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CC   The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC   whose expression is upregulated or downregulated in specific cancers or
CC   other diseases such as angiogenic or fibrotic disorders, and to methods
CC   of determining the presence or absence of a pathological cell in a
CC   patient by detecting a nucleic acid at least 80% identical to those of
CC   the invention. The
CC   invention also relates to expression vectors and host cells comprising a
CC   nucleic acid of the invention; antibodies which specifically bind a
CC   polypeptide of the invention; use of such antibodies for drug targeting;
CC   and methods of screening for modulators of activity or expression of the
CC   polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC   antibodies and methods are useful for diagnosing, prognosing and treating
CC   cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC   atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC   neovascularisation syndromes, scarring and uterine fibroids. They may
CC   also be useful in wound healing and in contraception. The present
CC   sequence represents a nucleic acid sequence of the invention.
XX
SQ   Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;
XX
```

```
Query Match             100.0%;  Score 1195;  DB 11;  Length 1195;
Best Local Similarity   100.0%;  Pred. No. 4.4e-276;
Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy    1 CCGAGACTCACGGTCAAGCTAAGGCGCGAAGAGTGGGTGGGTGGCCTGAAGCCATACTATTTTATAG   60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 CCGAGACTCACGGTCAAGCTAAGGCGCGAAGAGTGGGTGGGTGGCCTGAAGCCATACTATTTTATAG   60

Qy   61 AATTAATGGAAAGCACGAAAAGACAATCACAAACCAAGAAGAAGAACTTTGGAAAAATGAAGCCTA  120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AATTAATGGAAAGCACGAAAAGACAATCACAAACCAAGAAGAAGAACTTTGGAAAAATGAAGCCTA  120

Qy  121 GGAGAAAATTTAGAAGAAGACGAGATTATTTGCATAAGGACACACGGGGAGAGAGACCATGCTAA  180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GGAGAAAATTTAGAAGAAGACGAGATTATTTGCATAAGGACACACGGGGAGAGAGACCATGCTAA  180

Qy  181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGACCCCATGCTTGATGAAATTTGACTGCCCTT  240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGACCCCATGCTTGATGAAATTTGACTGCCCTT  240

Qy  241 CAGAGACTTCAGCACACACAGGAACCTCTTTCCACACAGTGCCACTTGCCAATTAAAATAGCTG  300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 CAGAGACTTCAGCACACACAGGAACCTCTTTCCACACAGTGCCACTTGCCAATTAAAATAGCTG  300

Qy  301 CTATTATAGACAATCTCTGACTTTTCTTTACACTCTCTTGAGGGAAGTAATTCACCCTTAG  360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 CTATTATAGACAATCTCTGACTTTTCTTTACACTCTCTTGAGGGAAGTAATTCACCCTTAG  360

Qy  361 CAAACTTCCCATCACACAATATTTTATAAAAATTCAAATCCTGGTCATCAACAAAGTCTTGC  420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 CAAACTTCCCATCACACAATATTTTATAAAAATTCAAATCCTGGTCATCAACAAAGTCTTGC  420

Qy  421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCCAGCAATTG  480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCCAGCAATTG  480

Qy  481 TCCAACTTCATTAAATGGAACCAAAGTATAAGAGAAGTTTCCACAATGGTTGGATAAGTGGATGT  540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 TCCAACTTCATTAAATGGAACCAAAGTATAAGAGAAGTTTCCACAATGGTTGGATAAGTGGATGT  540

Qy  541 TAACAAGAAAAGCAGTTTGGGCTTCAGTTTCTTCAGTTTGTTGTACTGCACTGCCAATTTATA  600
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 TAACAAGAAAAGCAGTTTGGGCTTCAGTTTCTTCAGTTTGTTGTACTGCACTGCCAATTTATA  600

Qy  601 GTCTCGTCTTACCCAATGAGCGGCGATCCTACAGATACAGATGTTGCTAAAACTGGGCATATCAAC  660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 GTCTCGTCTTACCCAATGAGCGGCGATCCTACAGATACAGATGTTGCTAAAACTGGGCATATCAAC  660

Qy  661 AGGTCCAACAAAATAAAGAAGAATGGCCTGGATTGAGCATGATGTTTGGAGAATGGAGAGATTT  720
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 AGGTCCAACAAAATAAAGAAGAATGGCCTGGATTGAGCATGATGTTTGGAGAATGGAGAGATTT  720

Qy  721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCGTGTTGGCTGTGACATCTATTC  780
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Qy 1021 AGAGTTAGACAtTGGTTGGGGAGACGGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 AGAGTTAGACAtTGGTTGGGGAGACGGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy 1081 TGTAGAATTACTGTTTACACACATTTTGTTCAATATATGATATATTTATCACCAACATT 1140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 TGTAGAATTACTGTTTACACACATTTTGTTCAATATATGATATATTTATCACCAACATT 1140

Qy 1141 TCAAGTTTGTTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAAA 1195
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 TCAAGTTTGTTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAAA 1195
```

RESULT 13

ADN39395

ID   ADN39395 standard; cDNA; 1195 BP.
XX
AC   ADN39395;
XX
DT   17-JUN-2004 (first entry)
XX
DE   Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:B79.
XX
KW   Human; differential expression; cancer; angiogenic disorder;
KW   fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW   inflammatory disease; autoimmune disease;
KW   retinal neovascularisation syndrome; scarring; uterine fibroid;
KW   detection; diagnosis; prognosis; drug screening; drug targeting;
KW   wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW   vulnerary; gene therapy; vaccine; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200304266l-A2.
XX
PD   22-MAY-2003.
XX
PF   13-NOV-2002; 2002WO-US036810.
XX
PR   13-NOV-2001; 2001US-0350666P.
PR   21-NOV-2001; 2001US-0324644P.
PR   29-NOV-2001; 2001US-0334393P.
PR   03-DEC-2001; 2001US-0335394P.
PR   14-DEC-2001; 2001US-0403768P.
PR   08-JAN-2002; 2002US-0347221P.
PR   10-JAN-2002; 2002US-0347349P.
PR   08-FEB-2002; 2002US-0355250P.
PR   13-FEB-2002; 2002US-0356774P.
PR   20-FEB-2002; 2002US-0359077P.
PR   29-MAR-2002; 2002US-0368809P.
PR   04-APR-2002; 2002US-0370110P.
PR   04-APR-2002; 2002US-0371244P.
PR   05-JUN-2002; 2002US-0386614P.
PR   16-JUL-2002; 2002US-0396839P.
PR   22-JUL-2002; 2002US-0397775P.
PR   22-JUL-2002; 2002US-0397845P.
PR   09-SEP-2002; 2002US-0409450P.
XX
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI   Afar D, Aziz N, Ginsburg WM, Gish KC, Glynne R, Hevezi PA;
PI   Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX
DR   WPI; 2003-486649/44.
DR   P-PSDB; ADN39396.
XX
PS   Claim 8; SEQ ID NO B79; 1385pp; English.
XX
CC   The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC   whose expression is upregulated or downregulated in specific cancers or
CC   other diseases such as angiogenic or fibrotic disorders, and to methods
CC   of determining the presence or absence of a pathological cell in a
CC   patient by detecting a nucleic acid at least 80% identical to those of
CC   the invention or by detecting a polypeptide of the invention. The
CC   invention also relates to expression vectors and host cells comprising a
CC   nucleic acid of the invention; antibodies which specifically bind a
CC   polypeptide of the invention; use of such antibodies for drug targeting;
CC   and methods of screening for modulators of activity or expression of the
CC   polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC   antibodies and methods are useful for diagnosing, prognosing and treating
CC   cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC   atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC   neovascularisation syndromes, scarring and uterine fibroids. They may
CC   also be useful in wound healing and in contraception. The present
CC   sequence represents a nucleic acid sequence of the invention.
XX
SQ   Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

Query Match   100.0%; Score 1195; DB 11; Length 1195;
Best Local Similarity   100.0%;
Matches 1195; Conservative   0; Mismatches   0; Indels   0; Gaps   0;
Pred. No. 4.4e-276;

Qy   1 CCGAGACTCACGGTCCAAGCTNAAGCGAGAGAGTGGGTGGCTGAAGCCGCCATACTATTTATAG 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CCGAGACTCACGGTCAAGCTNAAGCGGAGAGAGTGGGTGGCTGAAGCCGCCATACTATTTATAG 60

Qy   61 AATTNAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTTGGAAAAATGAAGCCTA 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AATTNAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAAATGAAGCCTA 120

Qy   121 GGAGAAATTTAGAGAAGAACGAGATTATTTTGCATAAGGACACACGGAGAGGACCAGCATGCTAA 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGAGAAATTTAGAGAAGAACGAGATTATTTTGCATAAGGACACACGGAGAGGACCAGCATGCTAA 180

Qy   181 AAAGAACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AAAGAACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy   241 CAGAGACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CAGAGACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy   301 CTATTATTAGCATCTCTGACTTTTCTTTACACTCTTTCTGAGGGAGAGTAATTCACCCTTTAG 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTATTATTAGCATCTCTGACTTTTCTTTACACTCTTTCTGAGGGAGAGTAATTCACCCTTTAG 360

Qy   361 CAACTTCCCATCAACAAATATTTTTATAAAAATTCCAAATCCTGGTCATCAACAAAGTCTTGC 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CAACTTCCCATCAACAAATATTTTTATAAAAATTCCAAATCCTGGTCATCAACAAAGTCTTGC 420

Qy   421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Db   721 ATGTGTCTCTGGGAATTGTGGGATTGGCAAATACTGGCTCTCGTTGGGCTTCTGACATCTATTC 780

Qy   781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy   841 TTGTTTCCCTTCTACTGGGCACAATACACGCCATTGACATTGATTTTTGCCTGGAATAAGTGGGATAG 900
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TTGTTTCCCTTCTACTGGGCACAATACACGCCATTGACATTGATTTTTGCCTGGAATAAGTGGGATAG 900

Qy   901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGTCTGTTTTCCTTCCAA 960
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGTCTGTTTTCCTTCCAA 960

Qy   961 TTGTTGTTGTCCCTGATATTTAAAAGCAATACTATTTCCTCTGCCATGCTTGAGGAAGAGATACTGA 1020
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TTGTTGTTGTCCCTGATATTTAAAAGCAATACTATTTCCTCTGCCATGCTTGAGGAAGAGATACTGA 1020

Qy   1021 AGATTAGACATCGGTTGGGAAGACGTCACCAAAAATTAACAAAACTGAGATATGTTGTTCCCAGT 1080
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 AGATTAGACATCGGTTGGGAAGACGTCACCAAAAATTAACAAAACTGAGATATGTTGTTCCCAGT 1080

Qy   1081 TGTAGAATTACTGTTTACACACATTTTGTTCAATATTGATATATTTATCACCAACATT 1140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TGTAGAATTACTGTTTACACACATTTTGTTCAATATTGATATATTTATCACCAACATT 1140

Qy   1141 TCAAGTTTGTATTTGTTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAAA 1195
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TCAAGTTTGTATTTGTTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAAA 1195

```
Qy    481  TCCAACTTCATATGGACCAAGTATAAGAGAAGTTTCCACATTGGTTGGTATAAGTGGGATGT  540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  TCCAACTTCATATGGACCAAGTATAAGAGAAGTTTCCACATTGGTTGGTATAAGTGGGATGT  540

Qy    541  TAACAAGAAAGCAGTTTGGGCCTTCTCAGTTTTCTTTTTGCTGTTACTGCATGCAATTTATA  600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  TAACAAGAAAGCAGTTTGGGCCTTCTCAGTTTTCTTTTTGCTGTTACTGCATGCAATTTATA  600

Qy    601  GTCTGTCTTTACCCAATGAGGCGGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC  660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  GTCTGTCTTTACCCAATGAGGCGGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC  660

Qy    661  AGGTCCAACAAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGATGAGATTT  720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  AGGTCCAACAAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGATGAGATTT  720

Qy    721  ATGTGTCTCTGGGGAATTGTGTGGAATACTGGCTCTGTTGGCTGTGTGACATCTATTC  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  ATGTGTCTCTGGGGAATTGTGTGGAATACTGGCTCTGTTGGCTGTGTGACATCTATTC  780

Qy    781  CATCTGTGAGTGACTCTTTGACATGGAGGAGAATTTCACTATATATTCAGAGACCAAGCTAGGAA  840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  CATCTGTGAGTGACTCTTTGACATGGAGGAGAATTTCACTATATATTCAGAGACCAAGCTAGGAA  840

Qy    841  TTGTTTCCCTTCTACTGGGCCACAATACACGCCATTGATTTTGGCCTGGAATAAGTGGGATAG  900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  TTGTTTCCCTTCTACTGGGCCACAATACACGCCATTGATTTTGGCCTGGAATAAGTGGGATAG  900

Qy    901  ATATAAAACAATTGTATGGTATACACCTCCAACTTTATGATAGCTGTTTTCCTTCCAA  960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  ATATAAAACAATTGTATGGTATACACCTCCAACTTTATGATAGCTGTTTTCCTTCCAA  960

Qy    961  TTGTTTGTCCTGATATTTAAAAGCATAACTACTATTCCTGCCAATGCTTGAGGAAGAGATACTGA  1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  TTGTTTGTCCTGATATTTAAAAGCATAACTACTATTCCTGCCAATGCTTGAGGAAGAGATACTGA  1020

Qy   1021  AGAATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAAACTGAGATATGTTCCCAGT  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  AGAATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAAACTGAGATATGTTCCCAGT  1080

Qy   1081  TGTAGAATTACTGTTTACACACATTTTTGTTCAATATATGATATTTTATCACCAACATT  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  TGTAGAATTACTGTTTACACACATTTTTGTTCAATATATGATATTTTATCACCAACATT  1140

Qy   1141  TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAA  1195
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAA  1195
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RESULT 14
ADP88258

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Query Match             100.0%;  Score 1195;  DB 11;  Length 1195;
Best Local Similarity   100.0%;  Pred. No. 4.4e-276;
Matches 1195;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     1  CCGAGACTCACGGTCAAGCTCAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  CCGAGACTCACGGTCAAGCTCAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG  60

Qy    61  AATTAATGAAAGCAGAAAGACATCACAAAACCAAGAAGAACTTTGGAAAATGAAGCCTA  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  AATTAATGAAAGCAGAAAGACATCACAAAACCAAGAAGAACTTTGGAAAATGAAGCCTA  120

Qy   121  GGAGAAATTTAGAGAAGACGATTATTTGCATAAGGACACGGGAGGACCAGCATGCTAA  180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  GGAGAAATTTAGAGAAGACGATTATTTGCATAAGGACACGGGAGGACCAGCATGCTAA  180

Qy   181  AAAGACCCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  AAAGACCCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT  240

Qy   241  CAGAACTTCAGCACACACACAGGAACTCTTTCCACAGTGGCCACTTCGCCAATTAAAATAGCTG  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  CAGAACTTCAGCACACACACAGGAACTCTTTCCACAGTGGCCACTTCGCCAATTAAAATAGCTG  300

Qy   301  CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAGTAATTCACCCTTTAG  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAGTAATTCACCCTTTAG  360

Qy   361  CAACTTCCATCAACAATATTTTATAAAATTCAATCCTGGTCATCAACAAAGTCTTGC  420
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Db   361 CAAACTTCCCATCAACAATATATTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   361 CAAACTTCCCATCAACAATATATTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Db   421 CAAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAAATTG 480
Qy   421 CAAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAAATTG 480

Db   481 TCCAACTTCATAATGGAACCAAGTATATAAGAAGAAGTTTCCACATTGGTTGGAATAAGTGGGATGT 540
Qy   481 TCCAACTTCATAATGGAACCAAGTATATAAGAAGAAGTTTCCACATTGGTTGGAATAAGTGGGATGT 540

Db   541 TAACAAGAAAAGCAGTTTGGGCCTTCTCACTTTTCTTTTTGTTTTTGCTGTGTACTGCCATGCAATTTATA 600
Qy   541 TAACAAGAAAAGCAGTTTGGGCCTTCTCACTTTTCTTTTTGTTTTTGCTGTGTACTGCCATGCAATTTATA 600

Db   601 GTCTGTCTTACCCAATGAGGCCGATCCTTCACAGATACAAGTTGCTAAAACTGGGCATATCAAC 660
Qy   601 GTCTGTCTTACCCAATGAGGCCGATCCTTCACAGATACAAGTTGCTAAAACTGGGCATATCAAC 660

Db   661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGAGTTTGGAGAATGGAGATTT 720
Qy   661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGAGTTTGGAGAATGGAGATTT 720

Db   721 ANGTGTCTTCTGGGAATTGTGGGAATTGGCAATACTGGCTCTGTTGTTGGGCTGTGACATCTATTC 780
Qy   721 ANGTGTCTTCTGGGAATTGTGGGAATTGGCAATACTGGCTCTGTTGTTGGGCTGTGACATCTATTC 780

Db   781 CATCTGTGAGTGACTCTTTGACATGGAGAAATTCACTATAATTCAGAGCAAGCTAGGAA 840
Qy   781 CATCTGTGAGTGACTCTTTGACATGGAGAAATTCACTATAATTCAGAGCAAGCTAGGAA 840

Db   841 TTGTTTCCCTTCTACTGGGGCACAAATACACGCATTGAATTGATTTTTGCCTGGAATAAGTGGGATAG 900
Qy   841 TTGTTTCCCTTCTACTGGGGCACAAATACACGCATTGAATTGATTTTTGCCTGGAATAAGTGGGATAG 900

Db   901 ATATAAAACAATTGTATGGTATACACCCCACACTTTTATGATAGACTGTTTTCCTTCCAA 960
Qy   901 ATATAAAACAATTGTATGGTATACACCCCACACTTTTATGATAGACTGTTTTCCTTCCAA 960

Db   961 TTGTTGTCCTGATATTTTAAAAGCATACTATTCCTGCCACTTTTATGATAGAGCTGTTTTCCTTCCAA 1020
Qy   961 TTGTTGTCCTGATATTTTAAAAGCATACTATTCCTGCCACTTTTATGATAGAGCTGTTTTCCTTCCAA 1020

Db   1021 AGATTAGACATGGTTGGGAAGAGACCTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
Qy   1021 AGATTAGACATGGTTGGGAAGAGACCTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Db   1081 TGTAGAATTACTCGTTTACACACATTTTGTTCAATAATTGATATATTTTATCACCAACATT 1140
Qy   1081 TGTAGAATTACTCGTTTACACACATTTTGTTCAATAATTGATATATTTTATCACCAACATT 1140

Db   1141 TCAAGTTTGTATTTGTTAATAAAATGATTTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195
Qy   1141 TCAAGTTTGTATTTGTTAATAAAATGATTTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195

XX
CC   The present invention relates to the isolation of human tumour-associated
CC   antigenic target (TAT) polynucleotide and polypeptide sequences. Also
CC   disclosed is an antibody that binds to a TAT polypeptide. The antibody is
CC   a monoclonal antibody, an antibody fragment, a chimeric antibody or a
CC   humanised antibody. It is conjugated to a growth inhibitory agent. It is
CC   produced in bacteria or in CHO cells and induces death of a cell to which
CC   it binds. The antibody is useful for preparing a composition for
CC   diagnosing or treating tumours and cancer. The present sequence
CC   represents a human TAT cDNA sequence of the invention.
XX
SQ   Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

PS   Claim 1; SEQ ID NO 42; 319pp; English.
XX
PT   New antibody that binds to a tumor-associated antigenic target (TAT)
PT   polypeptide, useful for preparing a composition for diagnosing or
PT   treating cancer.

Query Match   100.0%; Score 1195; DB 12; Length 1195;
Best Local Similarity 100.0%; Pred. No. 4.4e-276;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 CCGAGACTCACGGTCACGTCTAAGGCGAAGAGAGTGGGTGGGTGGCTGAAGCCATACTATTTTATAG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CCGAGACTCACGGTCACGTCTAAGGCGAAGAGAGTGGGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy   61 AATTAATGGAAAGCAGAAAAGACAATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AATTAATGGAAAGCAGAAAAGACAATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy   121 GGAGAAATTTAGAAGACGAATTATTTTCCATGCACAAAACCAAGAAGAACTTTGGAAAATGAAGCCTAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGAGAAATTTAGAAGACGAATTATTTTCCATGCACAAAACCAAGAAGAACTTTGGAAAATGAAGCCTAA 180

Qy   181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy   241 CAGAGACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CAGAGACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy   301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTCTGAGGGAAGTAATTCACCCTTTAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy   361 CAACTTCCCATCAACAATATATTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CAACTTCCCATCAACAATATATTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy   421 CAAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAAATTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CAAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAAATTG 480

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Qy    481 TCCAACTTCATAATGAACCAAGTAATAAGAAGTTTCCACATTGGTTGGATAAGTGGAATGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TCCAACTTCATAATGAACCAAGTAATAAGAAGTTTCCACATTGGTTGGATAAGTGGAATGT 540

Qy    541 TAACAAGAAAGCAGTTTGGGGCTTCTCAGTTTCTTTTTTGCTATCGCCATGCAATTTATA 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TAACAAGAAAGCAGTTTGGGGCTTCTCAGTTTCTTTTTTGCTATCGCCATGCAATTTATA 600

Qy    601 GTCTCTCTTACCCAATGAGGCGGATCCTTACAGATACAAAGTTGCTAAACTGGGCATATCAAC 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTCTCTGTCTTACCCAATGAGGCGGATCCTTACAGATACAAAGTTGCTAAACTGGGCATATCAAC 660

Qy    661 AGGTCCAACAAAAATAAAGAAGAAGAATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGGTCCAACAAAAATAAAGAAGAAGAATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy    721 ATGTGTCTCTGGGGAATTGTGGGGATTGGCAATACTGGCCTCTCGTTGGCTGTGTGACATCTATTC 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATGTGTCTCTGGGGAATTGTGGGGATTGGCAATACTGGCCTCTCGTTGGCTGTGTGACATCTATTC 780

Qy    781 CATCTGTGAGTGACTCTTTTGACATGGAGAGAAATTTCACTATTATTCAGAGCAAAGCTAGGAA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CATCTGTGAGTGACTCTTTTGACATGGAGAGAAATTTCACTATTATTCAGAGCAAAGCTAGGAA 840

Qy    841 TTGTTTCCCTTCTACTGGGGCACAATACACGGCATTGATTTTTTGCCTGGAATAAGTGGGATAG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TTGTTTCCCTTCTACTGGGGCACAATACACGGCATTGATTTTTTGCCTGGAATAAGTGGGATAG 900

Qy    901 ATATAAAAACAATTTGTATGGTATACACCCTCCAACTTTTATGATAGCTGTGTTTTCCTTCCAA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ATATAAAAACAATTTGTATGGTATACACCCTCCAACTTTTATGATAGCTGTGTTTTCCTTCCAA 960

Qy    961 TTGTTTGTCCTGATATTTAAAAGCATACTACTAATTCCTGCCATGCCTTGAGGGAAGAGATACTGA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TTGTTTGTCCTGATATTTAAAAGCATACTACTAATTCCTGCCATGCCTTGAGGGAAGAGATACTGA 1020

Qy   1021 AGATTAGACATGGTTGGGGAAGACGTCACCAAAAATTAACAAAACTGAGATAGTTCCCAGT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 AGATTAGACATGGTTGGGGAAGACGTCACCAAAAATTAACAAAACTGAGATAGTTCCCAGT 1080

Qy   1081 TGTAGAATTACTCGTTTACACACATTTTGTTCAATATTGATATTTATCACCAAACATT 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TGTAGAATTACTCGTTTACACACATTTTGTTCAATATTGATATTTATCACCAAACATT 1140

Qy   1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195
          |||||||||||||||||||||||||||||||||||||
Db   1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195
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Job time : 807.249 secs

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OM nucleic - nucleic search, using sw model.

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GenCore version 5.1.6

Run on: December 4, 2005, 20:37:01 ; Search time 6316.97 Seconds
                                              (without alignments)
                                              10753.247 Million cell updates/sec

Title: US-10-750-262-1
Perfect Score: 1195
Sequence: 1 ccgagactcacggtcaagct.........ggaaaaaaaaaaaaaaaa 1195

Scoring table: IDENTITY_NUC
Searched: Gapop 10.0 , Gapext 1.0
              5883141 seqs, 2842172565 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%   Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
              1: gb_ba:*
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              7: gb_ph:*
              8: gb_pr:*
              9: gb_ro:*
             10: gb_sts:*
             11: gb_sy:*
             12: gb_un:*
             13: gb_vi:*
             14: gb_htg:*
             15: gb_pl:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1195	100.0	1195	6	CQ776742	CQ776742 Sequence
2	1195	100.0	1195	6	AR366780	AR366780 Sequence
3	1195	100.0	1178	6	AR405830	AR405830 Sequence
4	1195	100.0	1195	6	AR564210	AR564210 Sequence
5	1195	100.0	1195	6	AR589196	AR589196 Sequence
6	1195	100.0	1195	6	AR654075	AR654075 Sequence
7	1195	100.0	1195	6	AX201105	AX201105 Sequence
8	1195	100.0	1195	6	AX267904	AX267904 Sequence
9	1195	100.0	1195	6	AX926483	AX926483 Sequence
10	1195	100.0	1195	6	AX951736	AX951736 Sequence
11	1195	100.0	1195	6	AX960014	AX960014 Sequence
12	1195	100.0	1195	8	AF186249	AF186249 Homo sapi
13	1195	100.0	1195	6	CQ981397	CQ981397 Sequence
14	1195	100.0	1330	6	CS031875	CS031875 Sequence
15	1195	100.0	1330	6	CS036259	CS036259 Sequence
16	1195	100.0	1330	6	CS040827	CS040827 Sequence
17	1195	100.0	1330	6	CS045211	CS045211 Sequence
18	1193	99.8	1193	6	BD232184	BD232184 Novel ser
19	1193	99.8	1193	6	AR617054	AR617054 Sequence
20	1193	99.8	1193	6	AX155243	AX155243 Sequence
21	1191.8	99.7	1240	8	BC011802	BC011802 Homo sapi
22	1178	98.6	1277	6	CQ412839	CQ412839 Sequence
23	946.6	79.2	1754	4	AF319659	AF319659 Sus scrof
24	825.6	69.1	3627	6	BD232188	BD232188 Novel ser
25	825.6	69.1	3627	6	AR366784	AR366784 Sequence
26	825.6	69.1	3627	6	AR617056	AR617056 Sequence
27	825.6	69.1	3627	6	AR654079	AR654079 Sequence
28	810.2	67.8	1234	9	AX155248	AX155248 Sequence
29	810.2	67.8	1234	6	BC061023	BC061023 Mus muscu
30	809.6	67.7	1175	9	AF297098	AF297098 Mus muscu
31	806	67.4	1211	6	CQ777614	CQ777614 Sequence
32	759.6	63.6	3627	6	BD192004	BD192004 Modulator
33	712	59.6	1198	9	AY029584	AY029584 Mus muscu
34	675.8	56.6	1209	8	BC066301	BC066301 Homo sapi
35	581	48.6	592	6	BD242240	BD242240 Compounds
36	581	48.6	592	6	AR278447	AR278447 Sequence
37	581	48.6	592	6	AR367143	AR367143 Sequence
38	581	48.6	592	6	AR371039	AR371039 Sequence
39	581	48.6	592	6	AR400179	AR400179 Sequence
40	581	48.6	592	6	AR405446	AR405446 Sequence
41	581	48.6	592	6	AR563826	AR563826 Sequence
42	581	48.6	592	6	AR588812	AR588812 Sequence
43	581	48.6	592	6	AR605632	AR605632 Sequence
44	581	48.6	592	6	AR656971	AR656971 Sequence
45	581	48.6	592	6	AX106561	AX106561 Sequence

ALIGNMENTS

RESULT 1
LOCUS   CQ776742   1195 bp   DNA   linear   PAT 11-MAR-2004
DEFINITION   Sequence 428 from Patent EP1394274.
ACCESSION   CQ776742
VERSION   CQ776742.1 GI:45380132
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Hominidae; Homo.
REFERENCE   1
AUTHORS   Ohtani,N., Sugita,Y., Yamaya,M., Kubo,H., Nagai,H. and Izuhara,K.
TITLE   Methods of testing for bronchial asthma or chronic obstructive
              pulmonary disease
JOURNAL   Patent: EP 1394274-A 428 03-MAR-2004;
              Genox Research, Inc. (JP)
FEATURES   Location/Qualifiers
source   1..1195
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
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Query Match   100.0%; Score 1195; DB 6; Length 1195;
Best Local Similarity   100.0%;
Matches 1195; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CCGAGACTCACGGTCAAGCTCAAGCTAAGGCGAAGAGTGGGTCGGCTGAAGCCATACTATT 60
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Db   1 CCGAGACTCACGGTCAAGCTCAAGCTAAGGCGAAGAGTGGGTCGGCTGAAGCCATACTATT 60

Qy   61 AATTAATGGAAAGCAGAAAAGCAGAAAACCAGAAGAGAACTTTGGAAAATGAAGCCTA 120
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Db   61 AATTAATGGAAAGCAGAAAAGCAGAAAACCAGAAGAGAACTTTGGAAAATGAAGCCTA 120

Qy   121 GGAGAAATTTAGAAGAGAAGACAGATTATTTGCATAAGGAGACACGGGAGAGACCAGCATGCTAA 180
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Db   121 GGAGAAATTTAGAAGAGAAGACAGATTATTTGCATAAGGAGACACGGGAGAGACCAGCATGCTAA 180

RESULT 2
AR366780
LOCUS   AR366780   1195 bp   DNA   linear   PAT 12-SEP-2003
DEFINITION Sequence 1 from patent US 6329503.
ACCESSION   AR366780
VERSION   AR366780.1 GI:34599746
KEYWORDS   Unknown.
SOURCE   Unknown.
  ORGANISM Unclassified.
REFERENCE   1 (bases 1 to 1195)
  AUTHORS   Afar,D.E., Hubert,R.S., Leong,K., Raitano,A.B., Saffran,D.C. and
            Mitchell,S.C.
  TITLE   Serpentine transmembrane antigens expressed in human cancers and
            uses thereof
  JOURNAL   Patent: US 6329503-A 1 11-DEC-2001;
            Agensys, Inc.; Santa Monica, CA;
            WOX;
FEATURES   Location/Qualifiers
     source   1..1195
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                     /mol_type="genomic DNA"
ORIGIN

Query Match   100.0%; Score 1195; DB 6; Length 1195;
Best Local Similarity   100.0%; Pred. No. 5.5e-238;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[Sequence alignment of query (Qy) to database (Db) sequence, positions 1–1195, with 100% identity matches indicated by vertical bars between the aligned nucleotide lines.]

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Db  721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTTCTGTTGGCTGTGACATCTATTC 780
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Qy  781 CATCCTGTGAGTGACTCTCTTTGACATGGAGAGGAAGAATTTCACTACTATATTCCAGGAA 840
Db  781 CATCCTGTGAGTGACTCTCTTTGACATGGAGAGGAAGAATTTCACTACTATATTCCAGGAA 840
Qy  841 TTGTTTCCCTTCTACTGGGGCACAATACACGGCATTGAGTTGATTTGCCTGGAATAAGTGG 900
Db  841 TTGTTTCCCTTCTACTGGGGCACAATACACGGCATTGAGTTGATTTGCCTGGAATAAGTGG 900
Qy  901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGTATAGCTGTTTTCCTTCCAA 960
Db  901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGTATAGCTGTTTTCCTTCCAA 960
Qy  961 TTGTGTGTCCTGATATTTAAAAGCATACTACTATTCCTCCCACTGCTTGAGGAGGAAGAAG 1020
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Db 1021 AGATTAGACATGGTTGGGGAAGAGCGTCACCCAAAAATTAACAAAAACTGAGATATGTTCC 1080
Qy 1081 TGTAGAATTACTGTTTACACACACATTTTTGTCAATATTGATATATTTTATCACCAACATT 1140
Db 1081 TGTAGAATTACTGTTTACACACACATTTTTGTCAATATTGATATATTTTATCACCAACATT 1140
Qy 1141 TCAAGTTTGTATTTGTTAATAAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195
Db 1141 TCAAGTTTGTATTTGTTAATAAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195
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RESULT 3
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LOCUS       AR405830              1195 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 878 from patent US 6630305.
ACCESSION   AR405830
VERSION     AR405830.1  GI:40154667
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1195)
  AUTHORS   Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
            Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
            Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A.W.,
            Hepler,W.T. and Henderson,R.A.
  TITLE     Compositions and methods for the therapy and diagnosis of prostate
            cancer
  JOURNAL   Patent: US 6630305-A 878 07-OCT-2003;
            Corixa Corporation; Seattle, WA;
            WOX;
FEATURES             Location/Qualifiers
     source          1..1195
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                     /mol_type="genomic DNA"
ORIGIN

Query Match             100.0%;  Score 1195;  DB 6;  Length 1195;
Best Local Similarity   100.0%;
Matches  1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Db    1 CCGAGACTCACGGTCAAGCTAAGGCGGAAGAGTGGGTGGGCTGAAGCCATACTACTATTTATAG 60
Qy   61 AATTAATGGAAAGCAGAAAAAGACATCACAAACCAAGAGACTTTGAAAAATGAACCTA 120
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Db   61 AATTAATGGAAAGCAGAAAAAGACATCACAAACCAAGAGACTTTGAAAAATGAACCTA 120
Qy  121 GGAGAAATTTAGAAGAAGAGACGATTATTTGCATAAGGACACCGGAGAGAGACCAGCCATGCTAA 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GGAGAAATTTAGAAGAAGAGACGATTATTTGCATAAGGACACCGGAGAGAGACCAGCCATGCTAA 180
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Qy  181 AAAGACCTGTGCTTTTGCATTTGCACCAAAGCAGCCCATGCTGATGAATTTGACTGCCCTT 240
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Db  181 AAAGACCTGTGCTTTTGCATTTGCACCAAAGCAGCCCATGCTGATGAATTTGACTGCCCTT 240
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Db  241 CAGAACTTCAGGCACACACAGGAGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
Qy  301 CTATTATAGCATCTCTGACTCTTTCTTTACACTCTCTTCAGAGCAAGTAAATTCACCCTTTAG 360
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Qy  361 CAACTTCCCATCAACAATATTTTTATAAAAATTCCAATCCTCGGTCATCAACAAAAGTCTTGC 420
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Qy  421 CAATGGTTTCCATCACTCTCTTTGGCATTGGTTTACCTGCCTGACACATGGGATAAGTGGGATAGCAGCAATTG 480
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Qy  481 TCCAACTTCATAATGGAACCAAGTAATAAGAAGTTGTTTACCTGCCACATTGGGATGGGATGGATGT 540
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Qy  661 AGGTCCAACAAAAATAAAGAAGAAGAATGCCTGGATTGAGCAGTGATGATGTTTGGAGAATGGAGATTT 720
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Qy  721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTTCTGTTGGCTGTGACATCTATTC 780
Db  721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTTCTGTTGGCTGTGACATCTATTC 780
Qy  781 CATCCTGTGAGTGACTCTCTTTGACATGGAGAGGAAGAATTTCACTATATTCCAGGAA 840
Db  781 CATCCTGTGAGTGACTCTCTTTGACATGGAGAGGAAGAATTTCACTATATTCCAGGAA 840
Qy  841 TTGTTTCCCTTCTACTGGGGCACAATACACGGCATTGAGTTGATTTGCCTGGAATAAGTGGGATAG 900
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Db 1141 TCAAGTTTGTATTTGTTAATAAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195
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RESULT 4
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LOCUS       AR564210              1195 bp    DNA     linear   PAT 08-OCT-2004
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DEFINITION Sequence 878 from patent US 6759515.
ACCESSION   AR564210
VERSION   AR564210.1 GI:53979261
KEYWORDS   Unknown.
SOURCE   Unknown.
  ORGANISM Unclassified.
REFERENCE   1 (bases 1 to 1195)
  AUTHORS   Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
            Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
            Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
            Hepler,W.T. and Henderson,R.A.
  TITLE   Compositions and methods for the therapy and diagnosis of prostate
            cancer
  JOURNAL   Patent: US 6759515-A 878 06-JUL-2004;
            Corixa Corporation; Seattle, WA
FEATURES   Location/Qualifiers
     source 1..1195
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ORIGIN

Query Match   100.0%; Score 1195; DB 6; Length 1195;
Best Local Similarity   100.0%; Pred. No. 5.5e-238;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    121  GGAGAAAATTTAGAAGAAGAAGACGGATTATTTGCATAAGGACACGGGAGAGACCAGCCATA   180
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Qy    181  AAAGACCCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAAATTTGACTGCCCTT   240
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Qy    481  TCCAACTTCATAATGGAACCAAGTATAAGAGATTTCCACATTGGTTGGATAAGTGGGATGT   540
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Qy    601  GTCTGTGTCTTACCCAATGAGGGCGATCCTACAGATACAAGTTGCTAAAACTGGGCATATCAAC   660
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Qy    721  ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCGTTGGCTGTGACATCTATTC   780
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Qy    781  CATCTGTGAGTGACTCTCTTTGACATGTGGAGAGAATTTCACTATATATTCAGAGACATTAGGAA   840
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Qy    841  TTGTTTCCCTTCTACTGGGGCACAATACACGGCATTGATTTGTTTGGCTTGGAATAAGTGGAATAG   900
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Qy    901  ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGTGTTTTCCTTCCAA   960
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Qy   1021  AGATTAGACATGGTTGGGGAAGACGTCACCAAAAATTAACAAAACTGAAGATATGTTCCAGT  1080
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Qy   1141  TCAAGTTTGTATTTGTTAATAAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAAA  1195
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Db   1141  TCAAGTTTGTATTTGTTAATAAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAAA  1195
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RESULT 5
AR589196

LOCUS   AR589196   1195 bp   DNA   linear   PAT 15-DEC-2004
DEFINITION Sequence 878 from patent US 6800746.
ACCESSION   AR589196
VERSION   AR589196.1 GI:56636093
KEYWORDS   Unknown.
SOURCE   Unknown.
  ORGANISM Unclassified.
REFERENCE   1 (bases 1 to 1195)
  AUTHORS   Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
            Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
            Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
            Hepler,W.T. and Henderson,R.A.
  TITLE   Compositions and methods for the therapy and diagnosis of prostate
            cancer
  JOURNAL   Patent: US 6800746-A 878 05-OCT-2004;
            Corixa Corporation; Seattle, WA
FEATURES   Location/Qualifiers
     source 1..1195
            /organism="unknown"
            /mol_type="genomic DNA"
ORIGIN

Query Match   100.0%; Score 1195; DB 6; Length 1195;
Best Local Similarity   100.0%; Pred. No. 5.5e-238;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1  CCGAGACTCACGGTCGAAGCTCAAGGCCGAAGAGTGGGGTGGGTGGGCCATACTAGTTTTATATG    60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  CCGAGACTCACGGTCGAAGCTCAAGGCCGAAGAGTGGGGTGGGTGGGCCATACTAGTTTTATATG    60

Qy     61  AATTAAATGGAAAGCAGAAAAAGACATCACAAACCAAGAAGAACTTTGGGAAAATGAAGCCTA   120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  AATTAAATGGAAAGCAGAAAAAGACATCACAAACCAAGAAGAACTTTGGGAAAATGAAGCCTA   120

Qy    121  GGAGAAAATTTAGAAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCCATAA   180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  GGAGAAAATTTAGAAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCCATAA   180
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RESULT 6
AR654075

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LOCUS           AR654075                1195 bp    DNA     linear   PAT 13-JUN-2005
DEFINITION      Sequence 1 from patent US 6887975.
ACCESSION       AR654075
VERSION         AR654075.1  GI:67584962
KEYWORDS        .
SOURCE          Unknown.
  ORGANISM      Unknown.
                Unclassified.
REFERENCE       1  (bases 1 to 1195)
  AUTHORS       Afar,D.E., Hubert,R.S., Leong,K., Raitano,A.B., Saffran,D.C. and
                Mitchell,S.C.
  TITLE         Peptides derived from STEAP1
  JOURNAL       Patent: US 6887975-A 1 03-MAY-2005;
                Agensys, Inc.; Santa Monica, CA
FEATURES             Location/Qualifiers
     source          1..1195
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Query Match     100.0%;  Score 1195;  DB 6;  Length 1195;
Best Local Similarity  100.0%;  Pred. No. 5.5e-238;
Matches 1195;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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(Alignment of Query (Qy) and Database (Db) nucleotide sequences, 100% identity over 1195 bp, shown in two paired blocks with connecting match bars (|). Nucleotide positions run from 1 to 1195.)

RESULT 7

LOCUS   AX201105   1195 bp   DNA   linear   PAT 29-AUG-2001
DEFINITION Sequence 735 from Patent WO0151633.
ACCESSION   AX201105
VERSION   AX201105.1   GI:15390890
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
            Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
            Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
  TITLE   Compositions and methods for the therapy and diagnosis of prostate
            cancer
  JOURNAL   Patent: WO 0151633-A 735 19-JUL-2001;
            CORIXA CORPORATION (US)
FEATURES   Location/Qualifiers
     source   1..1195
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

Query Match   100.0%; Score 1195; DB 6; Length 1195;
Best Local Similarity   100.0%;
Matches 1195; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGGGGCTGAACGCCATACTACTATTTTATAG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGGGGCTGAACGCCATACTACTATTTTATAG 60

Qy   61 AATTAAATGGAAAAGCAGAAAAAGACATTCACAAAACCAAGAAGAGAACTTTGGGAAAATGAAGCCTA 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AATTAAATGGAAAAGCAGAAAAAGACATTCACAAAACCAAGAAGAGAACTTTGGGAAAATGAAGCCTA 120

Qy   121 GGAGAAATTTAGAAGAAGAGACGATTATTTGCATAAGGACACGGGAGAGAGACCAGCATGCTAA 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGAGAAATTTAGAAGAAGAGACGATTATTTGCATAAGGACACGGGAGAGAGACCAGCATGCTAA 180

Qy   181 AAAGACCTGTGCTTTTGCATTTGCACCAAAACAGCCCCATGCTGATGAATTTGACTGCCCTT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AAAGACCTGTGCTTTTGCATTTGCACCAAAACAGCCCCATGCTGATGAATTTGACTGCCCTT 240

Qy   241 CAGAACTTCAGCACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CAGAACTTCAGCACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy   301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTCGAGGGAGTAATTCACCCTTTAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTCGAGGGAGTAATTCACCCTTTAG 360

Qy   361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCTCGGTCATCAACAAAAGTCTTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCTCGGTCATCAACAAAAGTCTTGC 420

Qy   421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGGTGTGACAATCATC 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGGTGTGACAATCATC 480

Qy   481 TCCAACTTCATAATGGAACCAAGTATAAAGAAGTTTCCACATTGGTTGGATAAGTGGGATGT 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TCCAACTTCATAATGGAACCAAGTATAAAGAAGTTTCCACATTGGTTGGATAAGTGGGATGT 540

Qy   541 TAACAAGAAAAGCAGTTGGGCCTTCTCAGTTTCTTTTTTTTGCTTGTGAAGTCAGTTATA 600
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Db   541 TAACAAGAAAAGCAGTTGGGCCTTCTCAGTTTCTTTTTTTTGCTTGTGAAGTCAGTTATA 600

Qy   601 GTCTGTCTTACCCAATGAGGCGGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTCTGTCTTACCCAATGAGGCGGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy   661 AGGTCCAACAAAATAAAGGAAGATGCCTGATTGAGCATATGTTGGACAATGAGATT 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 AGGTCCAACAAAATAAAGGAAGATGCCTGATTGAGCATATGTTGGACAATGAGATT 720

Qy   721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGGCTCTCTTGGCTGTGACACTCTATTC 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGGCTCTCTTGGCTGTGACACTCTATTC 780

Qy   781 CATCTGTGAGTGACTCTTTGACATGGAGAGAAATTTCACTATATATTCAGAGCCAAGCTAGGAA 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 CATCTGTGAGTGACTCTTTGACATGGAGAGAAATTTCACTATATATTCAGAGCCAAGCTAGGAA 840

Qy   841 TTGTTTCCCTTCTACTGGGGCACAATACACGCCATTGATTTTTGCCTGGAATAAGTGGGATAG 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TTGTTTCCCTTCTACTGGGGCACAATACACGCCATTGATTTTTGCCTGGAATAAGTGGGATAG 900

Qy   901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTATGATAAGCTGTTTTCCTTCCAA 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTATGATAAGCTGTTTTCCTTCCAA 960

Qy   961 TTGTTGTCCCTGATATTTAAAAAGCATACACTATTCCTGCCCATGCTTGAGGAAGATACTGA 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TTGTTGTCCCTGATATTTAAAAAGCATACACTATTCCTGCCCATGCTTGAGGAAGATACTGA 1020

Qy   1021 AGATTAGACATGGTTGGGGAGGACGTCACCAAAAATTAAACAGATATGTTCCCAGT 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 AGATTAGACATGGTTGGGGAGGACGTCACCAAAAATTAAACAGATATGTTCCCAGT 1080

Qy   1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATATTTTATCACCAACATT 1140
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Db   1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATATTTTATCACCAACATT 1140

Qy   1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195

RESULT 8
AX267904

```
LOCUS       AX267904                1195 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 878 from Patent WO0173032.
ACCESSION   AX267904
VERSION     AX267904.1  GI:16516522
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
            Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
            Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
            and Henderson,R.A.
  TITLE     Compositions and methods for the therapy and diagnosis of prostate
            cancer
  JOURNAL   Patent: WO 0173032-A 878 04-OCT-2001;
            CORIXA CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1..1195
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

Query Match             100.0%;  Score 1195; DB 6;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-238;
  Matches 1195; Conservative    0; Mismatches    0; Indels    0; Gaps    0;
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RESULT 10
LOCUS       AX951736                1195 bp    DNA     linear   PAT 08-JAN-2004
DEFINITION  Sequence 35 from Patent EP1367138.
ACCESSION   AX951736
VERSION     AX951736.1  GI:40782084
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Wang,Y.
  TITLE     Markers for breast cancer prognosis
  JOURNAL   Patent: EP 1367138-A 35 03-DEC-2003;
            Ortho Clinical Diagnostics Inc. (US)
FEATURES             Location/Qualifiers
     source          1..1195
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match            100.0%;  Score 1195;  DB 6;  Length 1195;
Best Local Similarity  100.0%;  Pred. No. 5.5e-238;
Matches 1195;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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(The remainder of the page consists of a Query/Db nucleotide sequence alignment presented in two columns, with Qy and Db rows of DNA sequence and base-position numbering from position 1 through 1195, all bases matching.)

RESULT 11

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LOCUS       AX960014                1195 bp    DNA        linear   PAT 14-JAN-2004
DEFINITION  Sequence 35 from Patent EP1349104.
ACCESSION   AX960014
VERSION     AX960014.1  GI:40880240
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jatkoe,T.
  TITLE     Method of selecting a portfolio of markers for use in a diagnostic
            application
  JOURNAL   Patent: EP 1349104-A 35 01-OCT-2003;
            Ortho-Clinical Diagnostics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1..1195
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN
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Query Match             100.0%;  Score 1195;  DB 6;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-238;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy    1 CCGAGACTCACGGTCAGCTGAGGCGAGAAGAGTGGGTGGCTGGCTGAGCCATACTATTTTATAG   60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 CCGAGACTCACGGTCAGCTGAGGCGAGAAGAGTGGGTGGCTGGCTGAGCCATACTATTTTATAG   60

Qy   61 AATTAATGGAAAGCAGAAAAACAAGAAGAGAACATCACAAAACCAAGAGAAAATGAAGCCTA  120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AATTAATGGAAAGCAGAAAAACAAGAAGAGAACATCACAAAACCAAGAGAAAATGAAGCCTA  120

Qy  121 GGAGAAATTTAGAGAAGACGAATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA  180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GGAGAAATTTAGAGAAGACGAATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA  180

Qy  181 AAAGACCTGTGCTTTTGCATTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTT  240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 AAAGACCTGTGCTTTTGCATTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTT  240

Qy  241 CAGAACTTCAGCACACACAGAGAACTCTTTCCACACTGCCACTTGCCAATTAAAATAGCTG  300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 CAGAACTTCAGCACACACAGAGAACTCTTTCCACACTGCCACTTGCCAATTAAAATAGCTG  300

Qy  301 CTATTATAGGCATCTCTGACTTTTCTTCTTGAGGAGGAAGTAATTCACCCCTTTAG  360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 CTATTATAGGCATCTCTGACTTTTCTTCTTGAGGAGGAAGTAATTCACCCCTTTAG  360

Qy  361 CAACTTCCCATCAACAATATTTTATAAAAATTCCAATCCTCTGAGAGTCATCAACAAAGTCTTGC  420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 CAACTTCCCATCAACAATATTTTATAAAAATTCCAATCCTCTGAGAGTCATCAACAAAGTCTTGC  420

Qy  421 CAATGGTTTCCATCACTCTCTGGCATTGGTTTACCTGCCAGGTGGTGATAGCAGCAAATTG  480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 CAATGGTTTCCATCACTCTCTGGCATTGGTTTACCTGCCAGGTGGTGATAGCAGCAAATTG  480

Qy  481 TCCAACTTCATAAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT  540
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Db  481 TCCAACTTCATAAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT  540

Qy  541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTTCTTTGCTGTACTGGTCATCGCAATTATA  600
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Db  541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTTCTTTGCTGTACTGGTCATCGCAATTATA  600

Qy  601 GTCCGTCTTACCCAATGAGCGCGATCCTACAGAATCACAAGTTGCTAAAACTGGGCCATATCAAC  660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 GTCCGTCTTACCCAATGAGCGCGATCCTACAGAATCACAAGTTGCTAAAACTGGGCCATATCAAC  660

Qy  661 AGGTCCAACAAAAATAAAGAAGAATGCCTGGATTGACGATGATGTTTGGGAGGAATGGAGATTT  720
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 AGGTCCAACAAAAATAAAGAAGAATGCCTGGATTGACGATGATGTTTGGGAGGAATGGAGATTT  720

Qy  721 ATGTGTCTCTGGGAATTGTGGGATGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC  780
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 ATGTGTCTCTGGGAATTGTGGGATGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC  780

Qy  781 CATCTGTGAGTGACTCTTTGACACTGGAGAGAATTTCACTATATCCAGAGCAAGCTAGGAA  840
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 CATCTGTGAGTGACTCTTTGACACTGGAGAGAATTTCACTATATCCAGAGCAAGCTAGGAA  840

Qy  841 TTGTTTCCCTTCTACTGGGCCACAATACACGGCCATTGATTTTTGCCTGGAATAAGTGGATAG  900
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 TTGTTTCCCTTCTACTGGGCCACAATACACGGCCATTGATTTTTGCCTGGAATAAGTGGATAG  900

Qy  901 ATATAAAAACAAATTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA  960
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 ATATAAAAACAAATTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA  960

Qy  961 TTGTTGTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCCTTGAGGAAGAAGATACTGA 1020
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 TTGTTGTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCCTTGAGGAAGAAGATACTGA 1020

Qy 1021 AGATTAGACATGGTTGGGGAAGACGTCACCAAAAATTAACAAAAACTGAGATATGTTCCCAGT 1080
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Db 1021 AGATTAGACATGGTTGGGGAAGACGTCACCAAAAATTAACAAAAACTGAGATATGTTCCCAGT 1080

Qy 1081 TGTAGAATTACTGTTTACACACATTTTGTTCAATAATTGATATATATTTATCACCAACATT 1140
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Db 1081 TGTAGAATTACTGTTTACACACATTTTGTTCAATAATTGATATATATTTATCACCAACATT 1140

Qy 1141 TCAAGTTTGTTATTTGTTAATAAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAAAA 1195
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 TCAAGTTTGTTATTTGTTAATAAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAAAA 1195
```

RESULT 12

AF186249

LOCUS   AF186249   1195 bp   mRNA   linear   PRI 14-DEC-1999

DEFINITION   Homo sapiens six transmembrane epithelial antigen of prostate
           (STEAP1) mRNA, complete cds.

ACCESSION   AF186249

VERSION   AF186249.1   GI:6572947

KEYWORDS   .

SOURCE   Homo sapiens (human)

ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominidae; Homo.

REFERENCE   1 (bases 1 to 1195)

AUTHORS   Hubert,R.S., Vivanco,I., Chen,E., Rastegar,S., Leong,K.,
           Mitchell,S.C., Madraswala,R., Zhou,Y., Kuo,J., Raitano,A.B.,
           Jakobovits,A., Saffran,D.C. and Afar,D.E.

TITLE   STEAP: a prostate-specific cell-surface antigen highly expressed in
           human prostate tumors

JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (25), 14523-14528 (1999)

PUBMED   10588738

REFERENCE   2 (bases 1 to 1195)

AUTHORS   Hubert,R.S., Vivanco,I., Chen,E., Rastegar,S., Leong,K.,
           Mitchell,S.C., Madraswala,R., Zhou,Y., Kuo,J., Raitano,A.B.,
           Jakobovits,A., Saffran,D.C. and Afar,D.E.H.

TITLE   Direct Submission

JOURNAL   Submitted (14-SEP-1999) UroGenesys Inc., 1701 Colorado Ave., Santa
           Monica, CA 90404, USA

FEATURES   Location/Qualifiers

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                 /map="7p22.3"

     gene   1..1195
                 /gene="STEAP1"

     CDS   66..1085
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                 prostate"
                 /protein_id="AAF17479.1"
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                 RKQFGLLSFFFAVLHAIYSLSYPMRRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI
                 YVSLGIVGLAILALLAVTSIPSVSDSLTWREFHYIQSKLGIVSLLLGTIHALIFAWNK
                 WIDIKQFVWYTPPTFMIAVFLPIVVLIFKSILFLPCLRKKILKIRHGWEDVTKINKTE
                 ICSQL"

ORIGIN

Query Match   100.0%; Score 1195; DB 8; Length 1195;
Best Local Similarity   100.0%; Pred. No. 5.5e-238;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     1 CCGAGACTCACGGTCAAGCTCAAGCGAAGAGTGGGTGGCTGGCTGAAGCCATACTATTTTTATAG 60
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Db     1 CCGAGACTCACGGTCAAGCTCAAGCGAAGAGTGGGTGGCTGGCTGAAGCCATACTATTTTTATAG 60

Qy    61 AATTAATGGAAAGCAGAAAAGACATCACAAAACCAAGAAGAACTTTGGAAAAATGAAGCCTA 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 AATTAATGGAAAGCAGAAAAGACATCACAAAACCAAGAAGAACTTTGGAAAAATGAAGCCTA 120

Qy   121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGACCAGCATGCTAA 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGACCAGCATGCTAA 180

Qy   181 AAAGACCTGTGCTTTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
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Db   181 AAAGACCTGTGCTTTTGCATTTGCACCAAAACAGCCAGCAGTGGCATGCTGATGAATTTGACTGCTG 240
Qy   241 CAGAACTTCAGCACACACAGGAGAACTCTTTCCACACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
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Db   361 CAACTTCCCATCAACACAAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
Qy   421 CAATGGTTTCCATCACTCCTTGGCATTGGTTTACCTGGCAGGTGTTGATTAGCAGCAATTG 480
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Qy   481 TCCAAACTTCATTAATGGACCAACCAGTATAAGAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
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Qy   541 TAACAAGAAAGCAGCAGTTTGGGGCTTCTCAGTTTCTCTTTTTTTTGCTGCATTGCAATTTATA 600
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Qy   661 AGGTTCCACAAAAAATAAAGAAGATGCCCTGGATTGAGCATGATGATGTTGGAGAAATGGAGATT 720
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Qy   781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTCACTTATATCATTCAGAGCAAGCTAGGAA 840
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Qy   841 TTGTTTCCCTTCTACTGGGCACAATACACGGCCATTGATTTTTGCCTGGAATAAGTGGATAG 900
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Qy   901 ATATAAAACAAATTTGTATGGTATAACCTTCCAACTTTTATGATAGCTGTTTTCTTCCAA 960
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Qy   961 TTGTTTGTCCTGATATTTAAAGCATACATTAAAAAGAATTAACAAAACTGAGATATTACTGA 1020
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Qy  1021 AGATTAGACATGGGTTGGGGAGGACGTCACCAAAAATTAACAAAACTGAGATAGTTCCAGT 1080
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RESULT 13

CQ981397

LOCUS   CQ981397   1330 bp   DNA   linear   PAT 25-JAN-2005

DEFINITION   Sequence 252 from Patent EP1498424.

ACCESSION   CQ981397

VERSION   CQ981397.1   GI:58190687

KEYWORDS
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Rosenthal,A., Hermann,K., Heiden,E., Pilarsky,C., Bruemmendorf,T.,
            Staub,E., Roepcke,S., Mennerich,D., Kinnemann,H. and Li,X.
  TITLE   Human nucleic acid sequences from lung tumours
  JOURNAL   Patent: EP 1498424-A 252 19-JAN-2005;
            Hinzmann, Bernd (DE); Hermann, Klaus (DE); Heiden, Esmeralda (DE);
            Rosenthal, Andre (DE)
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ORIGIN

Query Match   100.0%; Score 1195; DB 6; Length 1330;
Best Local Similarity 100.0%;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     61  AATTAATGGRAAAGCACGAAAAAGACATCACAAACCAAGAGAAGAACTTTGGAAAATGAAGCCTA   120
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Qy    121  GGAGAAATTTAGAAGAAGACGGATTATTTGCATAAGGACACGGGAGACAGCAGCCATGCTAA   180
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Qy    181  AAAGACCTGTCCTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT    240
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Qy    421  CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGTGTGTCATCAACAAAGTTG   480
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Db    856  ATGTGTCTCTGGGGAATTGTGGGCAATACTGGCTCTGTTGCTGCTGTGCACATCTATTC   915
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RESULT 14
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LOCUS       CS031875     Sequence 1381 from Patent WO2005016962.     1330 bp    DNA    linear    PAT 10-MAR-2005
DEFINITION  Sequence 1381 from Patent WO2005016962.
ACCESSION   CS031875
VERSION     CS031875.1  GI:60731699
KEYWORDS
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Abbas,A., Clark,H., Ouyang,W., Williams,M.P., Wood,W.I. and Wu,T.D.
  TITLE     Compositions and methods for the treatment of immune related
            diseases
  JOURNAL   Patent: WO 2005016962-A 1381 24-FEB-2005;
            Genentech, Inc. (US)
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ORIGIN

Query Match         100.0%;  Score 1195;  DB 6;  Length 1330;
Best Local Similarity  100.0%;
Matches 1195;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Db    256  GGAGAAATTTAGAAGAAGACGGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA   315
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RESULT 15
CS036259
LOCUS   CS036259   1330 bp   DNA   linear   PAT 10-MAR-2005
DEFINITION   Sequence 5765 from Patent WO2005016962.

ACCESSION   CS036259
VERSION   CS036259.1   GI:60733938
KEYWORDS   .
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE   1
AUTHORS   Abbas,A., Clark,H., Ouyang,W., Williams,M.P., Wood,W.I. and Wu,T.D.
TITLE   Compositions and methods for the treatment of immune related
             diseases
JOURNAL   Patent: WO 2005016962-A 5765 24-FEB-2005;
             Genentech, Inc. (US)
FEATURES   Location/Qualifiers
     source   1..1330
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ORIGIN

Query Match   100.0%; Score 1195; DB 6; Length 1330;
Best Local Similarity   100.0%;
Matches 1195; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CCGGAGACTCACGGTCAAGTCTAAGCGCAAGAGAGTGGGTGGCTGAAGCCCATGACTACTTTATAG 60

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Qy    781 CATCTGTGAGTGACTCCTTTGACATGGAGGAGAATTTCACTATATTCAGAGCAAGCTTAGGAA 840
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Db   1216 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTTATCACCAACATT 1275

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OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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c	3	39	3.3	2464	6	US-10-750-185-39315	Sequence 39315, A
c	4	38.6	3.2	2133	6	US-10-750-185-26044	Sequence 26044, A
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ALIGNMENTS

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; Publication No. US2005026060 3A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59979
; LENGTH: 1687
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-59979

Query Match 55.9%; Score 40; DB 6; Length 1687;
Best Local Similarity 55.9%;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   1060 AAACTGAGATATGTTCCCAGTTGTAGAAATTACTGTTTACACACATTTTTTGTTCAATATTG 1119
               ||  ||   |  || | || | |    || | ||  | | |||| ||   |||   |
Db    507 AACATTAATAATTTTATCTTTTATAATATATAAAATGATTAATTCAAGGAAATG 448

Qy   1120 ATATATTTATCACCAACATTTCAAGTTTTGTATTTGTTTATAATATATTATTCAACGAA 1179
          |||||| | || | ||| ||||| ||| | |||||| || |  || |||||| |||  |
Db    447 TTTCATTGTTTGACATTTGTTTTTTGTTTTATTTGTTGTTTTTAATATATTTATACTGAGAGA 388

Qy   1180 AAAAAAAAAAAAAAAAA 1195
          |  |||  ||| |||
Db    387 AGGAAGAGAGAAAAGA 372
```

RESULT 2
US-10-750-185-25365
; Sequence 25365, Application US/10750185

; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25365
; LENGTH: 1779
; TYPE: DNA
; ORGANISM: Bovine   198668060913
US-10-750-185-25365

Query Match   3.3%; Score 39.2; DB 6; Length 1779;
Best Local Similarity   54.1%; Pred. No 2.1;
Matches 80; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Qy   769 TGACATCTATTCCATCTGTGAGTGACTCTTTGACATGGAGGAATTTCACTATATTCAGA 828
              |||||| ||||| |||| ||||||||||||| ||||||||| ||||||||||||||||
Db   765 TGACATTAATTCTGTCTGTTACTGTTATTCTTACTTGTATCGGTTTTAATTATATCATTA 824

Qy   829 GCAAGCTAGGAGAATTGTTTCCCTTCTACTGGGCACAATACACGCATTGAATTTGCCTGGA 888
              ||||
Db   825 AAAAGCACATGACACTTAGTCTTTTGCTGTGCAAATAAGATAAAAAATGATTTGTCCTTTGT 884

Qy   889 ATAAGTGGGATAGAGAATATATAAAAACAATTTGT 916
              |||
Db   885 TAACTTATATTTTAAAAAAACAATGTTGT 912

RESULT 3
US-10-750-185-39315/c
Sequence 39315, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39315
; LENGTH: 2464
; TYPE: DNA
; ORGANISM: Bovine   1986688156421l
US-10-750-185-39315

Query Match   3.3%; Score 39; DB 6; Length 2464;
Best Local Similarity   50.3%; Pred. No 2.7;
Matches 96; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

Qy   899 AGATATAAAACAAATTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCC 958
              |||||| |||| ||||||
Db 1748 AGAGAAAGGGAAAAATTCTGGAATATATAAAAATGCCATTCTGCAGTGTATATCTGCAGTCTCAAT 1689

RESULT 4
US-10-750-185-26044
Sequence 26044, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26044
; LENGTH: 2133
; TYPE: DNA
; ORGANISM: Bovine   1986680786954
US-10-750-185-26044

Query Match   3.2%; Score 38.6; DB 6; Length 2133;
Best Local Similarity   47.0%; Pred. No 3.2;
Matches 119; Conservative 0; Mismatches 134; Indels 0; Gaps 0;

Qy   915 GTATCGTGATACACCTCCACACTTTTATGATAGCTGTTTTCCTTCCCAAATTGTTGTCCTGATA 974
Db   762 GTATTTAATTCAAATTTTAAAAGCATAATTTGTTGTCTTGGCTTTATTATAAAATTAACAAA 821

Qy   975 TTTAAAAGCATACTATTCCTGCCATGCTTGAGGAGAAGATACTGAAGATTAGACATGGT 1034
Db   822 TGCACATAATAAATTTTTCTAACAATACAGAAAAGTGTATAATATAGAAAGTTCCCCATCAT 881

Qy 1035 TGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTGTGTAGAATTACTGT 1094
Db   882 ATAACATAATCCAGAAGTGTATATAAAAACAGAAAATTCCTCATAATTCAAGAAAATAACTG 941

Qy 1095 TTACACACATTTTGTTCAATATATTGATATATTTATCACCAACATTTCAAGTTGTATTT 1154
Db   942 TTCTTAAAAATTTGGTTTATATTTTCCATTTTTCTATGCATATTTTAACATATATAAATAT 1001

Qy 1155 GTTAATAAAATGA 1167
Db 1002 GTAATTACTTTGA 1014

RESULT 5
US-11-145-703-1/c
Sequence 1, Application US/11145703
; Publication No. US20050260667A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya

APPLICANT: Bouguéleret, Lydie
APPLICANT: Bihain, Bernard
APPLICANT: Essioux, Laurent
TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
FILE REFERENCE: 53.US16.DIV
CURRENT APPLICATION NUMBER: US/11/145,703
CURRENT FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: US/10/147,603
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 09/539,333
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: US 60/126,903
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: US 60/131,971
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: US 60/132,065
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: US 60/143,928
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: US 60/145,915
PRIOR FILING DATE: 1999-07-27
PRIOR APPLICATION NUMBER: US 60/146,453
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: US 60/146,452
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: US 60/162,288
PRIOR FILING DATE: 1999-10-28
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 234
SOFTWARE: Patent.pm

SEQ ID NO 1
LENGTH: 319608
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 31..1107
OTHER INFORMATION: 5'regulatory region g35018 gene
FEATURE:
NAME/KEY: exon
LOCATION: 1108..1289
OTHER INFORMATION: exon A g35018 gene
FEATURE:
NAME/KEY: exon
LOCATION: 14877..14920
OTHER INFORMATION: exon B g35018 gene
FEATURE:
NAME/KEY: exon
LOCATION: 18778..18862
OTHER INFORMATION: exon Bbis g35018 gene
FEATURE:
NAME/KEY: exon
LOCATION: 25593..25740
OTHER INFORMATION: exon C g35018 gene
FEATURE:
NAME/KEY: exon
LOCATION: 29388..29502
OTHER INFORMATION: exon D g35018 gene
FEATURE:
NAME/KEY: exon
LOCATION: 29967..30282
OTHER INFORMATION: exon E g35018 gene
FEATURE:
NAME/KEY: exon
LOCATION: 64666..64812
OTHER INFORMATION: exon F g35018 gene
FEATURE:
NAME/KEY: exon
LOCATION: 65505..65853
OTHER INFORMATION: exon G g35018 gene
FEATURE:
NAME/KEY: misc_feature
LOCATION: 65854..67854

OTHER INFORMATION: 3'regulatory region g35018 gene
FEATURE:
NAME/KEY: exon
LOCATION: 94124..94964
OTHER INFORMATION: exon g35017
FEATURE:
NAME/KEY: exon
LOCATION: 201188..201234
OTHER INFORMATION: exon S g35030 gene
FEATURE:
NAME/KEY: exon
LOCATION: 214676..214793
OTHER INFORMATION: exon T g35030 gene
FEATURE:
NAME/KEY: exon
LOCATION: 215702..215746
OTHER INFORMATION: exon U g35030 gene
FEATURE:
NAME/KEY: exon
LOCATION: 216836..216915
OTHER INFORMATION: exon V g35030 gene
FEATURE:
NAME/KEY: misc_feature
LOCATION: 213818..215818
OTHER INFORMATION: 3'regulatory region g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 215819..215941
OTHER INFORMATION: exon R complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 215819..215975
OTHER INFORMATION: exon Rbis complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 216661..216952
OTHER INFORMATION: exon Q complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 216661..217061
OTHER INFORMATION: exon Q complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 217027..217061
OTHER INFORMATION: exon Q1 complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 229647..229742
OTHER INFORMATION: exon Qbis complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 216661..217061
OTHER INFORMATION: exon X complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 230408..230721
OTHER INFORMATION: exon P complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 231272..231412
OTHER INFORMATION: exon Obis complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 231787..231880
OTHER INFORMATION: exon O2 complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 231870..231879
OTHER INFORMATION: exon O1 complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 234174..234321
OTHER INFORMATION: exon O complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 237406..237428
OTHER INFORMATION: exon Nbis complement g34872 gene

FEATURE:
NAME/KEY: exon
LOCATION: 239719..239807
OTHER INFORMATION: exon N2 complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 239719..239853
OTHER INFORMATION: exon N complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 240528..240569
OTHER INFORMATION: exon M1117 complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 240528..240596
OTHER INFORMATION: exon M1090 complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 240528..240617
OTHER INFORMATION: exon M1069 complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 240528..240644
OTHER INFORMATION: exon M1 complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 240528..240692
OTHER INFORMATION: exon M692 complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 240528..240824
OTHER INFORMATION: exon M862 complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 240528..240994
OTHER INFORMATION: exon M692 complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 240528..241685
OTHER INFORMATION: exon M1 complement g34872 gene
FEATURE:
NAME/KEY: misc_feature
LOCATION: 241686..243685
OTHER INFORMATION: 5'regulatory region g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 240800..240993
OTHER INFORMATION: exon MS1 complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 240824..240993
OTHER INFORMATION: exon MS2 complement g34872 gene
FEATURE:
NAME/KEY: misc_feature
LOCATION: 290652..292652
OTHER INFORMATION: 3'regulatory region g34665 gene

Query Match   3.2%;   Score 38.6;   DB 7;   Length 319608;
Best Local Similarity   48.1%;   Pred. No. 25;
Matches 139;   Conservative   0;   Mismatches 149;   Indels   1;   Gaps   1;

```
Qy    905 AAAACAAATTTGTATCGGTATACACCTCCAACTTTTATGATAGACGTGTTTTCCTTCCAATTGT 964
          |||||||||| |||  ||| || ||| ||| | |||||| | ||| || ||| |||||||
Db  13082 AAACCAACTGTTATGTTTTCTTTTCCAGTGAGTTAGGTAGTCTTTTAAAATCACATTGG 13023

Qy    965 TGTCCTGATATTTAAAAGCATACTAATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGAT 1024
          ||||||||||||||
Db  13022 TGGAAATATGTATGTATATACAATACATCATCATATATATAATACATTATATATATATAT 12963

Qy   1025 TAGACATGGTTGGGAAGACGTCACCAAAAATTAACAAAACTGAGATATGTTCCCAGTTGTA 1084
          ||| |||
Db  12962 AAAATTATAATATATTATATTATGTATTATAAATTATATATATATATAAAATTATATTA 12903

Qy   1085 GAATTACTGTTTACACACANTTTTGTTCAATATTGATATAGACTGTTTTCCTTCCAATTTCAA 1144
          ||| |||
Db  12902 TATATAAATTATA-ATATATATTATAATATTATTATTATTACATATTTTATTATAACACAATTT 12843

Qy   1145 GTTTGTATTTGTTTAATAAAATGATTATTCAAGGAAAAAATGATTATATAATATTATTATAAA 1193
          ||| |||
Db  12843 TTATATATAATAAATTTATATAAATTATTATAATTATATATAATTATATTATTATAATTATAAA 12795
```

RESULT 6
US-10-750-185-36894/c
Sequence 36894, Application No. US2005026060A1
Publication No. US2005026060A1

GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
SEQ ID NO 36894
LENGTH: 1301
TYPE: DNA
ORGANISM: Bovine
US-10-750-185-36894   198668101688 6

Query Match   3.1%;   Score 37.6;   DB 6;   Length 1301;
Best Local Similarity   61.0%;   Pred. No. 4.6;
Matches 61;   Conservative   0;   Mismatches 39;   Indels   0;   Gaps   0;

```
Qy   1096 TACACACATTTTGTTCAAATATTGATATATTTATCACCAACACATTTCAAGTTTGTATTTG 1155
          |||||||||| || ||| ||||  |||  ||| || ||| ||||||||| ||
Db    851 TGCAGACATTTTAATTCTCCAAAATTGTGTTTTTGTGTTTAAATTCTCCAAGATTGTGTTCT 792

Qy   1156 TTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAA 1195
          ||||||||||||||||||||||||||||||||||||
Db    791 TGTTCTGAAGGTATAATCACAGCAAAAAAAAAAAAA 752
```

RESULT 7
US-10-750-185-57750
Sequence 57750, Application US/10750185
Publication No. US2005026060A1

GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
SEQ ID NO 57750
LENGTH: 1443
TYPE: DNA
ORGANISM: Bovine
US-10-750-185-57750   198668122939 5

Query Match   3.1%;   Score 37.4;   DB 6;   Length 1443;
Best Local Similarity   48.4%;   Pred. No. 5.3;
Matches 104;   Conservative   0;   Mismatches 111;   Indels   0;   Gaps   0;

```
Qy    980 AAGCATACTAATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATTAGACATGGTTGGGA 1039
          |||  || ||| || | | ||| ||||| || || ||| ||| || || |||
Db     50 AACCTAAGTGTCCATGACAGATGAACAGATAAAGAAAATGTGGAAAACACATACAATGGA 109
```

RESULT 8
US-10-750-185-32077/c
; Sequence 32077, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32077
; LENGTH: 1495
; TYPE: DNA
; ORGANISM: Bovine   1986688171280
US-10-750-185-32077

Query Match   3.1%;   Score 37; DB 6; Length 1495;
Best Local Similarity   53.0%; Pred. No. 6.8;
Matches   79; Conservative   0; Mismatches 70; Indels   0; Gaps   0;

Qy 1040 AGAGGTCACCAAAAATTAACAAAAACTGAGATATGTTCCCAGTGTGTAGAATTACTGTTTACA 1099
          ||||| | ||||||| |||||| | |||| | | |||| || | |||| ||||||||
Db   110 ATAGTGTAACAAAAGAAAACAGTCTGTTCATATGTTATACACAGATTATCCTTGAGGACA   169

Qy 1100 CACATTTTTGTTCAATATTGATATATTTTATCACCAACATTTCAAGTGTTGTATTTGTTAA 1159
          | | | | | ||| | || | ||| | || ||||| | |||
Db   170 CAATGCTAAGTCAAATAAGGCCAATCACAAAAAGGCAAACTCTGAATGATTTCACTTGTAT 229

Qy 1160 TAAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1194
          ||| ||| ||| || |||||||||| |||||
Db   230 TAAATATCTTAATACAATCAAACCAAAGAAAACAGAA 264

RESULT 9
US-10-750-185-51935
; Sequence 51935, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31

Qy 1046 CACCAAAAATTAACAAAAACTGAGATAGTAGTTCCCAGTGTGTAGAATTACTGTTTACACACATT 1105
          ||| ||||||| | ||| | | | || || | ||| || |||| | | |||||
Db 1068 CACTAAAAATTTTGAATTTCGTATCATTTTTAAGTCGTCCTAAAATAAACTGTTCTTAATTAAA 1009

Qy 1106 TTTGTTCAATATTGATATATTTTATCACCAACATTTCAAGTGTTGTATTTGTTAATAAAAAT 1165
          ||| | ||||| || | | || | | | | |||| || ||| | ||||||||
Db 1008 TTATTTCAACCATTTAAAAAATGCAAAATCTTTCTGTAAAGTAATTAATCCTTCAATAAAAA 949

Qy 1166 GATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1194
          | || | || ||||| |||||||| ||||
Db   948 ATAAATGCATTTTAAAAACAAAAAATAAAA 920

RESULT 10
US-10-750-185-46765
; Sequence 46765, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46765
; LENGTH: 1835
; TYPE: DNA
; ORGANISM: Bovine   1986680952210
US-10-750-185-46765

Query Match   3.1%;   Score 37; DB 6; Length 1835;
Best Local Similarity   62.4%; Pred. No. 7.3;
Matches   58; Conservative   0; Mismatches 35; Indels   0; Gaps   0;

Qy 1102 CATTTTTGTTCAATATTGATATATTTTATCACCAACATTTCAAGTTTGTATTTGTTAATA 1161
          ||||||| | ||||| | | | ||| | | | | | ||| ||||||
Db   155 CATTTTATCCTAAGTCAATTTAATTTATATAAGGAAGCGTATCAAAATAAATAGCTCTTGATT 214

Qy 1162 AAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1194
          | ||| ||| || | ||||||| ||||||
Db   215 CTATATTTCTTTATGGAAGAGAAAAAAGAACAAA 247

RESULT 11
US-10-750-185-51383/c
; Sequence 51383, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.

Qy 1044 GTCACCAAAAATTAACAAAAACTGAGATATGTTCCCAGTGTGTAGAATTACTGTTTACACACA 1103
          ||| | |||| | | | || | | | ||| ||| | | |||| || |||||| |||
Db 1322 GTCTTTATTATTATTAAAATATGAAATGTTGTTGTTGTTAGTTACTAATGCCAACTTCTTGACACTGC 1381

Qy 1104 TTTTGTTCAATATTGATATATTTTATCACCAACATTTCAAGTTTGTATTTGTTAATAAA 1163
          | ||| |||||| | | | || | | | | ||| ||| | | | | || ||||
Db 1382 CAAATAATTAATATTGTAAAAATTTACTGACTAGAAATATATATAATGTGGGGTGTAAAACATA 1441

Qy 1164 ATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
          | || |||| || ||||| |||||||| ||
Db 1442 AATATTATTACTGGGAAAAGGTTAAAAAATAAA 1473

; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 6922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51383
; LENGTH: 2081
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-51383   1986680958299

Query Match   3.1%;   Score 36.8;   DB 6;   Length 2081;
Best Local Similarity   58.0%;   Pred. No. 8.7;
Matches   65; Conservative   0; Mismatches   47; Indels   0; Gaps   0;

Qy   1084 AGAATTACTGTTTACACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATTTCA 1143
               |||| ||||||| | || || |||||| | ||||||||||||||||| |||||||||||||
Db   472 AAAATCAGTGTTGATTATGATAATCATTCAAATTTGATATATTCCTTATTTATTATACAA 1143

Qy   1144 AGTTTGTATTTGTTTAATAAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   412 ATTTAGAAAATAAAAACACATTAGGAAAGATTTTGGAAAAAAAAAAAAAAACAA 361

RESULT 12
US-10-750-185-52737/c
; Sequence 52737, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 6922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52737
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-52737   1986681330166

Query Match   3.1%;   Score 36.6;   DB 6;   Length 1620;
Best Local Similarity   57.4%;   Pred. No. 8.7;
Matches   66; Conservative   0; Mismatches   49; Indels   0; Gaps   0;

Qy   1080 TTGTAGAATTACTGTTTACACACACATTTTTGTTCAATATTGATATATTTTATCACCAACAT 1139
               | || |||||||||| | || ||||||||||| |||||||||||||||| ||||||||
Db   345 TTATAGCAAAATATATTTCCAGTATTTTTTAAAAAACTAGAGCTATTTTTATAGGGGATAC 286

Qy   1140 TTCAAGTTTGTATTTGTTTAATAAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1194
               |||| || || ||||||||||||||||||||||||||||||||||||||||||||||
Db   285 TTGAAGCCAGTATTTAAGCTTTAAATGACAGTAATATTGGCATAGAAGAAAAAAAAA 231

RESULT 13
US-11-099-691-22

; Sequence 22, Application US/11099691
; Publication No. US20050260644A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: BANDMAN, Olga
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: LAL, Preeti
; APPLICANT: YUE, Henry
; APPLICANT: TANG, Y. Tom
; APPLICANT: PATTERSON, Chandra
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: YANG, Junming
; TITLE OF INVENTION: CELL SIGNALING PROTEINS
; FILE REFERENCE: PF-0521 PCT
; CURRENT APPLICATION NUMBER: US/11/099,691
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: 60/085,343
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US/09/700,444
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/098,010
; PRIOR FILING DATE: 1998-08-26
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PERL Program
; SEQ ID NO 22
; LENGTH: 2948
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte Clone 1403604
US-11-099-691-22

Query Match   3.0%;   Score 36.4;   DB 7;   Length 2948;
Best Local Similarity   59.8%;   Pred. No. 13;
Matches   61; Conservative   0; Mismatches   41; Indels   0; Gaps   0;

Qy   1094 TTTACACACACATTTTTGTTCAATAATGATATATTTTATCACCAACATTTCAAGTTTGTATT 1153
               ||||||||| ||||||||||||| | ||||||| ||||||||||||||| | |||| |||
Db   2846 TTTACCAACATACTTTTTAAAATGTTTTTGCTATTGGGTTCCATATTTATTTAGAGTTTATAAG 2905

Qy   1154 TGTTAATAAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAAA 1195
               ||||||||||||||||||||||||||||||||||||||||||
Db   2906 TGTCAATAAAGCAAACTTTTGATCCCTCAAAAAAAAAAAAAAA 2947

RESULT 14
US-10-750-185-45671
; Sequence 45671, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 6922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45671
; LENGTH: 1577
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-45671   1986680420845

Query Match   3.0%;   Score 36.2;   DB 6;   Length 1577;

Qy   1012 AGATACTGAAGATTAGACATGGTTGGGAACGTCACCAAAATTAACAAAACTGAGATAT 1071
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Db   922 AGGCACTTATATTATTTAAAATTTTTGTACAAAAGTACAATTATGACCAAAATTAAAAGGTAA 981

Qy   1072 GTTCCCAGTTGTTAGAATTACTGTTTTACACACATTTTTGTTCAATATTGATATATTTTTATC 1131
           |||| ||||| |||| ||| ||| ||| |||||||| ||||| ||| || |||| |
Db   982 ACAAAAAATATTAGAGTTATATGTAGAAAAACAAAGGTGGAAGCTCTTTATTATTATATTATAT 1041

Qy   1132 ACCAACATTTCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAA 1188
           || ||||| ||||||||| ||| ||||| |||||||| ||| ||||| ||
Db   1042 ATATATATATATAATTTATATATTTACTAAATAAAATGAGTACATAAAGAAGAAAAAGTAA 1098

RESULT 15
US-10-750-185-42808/c
; Sequence 42808, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42808
; LENGTH: 1978
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-42808   198668806B1507

Query Match   3.0%;   Score 36.2;   DB 6;   Length 1978;
Best Local Similarity   62.2%;   Pred. No. 12;
Matches   74;   Conservative   0;   Mismatches   43;   Indels   2;   Gaps   1;

Qy   1079 GTTGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGA--TATATTTATCACCAA 1136
           ||| || | | | | || | |||||||||||||||| ||||||| ||||||
Db   1569 GTATTAAATCTCTGATTAATTAAATCTTGCTCTATATTGACTTAAATTTGCTTTGAA 1510

Qy   1137 CATTTCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAA 1195
           |||||||||||||||||| ||| ||||||||||||||||||||||||||||
Db   1509 CAATAGGGATTTCAATTGTTAAGAGTCTTATTTTGCCAGAAGCAAAAAAAAAAAAAAA 1451

Best Local Similarity   50.3%;   Pred. No. 11;
Matches   89;   Conservative   0;   Mismatches   88;   Indels   0;   Gaps   0;

Search completed: December 5, 2005, 08:05:49
Job time : 379.544 secs

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OM nucleic - nucleic search, using sw model

Run on: December 4, 2005, 20:43:36 ; Search time 238.244 Seconds
                                              (without alignments)
                                              8916.024 Million cell updates/sec

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GenCore version 5.1.6

Title: US-10-750-262-1
Perfect score: 1195
Sequence: 1 ccgagagactcacggtcaagct.........ggaaaaaaaaaaaaaaaaaa 1195

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 200000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
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                 2: /cgn2_6/ptcdata/1/ina/5_COMB.seq:*
                 3: /cgn2_6/ptcdata/1/ina/6A_COMB.seq:*
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                 5: /cgn2_6/ptcdata/1/ina/H_COMB.seq:*
                 6: /cgn2_6/ptcdata/1/ina/PCTUS_COMB.seq:*
                 7: /cgn2_6/ptcdata/1/ina/PP_COMB.seq:*
                 8: /cgn2_6/ptcdata/1/ina/RE_COMB.seq:*
                 9: /cgn2_6/ptcdata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	1195	100.0	1195	3	US-09-323-873A-1	Sequence 1, Appli
2	1195	100.0	1195	3	US-09-685-166A-878	Sequence 878, App
3	1195	100.0	1195	3	US-09-679-426-878	Sequence 878, App
4	1195	100.0	1195	3	US-09-759-143-878	Sequence 878, App
5	1195	100.0	1195	3	US-10-010-667A-1	Sequence 1, Appli
6	1195	100.0	1195	3	US-10-012-896-878	Sequence 878, App
7	1193	99.8	1193	3	US-09-455-486-1	Sequence 1, Appli
8	1143.4	95.7	1147	3	US-09-949-016-2686	Sequence 2686, Ap
9	1193	99.1	3627	3	US-09-323-873A-6	Sequence 6, Appli
10	825.6	69.1	3627	3	US-09-455-486-4	Sequence 4, Appli
11	825.6	69.1	3627	3	US-10-010-667A-6	Sequence 6, Appli
12	825.6	69.1	3627	3	US-09-439-313-342	Sequence 342, App
13	581	48.6	592	3	US-09-352-616A-342	Sequence 342, App
14	581	48.6	592	3	US-09-636-215-342	Sequence 342, App
15	581	48.6	592	3	US-09-685-166A-342	Sequence 342, App
16	581	48.6	592	3	US-09-679-426-342	Sequence 342, App
17	581	48.6	592	3	US-09-759-143-342	Sequence 342, App
18	581	48.6	592	3	US-09-651-236-342	Sequence 342, App
19	581	48.6	592	3	US-09-657-279-342	Sequence 342, App
20	581	48.6	592	3	US-10-012-896-342	Sequence 342, App
21	515.6	43.1	9073	3	US-09-949-016-14428	Sequence 14428, A
22	360.6	30.2	455	3	US-09-621-976-9264	Sequence 9264, Ap
23	266.6	22.3	2453	3	US-09-455-486-5	Sequence 5, Appli
24	266.6	22.3	2469	3	US-10-104-047-1185	Sequence 1185, Ap
25	265	22.2	1403	3	US-10-012-896-995	Sequence 995, App
26	229.6	19.2	848	3	US-10-012-896-993	Sequence 993, App
27	221.4	18.5	519	3	US-09-323-873A-7	Sequence 7, Appli
28	221.4	18.5	521	3	US-10-010-667A-7	Sequence 7, Appli
29	212.8	17.8	2714	3	US-09-562-930-5	Sequence 5, Appli
30	212.8	17.8	3884	3	US-09-562-930-10	Sequence 10, Appl
31	187.4	15.7	4429	3	US-09-455-486-3	Sequence 3, Appli
32	184.8	15.5	1213	3	US-09-083-521-1	Sequence 1, Appli
33	171	14.3	1886	3	US-09-562-930-1	Sequence 1, Appli
34	166.6	13.9	1203	3	US-09-544-616-6	Sequence 6, Appli
35	162.4	13.6	366	3	US-10-030-607-215	Sequence 215, App
36	162.4	13.6	366	3	US-09-433-313-215	Sequence 215, App
37	162.4	13.6	366	3	US-09-322-616A-215	Sequence 215, App
38	162.4	13.6	366	3	US-09-155-812-215	Sequence 215, App
39	162.4	13.6	366	3	US-09-232-149A-215	Sequence 215, App
40	162.4	13.6	366	3	US-09-636-215-215	Sequence 215, App
41	162.4	13.6	366	3	US-09-685-166A-215	Sequence 215, App
42	162.4	13.6	366	3	US-09-115-453-215	Sequence 215, App
43	162.4	13.6	366	3	US-09-688-408-215	Sequence 215, App
44	162.4	13.6	366	3	US-09-679-426-215	Sequence 215, App
45	162.4	13.6	366	3	US-09-759-143-215	Sequence 215, App

ALIGNMENTS

RESULT 1
US-09-323-873A-1
; Sequence 1, Application US/09323873A
; Patent No. 6329503
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Kahan Leong
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; APPLICANT: Steve Chappell Mitchell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 129.16USU2
; CURRENT APPLICATION NUMBER: US/09/323,873A
; CURRENT FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-323-873A-1

  Query Match   100.0%; Score 1195; DB 3; Length 1195;
  Best Local Similarity   100.0%;
  Matches 1195; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CCGAGAGACTCACGGTCAAGCTCAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTATAG 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CCGAGAGACTCACGGTCAAGCTCAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTATAG 60

Qy   61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAGAGAACTTTGGAAAAATGAAGCCTA 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAGAGAACTTTGGAAAAATGAAGCCTA 120

Qy   121 GGAGAAAATTTAGAAGAAGACGATTATTTTGCATAAGGACACACGGGAGAGACCACCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGAGAAAATTTAGAAGAAGACGATTATTTTGCATAAGGACACACGGGAGAGACCACCATGCTAA 180

Qy   181 AAAGACCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCGCCTT 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AAAGACCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCGCCTT 240

RESULT 2

Query Match   100.0%; Score 1195; DB 3; Length 1195;
Best Local Similarity   100.0%; Pred. No. 6.6e-301;
Matches 1195; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy      1 CCGAGACTCACGGTCAAGCTRAAGGCGGAAGAGAGTGGGTGGGCTGAAGCCCATACTATTTTATAG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CCGAGACTCACGGTCAAGCTRAAGGCCGAAGAGTGGGTGGGCTGAAGCCCATACTATTTTATAG 60

Qy     61 AATTAATGGAAAGCAGAAAAGACATCACAAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AATTAATGGAAAGCAGAAAAGACATCACAAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy    121 GGAGAAATTTAGAAGAAGACCAATTATTTGCATTGACAAAACAGCCCATGCTGATGAATTTGACTGCCCTT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GGAGAAATTTAGAAGAAGACCAATTATTTGCATTGACAAAACAGCCCATGCTGATGAATTTGACTGCCTAA 180

Qy    181 AAAGACCCTGTCCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AAAGACCCTGTCCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCTT 240

Qy    241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy    301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAAATTCACCCTTTAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAAATTCACCCTTTAG 360

Qy    361 CAACTTCCCATCACAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CAACTTCCCATCACAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy    421 CAATGGTTTCCATCACTCTCTTGGGCATTGGTTTACCTGCCCAGGTGTTGATAGCAGCAAATTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CAATGGTTTCCATCACTCTCTTGGGCATTGGTTTACCTGCCCAGGTGTTGATAGCAGCAAATTG 480

Qy    481 TCCAACTTCATAATGGAACCAAGTATAAGAGAGTTTCCACAATTGGATAAGAGTGGATGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TCCAACTTCATAATGGAACCAAGTATAAGAGAGTTTCCACAATTGGATAAGAGTGGATGT 540

Qy    541 TAACAAGAAAGCAGTTTGGGCCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAAATTTATA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TAACAAGAAAGCAGTTTGGGCCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAAATTTATA 600

Qy    601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCAATCAAC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCAATCAAC 660
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Db 601 GTCTGTGTTACCCAATGAGGGGATCCTACACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 661 AGGTCCAACAAAATAAAGAACGATGCCTGGATTGAGCATGAGTGATGTTGGAGAATGGAGATTT 720
Db 661 AGGTCCAACAAAATAAAGAACGATGCCTGGATTGAGCATGAGTGATGTTGGAGAATGGAGATTT 720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 721 ATGTGTCTTCTGGGAATTGTGGGATTGGCAATACTGGCTCTCGTTGGGCTGTGTGACATCTATTC 780
Db 721 ATGTGTCTTCTGGGAATTGTGGGATTGGCAATACTGGCTCTCGTTGGGCTGTGTGACATCTATTC 780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 781 CATCTGTGAGTGAGTCTCTTTGACATGGAGAGAATTTCACTATATTATTCAGAGCAAGCTAGGAA 840
Db 781 CATCTGTGAGTGACTCTTTGACATGGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
Qy 841 TTGTTTCCCTTCTACTGGGCACAATACACGGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
Db 841 TTGTTTCCCTTCTACTGGGCACAATACACGGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
Qy 901 ATATAAAAACAATTTGTATGGTTATACACCTCCAAACTTTTATGATAGCTGTTTTCCTTCCAA 960
Db 901 ATATAAAAACAATTTGTATGGTTATACACCTCCAAACTTTTATGATAGCTGTTTTCCTTCCAA 960
Qy 961 TTGTTGTCTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
Db 961 TTGTTGTCTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
Qy 1021 AGATTAGACATGGGTTGGGGAAGACGTCACCAAAAATTAACAAAAACTGAGATAGTTCCCAGT 1080
Db 1021 AGATTAGACATGGGTTGGGGAAGACGTCACCAAAAATTAACAAAAACTGAGATAGTTCCCAGT 1080
Qy 1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATAATCAATCCTGGTCATCAACAAGTCTTGC 1140
Db 1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATAATCAATCCTGGTCATCAACAAGTCTTGC 1140
Qy 1141 TCAAGTTGTGTATTTGTTAATAAAAATGATTTATTCCTGCCATGCTTGAGGAAGAAGAATTG 1195
Db 1141 TCAAGTTGTGTATTTGTTAATAAAAATGATTTATTCAAGGAAAAAAAAAAAAAAAAAAAAAA 1195

RESULT 3
US-09-679-426-878
; Sequence 878, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C20
; CURRENT APPLICATION NUMBER: US/09/679,426
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-679-426-878

Query Match 100.0%; Score 1195; DB 3; Length 1195;
Best Local Similarity 100.0%; Pred. No. 6.0e-301;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAAGAGTGGGTGGCCATACTATTTTATAG 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAAGAGTGGGTGGCCATACTATTTTATAG 60
Qy   61 AATTAATGGAAAGACAGAAAAACATCACAAAACCAAGAAGAACTTTGAAAATGAAGCCTA 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AATTAATGGAAAGACAGAAAAACATCACAAAACCAAGAAGAACTTTGAAAATGAAGCCTA 120
Qy 121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGAACACGGGAGAGAACCAGCATGCTAA 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGAACACGGGAGAGAACCAGCATGCTAA 180
Qy 181 AAAGACCTGTGCTTTTGCCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 AAAGACCTGTGCTTTTGCCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
Qy 241 CAGAACTTCAGCACACACAGAGAACTCTTTCCACAGTGGGCACTTGCCCAATTAAAATACCTG 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 CAGAACTTCAGCACACACAGAGAACTCTTTCCACAGTGGGCACTTGCCCAATTAAAATACCTG 300
Qy 301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
Qy 361 CAACTTCCCATCAACAATATTTTTATGAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 CAACTTCCCATCAACAATATTTTTATGAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
Qy 421 CAAATGGTTTTCATCACTCTCTTGGCATTGGTTTACCTGCCCAGGTGTGATAGCAGCAATTG 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 421 CAAATGGTTTTCATCACTCTCTTGGCATTGGTTTACCTGCCCAGGTGTGATAGCAGCAATTG 480
Qy 481 TCCAACTTCATAATGGAACCAAGTATAAGAAGAGTTTCCACATTGGTTGGATAAGTGGATGT 540
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Db 481 TCCAACTTCATAATGGAACCAAGTATAAGAAGAGTTTCCACATTGGTTGGATAAGTGGATGT 540
Qy 541 TAACAAGAAAGCAGAGTTGGGCCTTCTCCAGTTCTTCTTTTTCTTTTGTGTACTGCATGCAAAATTTATA 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 541 TAACAAGAAAGCAGAGTTGGGCCTTCTCCAGTTCTTCTTTTTCTTTTGTGTACTGCATGCAAAATTTATA 600
Qy 601 GTCTGTGTTACCCAATGAGGGGATCCTACACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 601 GTCTGTGTTACCCAATGAGGGGATCCTACACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
Qy 661 AGGTCCAACAAAATAAAGAACGATGCCTGGATTGAGCATGAGTGATGTTGGAGAATGGAGATTT 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 661 AGGTCCAACAAAATAAAGAACGATGCCTGGATTGAGCATGAGTGATGTTGGAGAATGGAGATTT 720
Qy 721 ATGTGTCTTCTGGGAATTGTGGGATTGGCAATACTGGCTCTCGTTGGGCTGTGTGACATCTATTC 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 721 ATGTGTCTTCTGGGAATTGTGGGATTGGCAATACTGGCTCTCGTTGGGCTGTGTGACATCTATTC 780
Qy 781 CATCTGTGAGTGAGTCTCTTTGACATGGAGAGAATTTCACTATATTATTCAGAGCAAGCTAGGAA 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 781 CATCTGTGAGTGAGTCTCTTTGACATGGAGAGAATTTCACTATATTATTCAGAGCAAGCTAGGAA 840
Qy 841 TTGTTTCCCTTCTACTGGGCACAATACACGGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 841 TTGTTTCCCTTCTACTGGGCACAATACACGGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
Qy 901 ATATAAAAACAATTTGTATGGTTATACACCTCCAAACTTTTATGATAGCTGTTTTCCTTCCAA 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 901 ATATAAAAACAATTTGTATGGTTATACACCTCCAAACTTTTATGATAGCTGTTTTCCTTCCAA 960
Qy 961 TTGTTGTCTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 961 TTGTTGTCTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy 1021 AGATTAGACATGGTTGGGGAAGAGACGTCACCAAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 AGATTAGACATGGTTGGGGAAGAGACGTCACCAAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy 1081 TGTAGAAATTACTGTTTACACACAATATTTTTATTTTTCAATATTGATATATTTTATCACCAACATT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 TGTAGAAATTACTGTTTACACACAATATTTTTATTTTTCAATATTGATATATTTTATCACCAACATT 1140

Qy 1141 TCAAGTTTCGTATTTGTTAATTAAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAA 1195
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 TCAAGTTTCGTATTTGTTAATTAAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAA 1195

RESULT 4
US-09-759-143-878
; Sequence 878, Application US/09759143
; Patent No. 6807746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-878

Query Match   100.0%; Score 1195; DB 3; Length 1195;
Best Local Similarity 100.0%; Pred. No. 6.6e-301;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 CCCGAGACTCACGGTCACGGTCAAGCTAAGGCCGGACGAAGAGTGGGGTGGCTCTGGCTGAGCCATACTACTATTTTATAG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CCCGAGACTCACGGTCACGGTCAAGCTAAGGCCGGACGAAGAGTGGGGTGGCTCTGGCTGAGCCATACTACTATTTTATAG 60

Qy   61 AATTAATCGGAAAAGCAGAAAAAGACATCACAAAACCAAGAGAAGAACTTTGGAAAAATGAAAGCCTA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AATTAATCGGAAAAGCAGAAAAAGACATCACAAAACCAAGAGAAGAACTTTGGAAAAATGAAAGCCTA 120

Qy   121 GGAGAAATTTAGAAGAAGACGATTATTTCGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGAGAAATTTAGAAGAAGACGATTATTTCGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy   181 AAAGACCTGTTGCTTTTGCATTTGCACCAAACACGCCCATCGTGATGAATTTGACTGCCCTT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AAAGACCTGTTGCTTTTGCATTTGCACCAAACACGCCCATCGTGATGAATTTGACTGCCCTT 240

Qy   241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGGCCACTTGCCCAATTAAAATAGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGGCCACTTGCCCAATTAAAATAGCTG 300

Qy   301 CTATTATAGCATCTCTGACTTTCTTCTTTACACTCTTCTGAGGGAGGAAGTAAATTCACCCTTTAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTATTATAGCATCTCTGACTTTCTTCTTTACACTCTTCTGAGGGAGGAAGTAAATTCACCCTTTAG 360

Qy   361 CAACTTCCCATCACACAACATATTTTTTATTAAAATTCCAATCCTTCTGTCATCACACAAAGTCTTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CAACTTCCCATCACACAACATATTTTTTATTAAAATTCCAATCCTTCTGTCATCACACAAAGTCTTGC 420

Qy   421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAAATTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAAATTG 480

Qy   481 TCCAACTTCATTAATGGAACCAAGTAATAAGAAGAGTTCCACATTGGTTGGATTAAGTGGATGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TCCAACTTCATTAATGGAACCAAGTAATAAGAAGAGTTCCACATTGGTTGGATTAAGTGGATGT 540

Qy   541 TAACAAGAAAGCAGTTTGGGCCTTCTCAGTTTCTTTTTTTGGCTTGTTACTGCATGCAATTATA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TAACAAGAAAGCAGTTTGGGCCTTCTCAGTTTCTTTTTTTGGCTTGTTACTGCATGCAATTATA 600

Qy   601 GTCTGTCTTACCCAATGAGCGCGATCCTACAGATACAAGTTGCTAAAACTGGGCATATCAAC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTCTGTCTTACCCAATGAGCGCGATCCTACAGATACAAGTTGCTAAAACTGGGCATATCAAC 660

Qy   661 AGGTCCAACAAAATAAAGAAGAATGCCTGGATTGAGCATGATGTTTGGGAGAATGGGAGATTT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 AGGTCCAACAAAATAAAGAAGAATGCCTGGATTGAGCATGATGTTTGGGAGAATGGGAGATTT 720

Qy   721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATAACTGGCTCTCGTTGGCTGTGACATCTATTC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATAACTGGCTCTCGTTGGCTGTGACATCTATTC 780

Qy   781 CATCTGTGAGTGACTCTTTGACATGGAGGAGAATTTCACTATATATTCAGAGCAAGCTAGGAA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 CATCTGTGAGTGACTCTTTGACATGGAGGAGAATTTCACTATATATTCAGAGCAAGCTAGGAA 840

Qy   841 TTGTTTCCCTTCTACTGGGGCACAATACACGGCCATTGAATTTTTGCCTGGAATAAGTGGATAG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TTGTTTCCCTTCTACTGGGGCACAATACACGGCCATTGAATTTTTGCCTGGAATAAGTGGATAG 900

Qy   901 ATATAAAACAATATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTCCTTCCAA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 ATATAAAACAATATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTCCTTCCAA 960

Qy   961 TTGTTGTCCTGATATTTAAAAGCATACTACTTATTCCTGCCATGCTTGAGGAGAAGAAGATACTGA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TTGTTGTCCTGATATTTAAAAGCATACTACTTATTCCTGCCATGCTTGAGGAGAAGAAGATACTGA 1020

Qy 1021 AGATTAGACATGGTTGGGGAAGAGACGTCACCAAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 AGATTAGACATGGTTGGGGAAGAGACGTCACCAAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy 1081 TGTAGAAATTACTGTTTACACACAATATTTTTATTTTTCAATATTGATATATTTTATCACCAACATT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 TGTAGAAATTACTGTTTACACACAATATTTTTATTTTTCAATATTGATATATTTTATCACCAACATT 1140

Qy 1141 TCAAGTTTGTATTTGTTAATTAAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
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Db 1141 TCAAGTTTGTATTTGTTAATTAAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195

RESULT 5
US-10-010-667A-1
; Sequence 1, Application US/10010667A
; Patent No. 6887975
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Hubert, Rene S.
; APPLICANT: Leong, Kahan
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Saffran, Douglas C.
; APPLICANT: Mitchell, Steve Chappell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS

```
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 511582001601
; CURRENT APPLICATION NUMBER: US/10/010,667A
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 09/323,873
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 1
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-010-667A-1

Query Match          100.0%;  Score 1195;  DB 3;  Length 1195;
Best Local Similarity  100.0%;  Pred. No. 6.6e-301;
Matches 1195;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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Qy     1 CCGAGACTCACGGTCAAGCTAAGGCGAGACAGTGGGTGGCTGGAGCCATACTATTTATAG    60
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Db     1 CCGAGACTCACGGTCAAGCTAAGGCGAGACAGTGGGTGGCTGGAGCCATACTATTTATAG    60

Qy    61 AATTAAATGGAAAGGCAGGAAAAGACATCACAAAACCAAGAGAACTTTGGAAAATGAAGCCTA   120
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Db    61 AATTAAATGGAAAGGCAGGAAAAGACATCACAAAACCAAGAGAACTTTGGAAAATGAAGCCTA   120

Qy   121 GGAGAAATTAGAAGAAGACGATATTTGCATAAGGACACGGAGAGACACCAGCACATGCTAA   180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGAGAAATTAGAAGAAGACGATATTTGCATAAGGACACGGAGAGACACCAGCACATGCTAA   180

Qy   181 AAAGACCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATGAATTTGACTGCCCTT   240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AAAGACCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATGAATTTGACTGCCCTT   240

Qy   241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG   300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG   300

Qy   301 CTATTATAGCATCTCTGACTTTTCTTTCTTTACACTCTTCTGAGGGGAAGTAATTCACCCTTTAG   360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTATTATAGCATCTCTGACTTTTCTTTCTTTACACTCTTCTGAGGGGAAGTAATTCACCCTTTAG   360

Qy   361 CAACTTCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC   420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CAACTTCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC   420

Qy   421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTTGATGCAGCAATTG   480
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Db   421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTTGATGCAGCAATTG   480

Qy   481 TCCAACTTCATAATGGAACCAAGTATATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT   540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TCCAACTTCATAATGGAACCAAGTATATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT   540

Qy   541 TAACAAGAAAAGCAGTTTGGGCTTCTTCAGTTCCTGTACTTGCTACTGCAATTTATA   600
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Db   541 TAACAAGAAAAGCAGTTTGGGCTTCTTCAGTTCCTGTACTTGCTACTGCAATTTATA   600

Qy   601 GTCTGTCTTACCCAATGAGGCGGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC   660
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Db   601 GTCTGTCTTACCCAATGAGGCGGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC   660

Qy   661 AGGTCCAACAAAATAAAGAAGAAGATGCCTGGATTGAGCATGATGATGTTTGGAGAATGGAGAGTT   720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 AGGTCCAACAAAATAAAGAAGAAGATGCCTGGATTGAGCATGATGATGTTTGGAGAATGGAGAGTT   720

Qy   721 ATGTGTCTCTGGGAATTGTGGGGATTGGCAATACTGGCTTCTGTTGGGCTGTGACATCTATTC   780
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Db   721 ATGTGTCTCTGGGAATTGTGGGGATTGGCAATACTGGCTTCTGTTGGGCTGTGACATCTATTC   780

Qy   781 CATCTGTGAGTGAGTCTTTTGACATGGCAGGAGGAGAATTTCACTATATTATTCAGAGCAAGCCTAGGAA   840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 CATCTGTGAGTGAGTCTTTTGACATGGCAGGAGGAGAATTTCACTATATTATTCAGAGCAAGCCTAGGAA   840

Qy   841 TTGTTTCCCTTCTACTGGGGCCAATACACCGGCATTGATGTTTTTGGCCTGGAATAAGTGGGATAG   900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TTGTTTCCCTTCTACTGGGGCCAATACACCGGCATTGATGTTTTTGGCCTGGAATAAGTGGGATAG   900

Qy   901 ATATAAAAACAAATTTGTATGGTATACACCCTCCAACTTTTTATGATAGTACCTGTTTTCCTTCCAA   960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 ATATAAAAACAAATTTGTATGGTATACACCCTCCAACTTTTTATGATAGTACCTGTTTTCCTTCCAA   960

Qy   961 TTGTTGTTCCTGATATTTAAAAGCATACTACTATTCCTGCCATGCTTGAGGAGGAAGAGAGATACTGA   1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TTGTTGTTCCTGATATTTAAAAGCATACTACTATTCCTGCCATGCTTGAGGAGGAAGAGAGATACTGA   1020

Qy  1021 AGATTAGACATGGTTGGGGAAGACGTCACCAAAAATTAACAAAACTGAGATATGTTCCCAGT   1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 AGATTAGACATGGTTGGGGAAGACGTCACCAAAAATTAACAAAACTGAGATATGTTCCCAGT   1080

Qy  1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATATTTTATATATTTTATCACCAACAACATT   1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATATTTTATATATTTTATCACCAACAACATT   1140

Qy  1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAAA   1195
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAAA   1195
```

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RESULT 6
US-10-012-896-878
; Sequence 878, Application US/10012896
; Patent No. 6943236
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Madeleine Joy
; APPLICANT: Meagher, Yoshihiro
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSEQ for Windows Version 3.0
;
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-878

Query Match          100.0%;  Score 1195;  DB 3;  Length 1195;
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Best Local Similarity 100.0%; Pred. No. 6.6e-301; Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CCGAGACTCACGGTCAAGCTAAGCCGGAAGAGTGGGTGGCTGAAGCCATACATATTTTATAG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CCGAGACTCACGGTCAAGCTAAGCCGGAAGAGTGGGTGGCTGAAGCCATACATATTTTATAG 60

Qy     61 AATTAATGGAAAGCAGAAAAAGACATCACAAACCAAGAAGAAGAAGAACTTTGGAAGCCTA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AATTAATGGAAAGCAGAAAAAGACATCACAAACCAAGAAGAAGAAGAACTTTGGAAGCCTA 120

Qy    121 GGAGAAATTTAGAAGAAGACCGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GGAGAAATTTAGAAGAAGACCGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy    181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy    241 CAGAACTTCACCACACACAGGAACTCTTTCCAGTGGCACTTGCCAATTAAAATAGCTG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CAGAACTTCAGCACACACAGGAACTCTTTCCAATTAAAATAGCTG 300

Qy    301 CTATTATAGCATCTCTGACTTTTCTTTCACTCTTTCGAGGGAAGTAATTCACCCTTTAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTATTATAGCATCTCTGACTTTTCTTTCACTCTTTCGAGGGAAGTAATTCACCCTTTAG 360

Qy    361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTTCATCAACAAAGTCTTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTTCATCAACAAAGTCTTGC 420

Qy    421 CAAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CAAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy    481 TCCAACTTCATAATGGAACCAAGTAATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TCCAACTTCATAATGGAACCAAGTAATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy    541 TAACAAGAGAAAAGCAGTTTGGGCCTTCCAGTTTCTTTTTTTGCTCGTTACTGCCATGCAATTTATA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TAACAAGAAGAAAGCAGTTTGGGCTTCCAGTTTCTTTTTTTGCTACTGCCATGCAATTTATA 600

Qy    601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAAGTTGCTAAAACTGGGCATATCAAC 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAAACTGGGCATATCAAC 660

Qy    661 AGGTCCAACACAAAATAAAGATGCCCTGGATTGAGCATGAGTTGTTTGGGAGGAAATGGAGATTT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGGTCCAACACAAAATAAAGATGCCCTGGATTGAGCATGAGTTGTTTGGGAGAAATGGAGATTT 720

Qy    721 ATGTGTCTCCTGGGGAATTGTGGGGATTGGCAATACTGGCTTCGTTGGCTCTGTGACATCTATTC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATGTGTCTCCTGGGGAATTGGCAATACTGGCTTCGTTGGCTCTGTGACATCTATTC 780

Qy    781 CATCTGTGAGTGACTCTTTGACATGGACGGAGAATTCACTATATTCAGAGCAAGCTAGGAA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CATCTGTGAGTGACTCTTTGACATGGACGGAGAATTCACTATATTCAGAGCAAGCTAGGAA 840

Qy    841 TTGTTTCCCTTCTACTCTACTGGGCACAATACAGGCATTGATTTTTTGCCTGGAATAAGTGGGATAG 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TTGTTTCCCTTCTACTCTACTGGGCACAATACAGGCATTGATTTTTTGCCTGGAATAGTGGGATAG 900

Qy    901 ATATAAAACAATTTGTATAGGTATACACCTCCACACTTTATGATTAGAGCTGTTTTCCTTCCAA 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ATATAAAACAATTTGTATAGGTATACACCTCCACACTTTATGATTAGAGCTGTTTTCCTTCCAA 960

Qy    961 TTGTTGTCCTGATATTTAAAAGCATAACTATTACTTCCTGCCAATCCTGGAGGAAGAGATACTGA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TTGTTGTCCTGATATTTAAAAGCATAACTATTACTTCCTGCCAATCCTGGAGGAAGAGATACTGA 1020

Qy   1021 AGATTAGAGACATGGTTGGGGAAGACGTCACCAAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 AGATTAGAGACATGGTTGGGGAAGACGTCACCAAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy   1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTATCCAACATT 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTATCCAACATT 1140

Qy   1141 TCAAGTTTGTTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAA 1195
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TCAAGTTTGTTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAA 1195
```

RESULT 7
US-09-455-486-1

```
;  Sequence 1, Application US/09455486
;  Patent No. 683438
;  GENERAL INFORMATION:
;  APPLICANT:  Daniel E. Afar
;  APPLICANT:  Rene S. Hubert
;  APPLICANT:  Arthur B. Raitano
;  APPLICANT:  Douglas C. Saffran
;  APPLICANT:  Stephen C. Mitchell
;  TITLE OF INVENTION:  NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
;  TITLE OF INVENTION:  EXPRESSED IN HUMAN CANCERS AND USES THEREOF
;  FILE REFERENCE:  129.17-US-11
;  CURRENT APPLICATION NUMBER:  US/09/455,486
;  CURRENT FILING DATE:  1999-12-06
;  PRIOR APPLICATION NUMBER:  09/323,873
;  PRIOR FILING DATE:  1999-06-01
;  NUMBER OF SEQ ID NOS:  34
;  SOFTWARE:  FastSEQ for Windows Version 4.0
;  SEQ ID NO 1
;    LENGTH: 1193
;    TYPE: DNA
;    ORGANISM: Homo sapiens
;    FEATURE:
;    NAME/KEY:  CDS
;    LOCATION:  (64)...(1083)
US-09-455-486-1
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Query Match 99.8%; Score 1193; DB 3; Length 1193;
Best Local Similarity 100.0%; Pred. No. 2.2e-300; Indels 0; Gaps 0;
Matches 1193; Conservative 0; Mismatches 0;

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Qy      3 GAGACTCACGGTCAAGCTAAGCCGGAAGAGTGGGTGGCTGAAGCCATACATATTTTATAGAA 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GAGACTCACGGTCAAGCTAAGCCGGAAGAGTGGGTGGCTGAAGCCATACATATTTTATAGAA 60

Qy     63 TTAATGGAAAGCAGAAAAAGACATCACAAACCAAGAAGAAGAAGAACTTTGGAAGCCTAGG 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TTAATGGAAAGCAGAAAAAGACATCACAAACCAAGAAGAAGAAGAACTTTGGAAGCCTAGG 120

Qy    123 AGAAATTTAGAAGAAGACCGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAA 182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGAAATTTAGAAGAAGACCGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAA 180

Qy    183 AGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCA 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCA 240

Qy    243 GAACTTCAGCACACACAGGAACTCTTTCCAGTGGCACTTGCCAATTAAAATAGCTGCT 302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GAACTTCAGCACACACAGGAACTCTTTCCAGTGGCACTTGCCAATTAAAATAGCTGCT 300

Qy    303 ATTATAGCATCTCTGACTTTTCTTTCACTCTTTCGAGGGAAGTAATTCACCCTTTAGCA 362
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ATTATAGCATCTCTGACTTTTCTTTCACTCTTTCGAGGGAAGTAATTCACCCTTTAGCA 360

Qy    363 ACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTTCATCAACAAAGTCTTGCCA 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTTCATCAACAAAGTCTTGCCA 420

Qy    423 ATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTC 482
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTC 480
```

RESULT 8
US-09-016-2686
Sequence 2686, Application US/0949016
Patent No. 6812339

GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: PatentIn for Windows Version 4.0
; SEQ ID NO 2686
; LENGTH: 1147
; TYPE: DNA

; ORGANISM: Human
US-09-949-016-2686

Query Match   95.7%;   Score 1143.4; DB 3; Length 1147;
Best Local Similarity 99.9%; Pred. No. 1.7e-287;
Matches 1144; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

[The remainder of the page consists of a dense nucleotide sequence alignment between Query (Qy) and Database (Db) sequences, presented in paired rows with match bars (|), numbered by position from 421/480 through 1141/1053.]

RESULT 9
US-09-323-873A-6

; Sequence 6, Application US/09323873A
; Patent No. 6329503
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Kahan Leong
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; APPLICANT: Steve Chappell Mitchell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 129.16USU2
; CURRENT APPLICATION NUMBER: US/09/323,873A
; CURRENT FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 3627
; TYPE: DNA
; ORGANISM: Homo Sapiens

US-09-323-873A-6

Query Match   69.1%;   Score 825.6;   DB 3;   Length 3627;
Best Local Similarity   99.5%;   Pred. No. 1.2e-204;
Matches 828; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy      1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAGCGAGCCATACTATTTATAG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     31 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAGCGAGCCATACTATTTATAG 90

Qy     61 AATTAATGGAAAAGCAGAGAAAAGACATCACAAAACCAAGAGAGAACTTTGGAAAAATGAAAGCCTA 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     91 AATTAATGAAAACCAGAAAAAGACATCACAAAACCAAGAGAGAACTTTGGAAAATGAAAGCCTA 150

Qy    121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACCAGGGAGAGACCATGCTAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    151 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCATGCTAA 210

Qy    181 AAAGACCTGTGCTTTTGCATTTGCACCAAAACAGCCCATCCTGATGAATTGACTGCCCTT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    211 AAAGACCTGTGCTTTTGCATTTGCACCAAAACAGCCCATCCTGATGAATTGACTGCCCTT 270

Qy    241 CAGAACTTCAGCACACAGGAACTCTTTCCACAGTGGCACTTCCCAATTAAAAATAGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    271 CAGAACTTCAGCACACAGGAACTCTTTCCACAGTGGCACTTCCCAATTAAAAATAGCTG 330

Qy    301 CTATTATAGCATCTCTGACTTTTCTTTTACACTCTTCTGAGGGGAAGTAATTCACCCTTTAG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    331 CTATTATAGCATCTCTGACTTTTCTTTTACACTCTTCTGAGGGGAAGTAATTCACCCTTTAG 390

Qy    361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
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Qy    391 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 450
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCCAGTGTGATAGCAGCAATTG 480

Qy    451 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCCAGTGTGATAGCAGCAATTG 510
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    451 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCCAGTGTGATAGCAGCAATTG

Qy    481 TCCAACTTCATAATGGAACCAAGTATAAGAAGAGTTCACATTGGTTGGATAAGTAAGTGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    511 TCCAACTTCATAATGGAACCAAGTATAAGAAGAGTTCACATTGGTTGGATAAGTAAGTGT 570

Qy    541 TAACAAGAAAGCAGTTTGGGGCTTCTCAGTTTCTTTTTTTGCTGTACTGCATGCAAATTATA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    571 TAACAAGAAAGCAGTTTGGGGCTTCTCAGTTTCTTTTTTTGCTGTACTGCATGCAAATTATA 630

Qy    601 GTCTGTCTTACCCAATGAGAGGCGATCCTACAGATACAAGATACAAGTTGCTAAAAACTGGGCATATCAAC 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    631 GTCTGTCTTACCCAATGAGAGGCGATCCTACAGATACAAGATACAAGTTGCTAAAAACTGGGCATATCAAC 690

Qy    661 AGGTCCAACAAAAATAAAGAAGAGATGCCTGGATTGAGCGATGAGTTGGGAGAATGGAGATTT 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    691 AGGTCCAACAAAAATAAAGAAGAGATGCCTGGATTGAGCGATGAGTTGGGAGAATGGAGATTT 750

Qy    721 ATGTTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCGTTGGCTCTGTTGGCATCTATTC 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    751 ATGTTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCGTTGGCTCTGTTGGCATCTATTC 810

Qy    781 CATCTGTGAGTGACTCTTTGACATGGAGGAGAATTTCACTATATATTCAGAGCAA 832
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    811 CATCTGTGAGTGACTCTTTGACATGGAGGAGAATTTCACTATATATTCAGAGCAA 862
```

RESULT 10
US-09-455-486-4

; Sequence 4, Application US/09455486
; Patent No. 6833438
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; APPLICANT: Stephen C. Mitchell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 129.17-US-11
; CURRENT APPLICATION NUMBER: US/09/455,486
; CURRENT FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/323,873
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 3627
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-455-486-4

Query Match   69.1%;   Score 825.6;   DB 3;   Length 3627;
Best Local Similarity   99.5%;   Pred. No. 1.2e-204;
Matches 828; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy      1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAGCGAGCCATACTATTTATAG 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     31 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAGCGAGCCATACTATTTATAG 90

Qy     61 AATTAATGGAAAAGCAGAGAAAAGACATCACAAAACCAAGAGAGAACTTTGGAAAAATGAAAGCCTA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     91 AATTAATGGAAAAGCAGAGAAAAGACATCACAAAACCAAGAGAGAACTTTGGAAAATGAAAGCCTA 150

Qy    121 GGAGAAATTTAGAGAAGAAGACGATTATTTGCATAAGGACACGGGAGGACAGCAGCCATGCTAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    151 GGAGAAATTTAGAGAAGAAGACGATTATTTGCATAAGGACACAGGGAGAGACCATGCTAA 210

Qy    181 AAAGACCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTGACTGCCCTT 240
```

Left column

Db 211 AAAGAACCTGTGCTTTGCATTGACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 270
Qy |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 241 CAGAACTTCAGCACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 271 CAGAACTTCAGCACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 330
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 301 CTATTATAGCATCTCTGACTTTTCTTACTCTTCTGAGGGGAAGTAAATTCACCCCTTAG 360
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 331 CTATTATAGCATCTCTGACTTTTCTTACTCTTCTGAGGGGAAGTAAATTCACCCCTTAG 390
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 361 CAACTTCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 391 CAACTTCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 450
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 421 CAATGGTTTCCATCACTCTCTTGGGCAATTGGTTTACCTGCCAAGGTGTGATACCAGCAAATTG 480
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 451 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAAGGTGTGATAGCAGCAAATTG 510
Qy |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 481 TCCAACTTCATAAATGGAACCAAGTATAAGAAGTTCCCACATTGGTTGGATAAGTGGATGT 540
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 511 TCCAACTTCATAAATGGAACCAAGTATAAGAAGTTCCCACATTGGTTGGATAAGTGGATGT 570
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 541 TAACAAGAAAAGCAGTTTGGGCTTCCAGTTCTTTTTTGCTGTACTGCTAAAACTGGGCATTCAC 600
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 571 TAACAAGAAAAGCAGTTTGGGCTTCCAGTTCTTTTTTGCTGTACTGCTAAAACTGGGCATATCA 630
Qy |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 601 GTCTGTCTTACCCAATGAGGCGGATCCTACAGATACACAAGTTGCTAAAACTGGGCATATCAAC 660
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 631 GTCTGTCTTACCCAATGAGGCGGATCCTACAGATACACAAGTTGCTAAAACTGGGCATATCAAC 690
Qy |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 661 AGGTCCAACAAAAATAAAGAAGAGATGCCTGGATTGAGCCATGATTGTTGGAGAATGGAGATTT 720
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 691 AGGTCCAACAAAAATAAAGAAGAGATGCCTGGATTGAGCCATGATTGTTGGAGAATGGAGATTT 750
Qy |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 721 ATGTGTCTCTCGGGAATTGTGGGGATTGGGCAATACTGGCCTCGTTGGGCTGTGACATCTATTC 780
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 751 ATGTGTCTCTCGGGAATTGTGGGGATTGGGCAATACTGGCCTCGTTGGGCTGTGACATCTATTC 810
Qy |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 781 CATCTGTGAGTGAGTGACTCTTTGACATGGAGAGAGAATTTCACTATATATTCAGAGAGCAA 832
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||

Db 811 CATCTGTGAGTGAGTGACTCTTTGACATGGAGAGAGAATTTCACTATATATTCAGGTAA 862

RESULT 11
US-10-010-667A-6
Sequence 6, Application US/10010667A
Patent No. 6887975
GENERAL INFORMATION:

APPLICANT: Afar, Daniel
APPLICANT: Hubert, Rene S.
APPLICANT: Leong, Kahan
APPLICANT: Raitano, Arthur B.
APPLICANT: Saffran, Douglas C.
APPLICANT: Mitchell, Steve Chappell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
                    EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 5115820001601
CURRENT APPLICATION NUMBER: US/10/010,667A
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 3627
TYPE: DNA
ORGANISM: Homo sapiens
US-10-010-667A-6

Right column

Query Match   69.1%;   Score 825.6; DB 3;   Length 3627;
Best Local Similarity 99.5%; Pred. No. 1.2e-204;
Matches 828;   Conservative 0;   Mismatches 4;   Indels 0;   Gaps 0;

Qy   1 CCGAGACTCACGGTCAAGCTAAGGCGGAGAGTGGGGTGGCCATACTATTTATAG 60
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   31 CCGAGACTCACGGTCAAGCTAAGGCGGAAGAGTGGGGTGGCCATACTATTTATAG 90
Qy |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   61 AATTAATGGAAAGCAGAAAAGACATCACAAAACCAAGAGAACTTTGGAAAATGAAGCCTA 120
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   91 AATTAATGGAAAGCAGAAAAGACATCACAAAACCAAGAGAACTTTGGAAAATGAAGCCTA 150
Qy |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 121 GGAGAAATTTAGAAGAGAACGGATTATTTGCATTAAGGACACGGGAGAGACCAGCATGCCTAA 180
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 151 GGAGAAATTTAGAAGAGAACGGATTATTTGCATTAAGGACACGGGAGAGACCAGCATGCCTAA 210
Qy |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 181 AAAGACCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 211 AAAGACCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTT 270
Qy |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 241 CAGAACTTCAGCACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 271 CAGAACTTCAGCACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 330
Qy |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 301 CTATTATAGCATCTCTGACTTTTCTTACTCTTCTGAGGGGAAGTAAATTCACCCCTTAG 360
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 331 CTATTATAGCATCTCTGACTTTTCTTACTCTTCTGAGGGGAAGTAAATTCACCCCTTAG 390
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Qy 361 CAACTTCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 391 CAACTTCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 450
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Qy 421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAAGGTGTGATAGCAGCAAATTG 480
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 451 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAAGGTGTGATAGCAGCAAATTG 510
Qy |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 481 TCCAACTTCATAAATGGAACCAAGTATAAGAAGTTCCCACATTGGTTGGATAAGTGGATGT 540
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 511 TCCAACTTCATAAATGGAACCAAGTATAAGAAGTTCCCACATTGGTTGGATAAGTGGATGT 570
Qy |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 541 TAACAAGAAAAGCAGTTTGGGCTTCCAGTTCTTTTTTGCTGTACTGCAAAAACTGGGCATTCAC 600
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 571 TAACAAGAAAAGCAGTTTGGGCTTCTCAGTTCTTTTTTGCTGTACTGCAAAAACTGGGCATTCAC 630
Qy |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 601 GTCTGTCTTACCCAATGAGGCGGATCCTACAGATACACAAGTTGCTAAAACTGGGCATATCAAC 660
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 631 GTCTGTCTTACCCAATGAGGCGGATCCTACAGATACACAAGTTGCTAAAACTGGGCATATCAAC 690
Qy |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 661 AGGTCCAACAAAAATAAAGAAGAGATGCCTGGATTGAGCCATGATTGTTGGAGAATGGAGATTT 720
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Db 691 AGGTCCAACAAAAATAAAGAAGAGATGCCTGGATTGAGCCATGATTGTTGGAGAATGGAGATTT 750
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Qy 721 ATGTGTCTCTCGGGAATTGTGGGGATTGGGCAATACTGGCCTCGTTGGGCTGTGACATCTATTC 780
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Db 751 ATGTGTCTCTCGGGAATTGTGGGGATTGGGCAATACTGGCCTCGTTGGGCTGTGACATCTATTC 810
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Qy 781 CATCTGTGAGTGAGTGACTCTTTGACATGGAGAGAGAATTTCACTATATATTCAGAGAGCAA 832
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Db 811 CATCTGTGAGTGAGTGACTCTTTGACATGGAGAGAGAATTTCACTATATATTCAGGTAA 862

RESULT 12
US-09-439-313-342/c
Sequence 342, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yuqui
APPLICANT: Reed, Steven G.

; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSEQ for Windows Version 3.0
;
; SEQ ID NO 342
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-342

Query Match   48.6%; Score 581; DB 3; Length 592;
Best Local Similarity 99.7%; Pred. No. 2.6e-141;
Matches 581; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db   583 CCGAGACTCACGGTCAAGCTAAGGCGAAGGAGAAGAGTGGGGTGGCTGAAGCCATACTATTTTATAG 524

Qy    61 AATTAATGGAAAGCAGAAAAAGACATCACAAAACCAAGAAGAAGAACTTTGGAAAATGAAAGCCTA 120
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Db   523 AATTAATGGAAAGCAGAAAAAGACATCACAAAACCAAGAAGAAGAACTTTGGAAAATGAAAGCCTA 464

Qy   121 GGAGAAATTTAGAAGAAGAACGATTATTTGCATAAGGACACGGGAGAGAGACCAGCATGCTAA 180
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Db   463 GGAGAAATTTAGAAGAAGAACGATTATTTGCATAAGGACACGGGAGAGAGACCAGCATGCTAA 404

Qy   181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   403 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 344

Qy   241 CAGAACTTCAGCACACACAGGGACTCTTCCACAGTGGCACTTGCCCAATTAAAATAGCTG 300
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Db   343 CAGAACTTCAGCACACACAGGGACTCTTCCACAGTGGCACTTGCCCAATTAAAATAGCTG 284

Qy   301 CTATTATAGCATCTCTGACTTTCTTTTACACTCTTCTGAGGGGAAGTAATTCACCCTTTAG 360
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Db   283 CTATTATAGCATCTCTGACTTTCTTTTACACTCTTCTGAGGGGAAGTAATTCACCCTTTAG 224

Qy   361 CAACTTCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
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Db   223 CAACTTCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 164

Qy   421 CAATGGTTTCCATCACACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
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Db   163 CAATGGTTTCCATCACACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 104

Qy   481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGGATGT 540
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Db   103 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGGATGT 44

Qy   541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTTGCTGT 583
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Db    43 TAACAAGAAAGCARATTGGGCTTCTCAGTTTCTTTTTTGCTGT 1
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RESULT 13
US-09-352-616A-342/c
; Sequence 342, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqui
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSEQ for Windows Version 3.0
;
; SEQ ID NO 342
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-342

Query Match   48.6%; Score 581; DB 3; Length 592;
Best Local Similarity 99.7%; Pred. No. 2.6e-141;
Matches 581; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy     1 CCGAGACTCACGGTCAAGCTAAGGCGAAGGAGAAGAGTGGGGTGGCTGGCTGAAGCCATACTATTTTATAG 60
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Db   583 CCGAGACTCACGGTCAAGCTAAGGCGAAGGAGAAGAGTGGGGTGGCTGAAGCCATACTATTTTATAG 524

Qy    61 AATTAATGGAAAGCAGAAAAAGACATCACAAAACCAAGAAGAAGAACTTTGGAAAATGAAAGCCTA 120
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Db   523 AATTAATGGAAAGCAGAAAAAGACATCACAAAACCAAGAAGAAGAACTTTGGAAAATGAAAGCCTA 464

Qy   121 GGAGAAATTTAGAAGAAGAACGATTATTTGCATAAGGACACGGGAGAGAGACCAGCATGCTAA 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   463 GGAGAAATTTAGAAGAAGAACGATTATTTGCATAAGGACACGGGAGAGAGACCAGCATGCTAA 404

Qy   181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
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Qy   301 CTATTATAGCATCTCTGACTTTCTTTTACACTCTTCTGAGGGGAAGTAATTCACCCTTTAG 360
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Db   283 CTATTATAGCATCTCTGACTTTCTTTTACACTCTTCTGAGGGGAAGTAATTCACCCTTTAG 224

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Db   223 CAACTTCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 164

Qy   421 CAATGGTTTCCATCACACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
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Db   163 CAATGGTTTCCATCACACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 104

Qy   481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGGATGT 540
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RESULT 14
US-09-636-215-342/c
; Sequence 342, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.

RESULT 15
US-09-685-166A-342/c
Sequence 342, Application US/09685166A
; Patent No. 663305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSEQ for Windows Version 3.0
US-09-636-215-342
; SEQ ID NO 342
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-636-215-342

Query Match   48.6%;   Score 581;   DB 3;   Length 592;
Best Local Similarity   99.7%;   Pred. No. 2.6e-141;
Matches 581;   Conservative 1;   Mismatches 1;   Indels 0;   Gaps 0;

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Qy    61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAAATGAAGCCTA 120
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Db   523 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAAATGAAGCCTA 464

Qy   121 GGAGAAAATTAGAAGAAGACGAGATTATTTGCATTAAGGACACGGGAGGAGAGACCATGCT 180
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Db   463 GGAGAAAATTAGAAGAAGACGAGATTATTTGCATTAAGGACACGGGAGGAGAGACCATGCT 404

Qy   181 AAAGACCTGTGCTTTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCCTT 240
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Db   403 AAAGACCTGTGCTTTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCCTT 344

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Db   343 CAGAACTTCAGCACACACAGGGAACTCTTTCCACAGTGGGCACTTGCCAATTAAAAATAGCTG 284

Qy   301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
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Db   283 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 224

Qy   361 CAACTTCCCATCAACAATATTTTTATAAAAAATTCCAATCCTGGTCATCACACAAAGTCTTGC 420
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Db   223 CAACTTCCCATCAACAATATTTTTATAAAAAATTCCAATCCTGGTCATCACACAAAGTCTTGC 164

Qy   421 CAATGGTTTCCATCACTCTCTTGGCCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
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Db   163 CAATGGTTTCCATCACTCTCTTGGCCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 104

Qy   481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGGATGT 540
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Db   103 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGGATGT 44

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Db    43 TAACAAGAAAGCARATTGGGGCTTCTCAGTTTCTTTTTTGCCTGT 1
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OM nucleic - nucleic search, using sw model

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Run on: December 5, 2005, 00:23:57 ; Search time 1115.59 Seconds
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Perfect score: 1195
Sequence: 1 ccgagaccacggtcaagct..........ggaaaaaaaaaaaaaaaa 1195
Scoring table: IDENTITY_NUC
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Searched: 9793542 seqs, 4134689005 residues
Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	Match DB	DB ID	Description
1	1195	100.0	1195	3	US-09-759-143-878	Sequence 878, App
2	1195	100.0	1195	3	US-09-780-669-878	Sequence 878, App
3	1195	100.0	1195	3	US-09-822-827-878	Sequence 878, App
4	1195	100.0	1195	3	US-09-895-793-878	Sequence 878, App
5	1195	100.0	1195	3	US-09-895-814-878	Sequence 878, App
6	1195	100.0	1195	3	US-10-012-896-878	Sequence 878, App
7	1195	100.0	1195	5	US-10-011-095-1	Sequence 1, Appli
8	1195	100.0	1195	5	US-10-010-667A-1	Sequence 1, Appli
9	1195	100.0	1195	6	US-10-205-823-396	Sequence 396, App
10	1195	100.0	1195	6	US-10-144-678A-878	Sequence 878, App
11	1195	100.0	1195	6	US-10-294-025-878	Sequence 878, App
12	1195	100.0	1195	6	US-10-393-590-35	Sequence 35, Appl
13	1195	100.0	1195	6	US-10-393-567-35	Sequence 35, Appl
14	1195	100.0	1195	6	US-10-394-087-35	Sequence 35, Appl
15	1195	100.0	1195	6	US-10-295-027-713	Sequence 713, App
16	1195	100.0	1195	6	US-10-295-027-1130	Sequence 1130, Ap
17	1195	100.0	1195	8	US-10-643-795A-16	Sequence 16, Appl
18	1195	100.0	1195	9	US-10-643-795A-42	Sequence 42, Appl
19	1195	100.0	1195	9	US-10-750-262-1	Sequence 1, Appli
20	1195	100.0	1195	9	US-10-948-518-16	Sequence 16, Appl
21	1195	100.0	1195	9	US-10-948-518-42	Sequence 42, Appl
22	1195	100.0	1195	9	US-10-956-157-1811	Sequence 1811, Ap
23	1195	100.0	1195	9	US-10-956-157-7046	Sequence 7046, Ap
24	1195	100.0	1195	9	US-10-858-887-1	Sequence 1, Appli
25	1195	100.0	1195	9	US-10-631-467-428	Sequence 428, App
26	1195	100.0	1195	10	US-11-051-454-396	Sequence 396, App
27	1195	100.0	1330	7	US-10-755-889-191	Sequence 191, App
28	1193	99.8	1193	7	US-10-165-044-1	Sequence 1, Appli
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31	1193	99.8	1193	8	US-10-856-109-1	Sequence 1, Appli
32	1193	99.8	1193	8	US-10-753-195-1	Sequence 1, Appli
33	1193	99.8	1193	8	US-10-752-421-1	Sequence 1, Appli
34	1193	99.8	1193	8	US-10-830-899-2	Sequence 2, Appli
35	1181.8	98.9	1193	9	US-10-861-662-2	Sequence 2, Appli
36	1178	98.9	1277	3	US-09-914-353-19910	Sequence 19910, A
37	1177	98.5	1201	7	US-10-696-639-15	Sequence 15, Appl
38	1177	98.5	1177	3	US-10-425-1114-16445	Sequence 16445, A
39	1166	97.6	1354	8	US-10-723-860-5120	Sequence 5120, Ap
40	1048	87.7	1365	9	US-10-861-662-6	Sequence 6, Appli
41	1048	87.7	1365	9	US-10-830-899-6	Sequence 6, Appli
42	827.2	69.2	3627	8	US-10-830-899-10	Sequence 10, Appl
43	827.2	69.2	3627	8	US-10-861-662-10	Sequence 10, Appl
44	825.6	69.1	3627	5	US-10-011-095-6	Sequence 6, Appli
45	825.6	69.1	3627	5	US-10-010-667A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-759-143-878
; Sequence 878, Application US/09759143
; Patent No. US20020022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-878

Query Match   100.0%; Score 1195; DB 3; Length 1195;
Best Local Similarity 100.0%; Pred. No. 1.1e-281;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 CCGAGACTCACGGTCAAGCTCAAGGCGAAGAGTGGGTGGCTGAAGCCATACTACTATTTATAG 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CCGAGACTCACGGTCAAGCTCAAGGCGAAGAGTGGGTGGCTGAAGCCATACTACTATTTATAG 60

Qy   61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTTGGAAAAATGAGGCCTA 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTTGGAAAAATGAGGCCTA 120

Qy   121 GGAGAAATTTAGAAGAAGACGGATTATTTGCATAAGGACACGGGGAGAGACCAGCATGCTAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGGAGAGACCAGCATGCTAA 180

Qy   181 AAAGACCTGTGCTTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AAAGACCTGTGCTTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy   241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG   300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG   300

Qy   301 CTATTATAGGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAGAGTAATTCACCCTTTAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTATTATAGGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAGAGTAATTCACCCTTTAG 360

Qy   361 CAACTTCCCATCAACAAATATTTTTATAAAAATTCCAATCCTTGGTCATCACAAGTCTTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CAACTTCCCATCAACAAATATTTTTATAAAAATTCCAATCCTTGGTCATCACAAGTCTTGC 420

Qy   421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTACCTGCCAGGTGTGATAGCAGCAATTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy   481 TCCAACTTCATATAATGGAACCAAAGTATAAAGAAGTTTCCACATTGGTTGGGATAAGTGGATGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TCCAACTTCATAATGGAACCAAAGTATAAAGAAGTTTCCACATTGGTTGGGATAAGTGGATGT 540

Qy   541 TAACAAGAAAAGCACGTTTGGGCTTCTCCAGTTTCTTTTTGCTGTACTGCAATGCCAATTTATA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TAACAAGAAAAGCAGTTTGGGCTTCTCCAGTTTCTTTTTGCTGTACTGCAATGCCAATTTATA 600

Qy   601 GTCTGTCTTACCCAATGAGGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTCTGTCTTACCCAATGAGGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy   661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGACGATGGTGTTGGGAGAATGGAGATTT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGACGATGGTGTTGGGAGAATGGAGATTT 720

Qy   721 ATGTGTCTCTGGGAATTGTGGGAATTGGCAATACTGGCTCTCGTTGGCTGTGCATCTTATTC 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATGTGTCTCTGGGAATTGTGGGAATTGGCAATACTGGCTCTCGTTGGCTGTGCATCTTATTC 780

Qy   781 CATCTGTGAGTGACTCTTTGACAATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 CATCTGTGAGTGACTCTTTGACAATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy   841 TTGTTTCCCTTCTACTGGGCACAATACACGCCATTCAATTTATTTTGCCTGGAATAAGTGGATAG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TTGTTTCCCTTCTACTGGGCACAATACACGCCATTCAATTTATTTTGCCTGGAATAAGTGGATAG 900

Qy   901 ATATAAAACAATTTGTATGTGATATACGGCTATTTATGATAGTTCCTTCCAA 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 ATATAAAACAATTTGTATGTGATATACGGCTATTTATGATAGTTCCTTCCAA 960

Qy   961 TTGTTGTCCTGATATTTAAAGCATAACATTCCTGCCATGCTTGAGGAAGAGATACTGA 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TTGTTGTCCTGATATTTAAAGCATAACATTCCTGCCATGCTTGAGGAAGAGATACTGA 1020

Qy 1021 AGATTAGACATGGTTGGGGAGAGCGTCACCAAAATTAACAAAAACTGAGATATGTTCCCAGT 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 AGATTAGACATGGTTGGGGAGAGCGTCACCAAAATTAACAAAAACTGAGATATGTTCCCAGT 1080

Qy 1081 TGTAGAATTACTGTTTACACACATTTTGTTCAATATTGATATATTTTATCACCAAACATT 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 TGTAGAATTACTGTTTACACACATTTTGTTCAATATTGATATATTTTATCACCAAACATT 1140

Qy 1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAAAAA 1195
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAAAAA 1195

RESULT 2

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

Query Match   100.0%; Score 1195; DB 3; Length 1195;
Best Local Similarity   100.0%; Pred. No. 1.1e-281;
Matches 1195; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CCGAGACTCACGGTCAAGCTAAGCGCGAAGAGTGGGTGGCTGAAGCCAATACTATTTTATAG   60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CCGAGACTCACGGTCAAGCTAAGCGCGAAGAGTGGGTGGCTGAAGCCAATACTATTTTATAG   60

Qy   61 AATTAATGGAAAGCAGAAAAAGACAATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AATTAATGGAAAGCAGAAAAAGACAATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy   121 GGAGAAATTTAGAAGAAGACGGATTATTTGCATAAGGACACGGGGAGAGACCAGCATGCTAA 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGGAGAGACCAGCATGCTAA 180

Qy   181 AAAGACCTGTGCTTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AAAGACCTGTGCTTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy   241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG   300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG   300

Qy   301 CTATTATAGGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAGAGTAATTCACCCTTTAG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTATTATAGGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAGAGTAATTCACCCTTTAG 360

Qy   361 CAACTTCCCATCAACAAATATTTTTATAAAAATTCCAATCCTTGGTCATCACAAGTCTTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CAACTTCCCATCAACAAATATTTTTATAAAAATTCCAATCCTTGGTCATCACAAGTCTTGC 420

Qy   421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

US-09-822-827-878
; Sequence 878, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-878

RESULT 3

Query Match   100.0%; Score 1195; DB 3; Length 1195;
Best Local Similarity   100.0%; Pred. No. 1.1e-281;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db    421 CAATGGTTTCCATCACTTCTCTTGGGCATTGGGTTTACCTGCATGGTTGGATAGTGATAGCAATTG 480

Qy    481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAGTAGTGGATGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAGTAGTGGATGT 540

Qy    541 TAACAAGAAAGCAGTTTGGGGCTTCTCAGTTTCTTCTTTTTTGTCCTGCATGCAAATTTATA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TAACAAGAAAGCAGTTTGGGGCTTCTCAGTTTCTTCTTTTTTGTCCTGCATGCAAATTTATA 600

Qy    601 GTCTGTCTTACCCAATGAGGCGATCCTTACAGATACAAGTTGCTAAAACTGGGCCATATCAAC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTCTGTCTTACCCAATGAGGCGATCCTTACAGATACAAGTTGCTAAAACTGGGCCATATCAAC 660

Qy    661 AGGTCCAACAAAATAAAGAAGAATGCCTGGATTGGCAAATACTGGGCCATATCAAC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGGTCCAACAAAATAAAGAAGAATGCCTGGATTGGCAAATACTGGGCCATATCAAC 720

Qy    721 ATGTGTCTCTGGGAATTGTGGGATTGGCAAATGGTTTGGGAGAATGGAGATTT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATGTGTCTCTGGGAATTGTGGGATTGGCAAATGGTTTGGGAGAATGGAGATTT 780

Qy    781 CATCTCGTGAGTGACTCTTTTGACATGGAGAGAATTTCACTATATTTCAGAGCAAGCTAGGAA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CATCTCGTGAGTGACTCTTTTGACATGGAGAGAATTTCACTATATTTCAGAGCAAGCTAGGAA 840

Qy    841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy    901 ATATAAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTCCTTCCAA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ATATAAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTCCTTCCAA 960

Qy    961 TTGTTGTGTCCTGATATTTTAAAAGCATACTAATTCCTGCCATTGGTTGGATAGTACTGA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TTGTTGTGTCCTGATATTTTAAAAGCATACTAATTCCTGCCATTGGTTGGATAGTACTGA 1020

Qy   1021 AGATTAGACATGGTTGGGGAAGACGTCACCAAAAATTAACAAAAACTGAGATATGTTCCCAGT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 AGATTAGACATGGTTGGGGAAGACGTCACCAAAAATTAACAAAAACTGAGATATGTTCCCAGT 1080

Qy   1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATATTTTATCACCAACATT 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATATTTTATCACCAACATT 1140

Qy   1141 TCAAGTTTGTATTTGTTTAATAAAAATGATTATTCAAGGAAAAAAAAAAAAAAAA 1195
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TCAAGTTTGTATTTGTTTAATAAAAATGATTATTCAAGGAAAAAAAAAAAAAAAA 1195
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Qy      1 CCGGAGACTTCACGGTCAAGCTAAGGCGGAGGAGTGGGTGGCTGAAGCCAATACTATTTTTATAG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CCGGAGACTTCACGGTCAAGCTAAGGCGGAGGAGTGGGTGGCTGAAGCCAATACTATTTTTATAG 60

Qy     61 AATTAATGGAAAGCAGAAAAAGACATCACAAAACCAAGAAGAGAACTTTGGAAAAATGAAGCCTA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AATTAATGGAAAGCAGAAAAAGACATCACAAAACCAAGAAGAGAACTTTGGAAAAATGAAGCCTA 120

Qy    121 GGAGAAATTTAGAAGAGACGATTATTTGCATAAGGACACGGAGAGACCAGCAGTGCTAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GGAGAAATTTAGAAGAGACGATTATTTGCATAAGGACACGGAGAGACCAGCAGTGCTAA 180

Qy    181 AAAGACCTGTGCTTTTGCCAAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AAAGACCTGTGCTTTTGCCAAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy    241 CAGAACTTCAGCACACACAAGGAAACTCTTTCCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CAGAACTTCAGCACACACAAGGAAACTCTTTCCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy    301 CTATTAATAGCATCTCTGACTTTTCTTTTACACTCTTCCGAGGGAAGTAATTCACCCTTTAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTATTAATAGCATCTCTGACTTTTCTTTTACACTCTTCCGAGGGAAGTAATTCACCCTTTAG 360

Qy    361 CAACTTCCCATCAAACAATATTTTTATAAAATTCCAATCCTGGTCATCAAACAAAGTCTTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CAACTTCCCATCAAACAATATTTTTATAAAATTCCAATCCTGGTCATCAAACAAAGTCTTGC 420

Qy    421 CAATGGTTTCCATCACTTCTCTTGGGCATTGGGTTTACCTGCATGGTTGGATAGTGATAGCAATTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CAATGGTTTCCATCACTTCTCTTGGGCATTGGGTTTACCTGCATGGTTGGATAGTGATAGCAATTG 480

Qy    481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAGTAGTGGATGT 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAGTAGTGGATGT 540

Qy    541 TAACAAGAAAGCAGTTTGGGGCTTCTCAGTTTCTTCTTTTTTGTCCTGCATGCAAATTTATA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TAACAAGAAAGCAGTTTGGGGCTTCTCAGTTTCTTCTTTTTTGTCCTGCATGCAAATTTATA 600

Qy    601 GTCTGTCTTACCCAATGAGGCGATCCTTACAGATACAAGTTGCTAAAACTGGGCCATATCAAC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTCTGTCTTACCCAATGAGGCGATCCTTACAGATACAAGTTGCTAAAACTGGGCCATATCAAC 660

Qy    661 AGGTCCAACAAAATAAAGAAGAATGCCTGGATTGGCAAATACTGGGCCATATCAAC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGGTCCAACAAAATAAAGAAGAATGCCTGGATTGGCAAATACTGGGCCATATCAAC 720

Qy    721 ATGTGTCTCTGGGAATTGTGGGATTGGCAAATGGTTTGGGAGAATGGAGATTT 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATGTGTCTCTGGGAATTGTGGGATTGGCAAATGGTTTGGGAGAATGGAGATTT 780

Qy    781 CATCTCGTGAGTGACTCTTTTGACATGGAGAGAATTTCACTATATTTCAGAGCAAGCTAGGAA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CATCTCGTGAGTGACTCTTTTGACATGGAGAGAATTTCACTATATTTCAGAGCAAGCTAGGAA 840

Qy    841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy    901 ATATAAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTCCTTCCAA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ATATAAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTCCTTCCAA 960

Qy    961 TTGTTGTGTCCTGATATTTTAAAAGCATACTAATTCCTGCCATTGGTTGGATAGTACTGA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TTGTTGTGTCCTGATATTTTAAAAGCATACTAATTCCTGCCATTGGTTGGATAGTACTGA 1020

Qy   1021 AGATTAGACATGGTTGGGGAAGACGTCACCAAAAATTAACAAAAACTGAGATATGTTCCCAGT 1080
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Db   1021 AGATTAGACATGGTTGGGGAAGACGTCACCAAAAATTAACAAAAACTGAGATATGTTCCCAGT 1080
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RESULT 4
US-09-793-878
; Sequence 878, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Sheiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-793-878

Query Match   100.0%; Score 1195; DB 3; Length 1195;
Best Local Similarity   100.0%; Pred. No. 1.1e-281;
Matches 1195; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy         1 CCGAGACTCACGGTCAACGTCAAGCGAAGAAGTGGGTGGCTGGCTGAGAGGCCATACTACTATTTTATAG   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 CCGAGACTCACGGTCAACGTCAAGCGAAGAAGTGGGTGGCTGGCTGAGAGGCCATACTACTATTTTATAG   60

Qy        61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAGAAGAACTTTGGAAAATGAAGCCTA      120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAGAAGAACTTTGGAAAATGAAGCCTA      120

Qy       121 GGAGAAATTAGAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGAGCAGCATGCTAA       180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 GGAGAAATTAGAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGAGCAGCATGCTAA       180

Qy       181 AAAGACCCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTT       240
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 AAAGACCCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTT       240

Qy       241 CAGAACTTCAGCACACAGGAACTCTTTCCACAGTGGGCACTTGCCAATTAAAAATAGCTG       300
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 CAGAACTTCAGCACACAGGAACTCTTTCCACAGTGGGCACTTGCCAATTAAAAATAGCTG       300

Qy       301 CTATTATAGCAATCTCTGACTCTTCTTCTTTACACTCTTCTGAGGAGGAAGTAATTCACCCTTTAG       360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 CTATTATAGCAATCTCTGACTCTTCTTCTTTACACTCTTCTGAGGAGGAAGTAATTCACCCTTTAG       360

Qy       361 CAACTTCCCATCAACAACAATATTTTTATAAAATTCCAAATCCTGGTCATCAACAAAAGTCTTGC       420
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 CAACTTCCCATCAACAACAATATTTTTATAAAATTCCAAATCCTGGTCATCAACAAAAGTCTTGC       420

Qy       421 CAATGGTTTCCATCACTCTCTTCTGGCATTGGTTTACCTGCCCAGGTGTGATAGCAGCAAATTG       480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 CAATGGTTTCCATCACTCTCTTCTGGCATTGGTTTACCTGCCCAGGTGTGATAGCAGCAAATTG       480

Qy       481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGAATGT       540
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGAATGT       540

Qy       541 TAACAAGAAAGCAGTTTGGGCTTCTCCAGTTTCTTTTTTGCTGTACTGCATGCAATTATA       600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 TAACAAGAAAGCAGTTTGGGCTTCTCCAGTTTCTTTTTTGCTGTACTGCATGCAATTATA       600

Qy       601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAAACTGGGCATATCAAC       660
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAAACTGGGCATATCAAC       660

Qy       661 AGGTCCAACAAAAATAAAGAAGATGCCTGGATGTGAGCATGAGTGTTTGGAGAATGGGAGATTT       720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 AGGTCCAACAAAAATAAAGAAGATGCCTGGATGTGAGCATGAGTGTTTGGAGAATGGGAGATTT       720

Qy       721 ATGTGTCTCTCTGGGAATTGTGGGAATTGGCCTGAATTCCACTATATTTTATTC       780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 ATGTGTCTCTCTGGGAATTGTGGGAATTGGCCTGAATTCCACTATATTTTATTC       780

Qy       781 CATCTCTGTGAGTGACTCTTTGACATGGAGAGAAATTTCACTATATTCAGAGCAAGCTAGGAA       840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 CATCTCTGTGAGTGACTCTTTGACATGGAGAGAAATTTCACTATATTCAGAGCAAGCTAGGAA       840

Qy       841 TTGTTTCCCTTCTACTGGGGCACAATACAGCCATTGATTTTGCCTGGAATAAGTGGATAG       900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 TTGTTTCCCTTCTACTGGGGCACAATACAGCCATTGATTTTGCCTGGAATAAGTGGATAG       900

Qy       901 ATATAAAACAAATTTGTATGGTATACACCTCCAACTTTTATGATAAGCTGTTTTCCTTCCAA       960
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 ATATAAAACAAATTTGTATGGTATACACCTCCAACTTTTATGATAAGCTGTTTTCCTTCCAA       960

Qy       961 TTGTTGTCCTGATATTTAAAAGCATACTATATTCCTGCCATGCCTTGAGGAGGAAGATACTGA      1020
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 TTGTTGTCCTGATATTTAAAAGCATACTATATTCCTGCCATGCCTTGAGGAGGAAGATACTGA      1020

Qy      1021 AGATTAGACATGGTTGGGAGGACGTCACCAAAAATTAACAAAAACTGAGATATGTTCCAGT      1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 AGATTAGACATGGTTGGGAGGACGTCACCAAAAATTAACAAAAACTGAGATATGTTCCAGT      1080

Qy      1081 TGTAGAATTACTGTTTACACACATTTTGTTCAATATGATATATTTATCACCAACATT      1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 TGTAGAATTACTGTTTACACACATTTTGTTCAATATGATATATTTATCACCAACATT      1140

Qy      1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA      1195
             |||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA      1195
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RESULT 5
US-09-895-814-878
; Sequence 878, Application US/09895814
; Publication No. US20020192296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-814-878

Query Match   100.0%; Score 1195; DB 3; Length 1195;
Best Local Similarity 100.0%; Pred. No. 1.1e-281;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 CCGAGACTCACGGTCAAGCTAAGGGAGGAAGAGTGGGTGGGTGAGGCCATACTACTATTTTATAG 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CCGAGACTCACGGTCAAGCTAAGGGAGGAAGAGTGGGTGGGTGAGGCCATACTACTATTTTATAG 60

Qy   61 AATTAATGGAAAGACGAAAAAGACAATCACAAAACCAAGAGAGAACTTTGGAAATGAAGCCTA 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AATTAATGGAAAGACGAAAAAGACAATCACAAAACCAAGAGAGAACTTTGGAAATGAAGCCTA 120

Qy   121 GGAGAAAATTTAGAAGAAGACGAATTATTTCGCATAAGGACACGGGGAGGAGAGCCAGCATGCTAA 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGAGAAAATTTAGAAGAAGACGAATTATTTCGCATAAGGACACGGGGAGGAGAGCCAGCATGCTAA 180

Qy   181 AAAGACCTGTGCTTTGCATTGCACCAAAACAGCCCATGCCTGATGAATTTGACTGCCCTT 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AAAGACCTGTGCTTTGCATTGCACCAAAACAGCCCATGCCTGATGAATTTGACTGCCCTT 240

Qy   241 CAGAACTTCAGCACACACAGGAGAACTCTTTCCACAGTGGCACTTCCCAATTAAAATAGCTG 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CAGAACTTCAGCACACACAGGAGAACTCTTTCCACAGTGGCACTTCCCAATTAAAATAGCTG 300

Qy   301 CTATTAATAGCATCTCTGACTTTTCTTTACACTCTTCTCTGAGGGAAGTAATTCACCCTTTAG 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTATTAATAGCATCTCTGACTTTTCTTTACACTCTTCTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy   361 CAACTTCCCATCAACAATATTTTATAAAATTCCAATCCTGGTCATCAACAAAAGTCTTGC 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CAACTTCCCATCAACAATATTTTATAAAATTCCAATCCTGGTCATCAACAAAAGTCTTGC 420

Qy   421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCACGCAATTG 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCACGCAATTG 480

Qy   481 TCCAACTTCATAATGGAACCAAGTATAAGAAAGTTTCCAACATTGGTTTGATAAGTGGATGT 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TCCAACTTCATAATGGAACCAAGTATAAGAAAGTTTCCAACATTGGTTTGATAAGTGGATGT 540

Qy   541 TAACAAGAAAAGCAGTTTGGGCCTTCTCAGTTTCTTTTTGCTGTACTGCATGCAATTTATA 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TAACAAGAAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTGCTGTACTGCATGCAATTTATA 600

Qy   601 GTCTGCTTCTTACCCAAATGAGGCGATCCTACAGAATACAAGTTGCTAAACTGGGCATATCAAC 660

RESULT 6
US-10-012-896-878
; Sequence 878, Application US/10/012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896

Db   601 GTCTGCTTCTTACCCAAATGAGGCGATCCTACAGAATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy   661 AGGTCCAACAAAATAAAGAAGAAGATGCCCTGGATTGAGCATGACGATGGGAGAATTT 720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 AGGTCCAACAAAATAAAGAAGAAGATGCCCTGGATTGAGCATGACGATGGGAGAATTT 720

Qy   721 ATGTGTCTTCTGGGAATTGTGGGATTGGCAATACTCGGCCTCTGTTGTTGGGCTGTGACATCTATTC 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATGTGTCTTCTGGGAATTGTGGGATTGGCAATACTCGGCCTCTGTTGTTGGGCTGTGACATCTATTC 780

Qy   781 CATCTGTGAGTGACTCTTTGACATGGAGAATTTCACTATATATTCAGAGCAAGCTAGGAA 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 CATCTGTGAGTGACTCTTTGACATGGAGAATTTCACTATATATTCAGAGCAAGCTAGGAA 840

Qy   841 TTGTTTCCCTTCTACTGGGCACATACACCCATTGATTTTTTGCCTGGAATTAAGTGGATAG 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TTGTTTCCCTTCTACTGGGCACATACACCCATTGATTTTTTGCCTGGAATTAAGTGGATAG 900

Qy   901 ATATAAAACAAATTTGTATGGGTATACACCTCCAACTTTATGTAGCTGTGTTTCTTCCTTCCAA 960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 ATATAAAACAAATTTGTATGTTATACACCTCCAACTTTATGTAGCTGTGTTTCTTCCTTCCAA 960

Qy   961 TTTGTGTCCTGATATTAAAAGCATACTATTCCTGCCATGCTTGAGGAATAAGTCCCAGT 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TTTGTGTCCTGATATTAAAAGCATACTATTCCTGCCATGCTTGAGGAATAAGTCCCAGT 1020

Qy 1021 AGATTAGACACATGGTTGGGGAGACCGTCACCAAAAATTAACAAAAACTGAGATATGTTCCCAGT 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 AGATTAGACATGGTTGGGGAGACGTCACCAAAAATTAACAAAAACTGAGATATGTTCCCAGT 1080

Qy 1081 TGTAGAATTACTGTTTACACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 TGTAGAATTACTGTTTACACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy 1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAAAGT 1195
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAAAGT 1195

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; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSEQ for Windows Version 3.0
;
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-878

Query Match           100.0%;  Score 1195;  DB 5;  Length 1195;
Best Local Similarity 100.0%;  Pred. No. 1.1e-281;
Matches 1195;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy      1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTA 60

Qy     61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGAAAAATGAAGCCTA 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGAAAAATGAAGCCTA 120

Qy    121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGGAGAACCAGCATGCTAA 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGGAGAACCAGCATGCTAA 180

Qy    181 AAAGACCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Db    181 AAAGACCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy    241 CAGAACTTCAGCACACCACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAAATAGCTG 300

Db    241 CAGAACTTCAGCACACCACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAAATAGCTG 300

Qy    301 CTATTATAGACATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Db    301 CTATTATAGACATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy    361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTCTGGTCATCAACAAAGTCTTGC 420

Db    361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTCTGGTCATCAACAAAGTCTTGC 420

Qy    421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTGTTTACCTCCCAGTGTGTGATAGCAGCAATTG 480

Db    421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTGTTTACCTCCCAGTGTGTGATAGCAGCAATTG 480

Qy    481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Db    481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy    541 TAACAAGAAAAGACAGTTTGGGCCTTCCAGTTTCTTCTTTTTTTGCTGTACTGCAAATTTATA 600

Db    541 TAACAAGAAAAGACAGTTTGGGCCTTCCAGTTTCTTCTTTTTTTGCTGTACTGCAAATTTATA 600

Qy    601 GTCTGTCTTACCCAATGAGGGCGATCCTACAGATAACAAGTTGCTAAACTGGGCATTATCAAC 660

Db    601 GTCTGTCTTACCCAATGAGGGCGATCCTACAGATAACAAGTTGCTAAACTGGGCATTATCAAC 660

Qy    661 AGGTCCACAACAAAATAAAGAAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGGAGATTT 720

Db    661 AGGTCCACAACAAAATAAAGAAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGGAGATTT 720

Qy    721 ATGTGTCTCTGGGAAATTGTGGGAATTGGGAATGGCATGATGTTGGACAATCTATTC 780

Db    721 ATGTGTCTCTGGGAAATTGTGGGAATTGGGAATGGCATGATGTTGGACAATCTATTC 780

Qy    781 CAATCTGTGAGTGACTTCTTTGACATGGAGAGAAATTTCACTATATTATTCAGATAGCTAGGAA 840

Db    781 CAATCTGTGAGTGACTTCTTTGACATGGAGAGAAATTTCACTATATTATTCAGATAGCTAGGAA 840

Qy    841 TTGTTTCCCTTCTACTGGGGCACAATACACCGCCATTGAATTTTTGCCTGGAATAAGTGGATAG 900

Db    841 TTGTTTCCCTTCTACTGGGGCACAATACACCGCCATTGAATTTTTGCCTGGAATAAGTGGATAG 900
```

RESULT 7
US-10-011-095-1
; Sequence 1, Application US/10011095
; Publication No. US20030456B2A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Hubert, Rene S.
; APPLICANT: Leong, Kahan
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Saffran, Douglas C.
; APPLICANT: Mitchell, Steve Chappell
; TITLE OF INVENTION: ANTIBODIES IMMUNOSPECIFIC FOR STEAP1 (AS AMENDED)
; FILE REFERENCE: 511582001610
; CURRENT APPLICATION NUMBER: US/10/011,095
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 09/323,873
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-011-095-1

Query Match   100.0%; Score 1195; DB 5; Length 1195;
Best Local Similarity 100.0%; Pred. No. 1.1e-281;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTA 60

Qy     61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGAAAAATGAAGCCTA 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGAAAAATGAAGCCTA 120

Qy    121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGGAGAACCAGCATGCTAA 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGGAGAACCAGCATGCTAA 180

Qy    181 AAAGACCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AAAGACCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy    241 CAGAACTTCAGCACACCACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAAATAGCTG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CAGAACTTCAGCACACCACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAAATAGCTG 300
```

```
Qy    901 ATATAAAACAATTTGTATGGTATACACGTTCACCTTCCAAACTTTTATGATTAGCTGTTTTCCTTCCAA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ATATAAAACAATTTGTATGGTATACACGTTCACCTTCCAAACTTTTATGATTAGCTGTTTTCCTTCCAA 960

Qy    961 TTGTTGTCCTGATATTTAAAAGCCATACTATTCCTTCCTGCCATGCTTGAGGAAGAAGAAGATACTGA 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TTGTTGTCCTGATATTTAAAAGCCATACTATTCCTTCCTGCCATGCTTGAGGAAGAAGAAGATACTGA 1020

Qy   1021 AGATTAGACACATGGTTGGGGAAGAGCGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 AGATTAGACACATGGTTGGGGAAGAGCGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy   1081 TGTAGAATTACTGTTTACACACATTTTGTTCAATATTGATTATTTTTATCACCAAACATT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TGTAGAATTACTGTTTACACACATTTTGTTCAATATTGATTATTTTTATCACCAAACATT 1140

Qy   1141 TCAAGTTTGTTATTTGTTAATAAAAATGATTAATTCAAGGAAAAAAAAAAAAAAA 1195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TCAAGTTTGTTATTTGTTAATAAAAATGATTAATTCAAGGAAAAAAAAAAAAAAA 1195
```

; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 5115B2001601
; CURRENT APPLICATION NUMBER: US/10/010,667A
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 09/323,873
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 1
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-010-667A-1

Query Match   100.0%; Score 1195; DB 5; Length 1195;
Best Local Similarity   100.0%; Pred. No. 1.1e-281;
Matches 1195; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CCGAGACTCACGGTCAAGCTAAGGCCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CCGAGACTCACGGTCAAGCTAAGGCCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy   61 AATTAATAGGAAAGCAGAAAAAGACATCACAAAACCAAGAAGAGAAGAACTTTGAAAATGAAGCCTA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AATTAATAGGAAAGCAGAAAAAGACATCACAAAACCAAGAAGAGAAGAACTTTGAAAATGAAGCCTA 120

Qy   121 GGAGAAATTTAGAAGAGGAGACGGATTAATTGGCATTAAGGACACACGGGGACGAGGAGGA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGAGAAATTTAGAAGAGGAGACGGATTAATTGGCATTAAGGACACACGGGGACGAGGAGGA 180

Qy   181 AAAGACCTGTGCTTTTGCATTTGCAACCAAAACAGCCCATGCTGATGAATTTGACTGGCCTT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AAAGACCTGTGCTTTTGCATTTGCAACCAAAACAGCCCATGCTGATGAATTTGACTGGCCTT 240

Qy   241 CAGAACTTCAGCACACACAGGAACCTCTTCCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CAGAACTTCAGCACACACAGGAACCTCTTCCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy   301 CTATTATAGCAATCTCTGACTTTTCTTCTTTACACTCTTCTCTGAGGGAGGAAGTAATTCACCCTTTAG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTATTATAGCAATCTCTGACTTTTCTTCTTTACACTCTTCTCTGAGGGAGGAAGTAATTCACCCTTTAG 360

Qy   361 CAACTTCCCATCAACAAATATTTTATAAAATTCAATCCTGGTCATCAACAAAGTCTTGC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CAACTTCCCATCAACAAATATTTTATAAAATTCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy   421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAAATTG 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAAATTG 480

Qy   481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy   541 TAACAAGAAAGCAGTTGGGCCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TAACAAGAAAGCAGTTGGGCCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy   601 GTCTGTCTTACCCAATGAGCGGATCCTACAGATACAAGTTGCTAAACTGGGCCATATCAAC 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTCTGTCTTACCCAATGAGCGGATCCTACAGATACAAGTTGCTAAACTGGGCCATATCAAC 660

Qy   661 AGGTCCAACAAAAATAAAGAAGAAGATGCCTGATTGAGCATGATGTTTGGAGAAGTGGAGATTT 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 AGGTCCAACAAAAATAAAGAAGAAGATGCCTGATTGAGCATGATGTTTGGAGAAGTGGAGATTT 720

Qy   721 ATGTGTCTCTGGGGAATTGTGGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATGTGTCTCTGGGGAATTGTGGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy   781 CATCTGTGAGTGACTCCTTTGACATGGAGGAATTTCACTATTATTCAGAGCAAGCTAGGAA 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 CATCTGTGAGTGACTCCTTTGACATGGAGGAATTTCACTATTATTCAGAGCAAGCTAGGAA 840

Qy   841 TTGTTTCCCTTCTACTGGGCCACAATACACGGCCATTGAATTTCACTAACTTTATGATGAG 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TTGTTTCCCTTCTACTGGGCCACAATACACGGCCATTGAATTTCACTAACTTTATGATGAG 900

Qy   901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTAAGGCAACCGTGTTTTCCTTCCAA 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTAAGGCAACCGTGTTTTCCTTCCAA 960

Qy   961 TTGTTGTCCTGATATTTAAAAGCATAACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TTGTTGTCCTGATATTTAAAAGCATAACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy   1021 AGATTAGACATGGTTGGGGAAGACGTCACCAAAAATTAACAAAAACTGAGATAATGTTCCAGT 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 AGATTAGACATGGTTGGGGAAGACGTCACCAAAAATTAACAAAAACTGAGATAATGTTCCAGT 1080

Qy   1081 TGTAGAATTACTGTTTACACACATTTTGTTCAATAATTGATATAATTTTATCACCAACATT 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TGTAGAATTACTGTTTACACACATTTTGTTCAATAATTGATATAATTTTATCACCAACATT 1140

Qy   1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAAGGAAAAAAAAAAAAAAAAAAA 1195
           ||||||||||||||||||||||||||||||||||||||||||
Db   1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAAGGAAAAAAAAAAAAAAAAAAA 1195

RESULT 8
US-10-010-667A-1
Sequence 1, Application US/100/10667A
; Publication No. US20030052217A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Hubert, Rene S.
; APPLICANT: Leong, Kahan
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Saffran, Douglas C.
; APPLICANT: Mitchell, Steve Chappell

Qy   541 TAACAAGAAAGCAGTTGGGCCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TAACAAGAAAGCAGTTGGGCCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy   601 GTCTGTCTTACCCAATGAGCGGATCCTACAGATACAAGTTGCTAAACTGGGCCATATCAAC 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTCTGTCTTACCCAATGAGCGGATCCTACAGATACAAGTTGCTAAACTGGGCCATATCAAC 660

Qy   661 AGGTCCAACAAAAATAAAGAAGAAGATGCCTGATTGAGCATGATGTTTGGAGAAGTGGAGATTT 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 AGGTCCAACAAAAATAAAGAAGAAGATGCCTGATTGAGCATGATGTTTGGAGAAGTGGAGATTT 720

Qy   721 ATGTGTCTCTGGGGAATTGTGGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

```
US-10-205-823-396
; Sequence 396, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbatcheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wonsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 396
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-823-396

Query Match             100.0%;  Score 1195;  DB 5;  Length 1195;
Best Local Similarity   100.0%;  Pred. No. 1.1e-281;

Matches 1195;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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RESULT 9

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Qy          1  CCGGAGCTCACGGTTCAAGTCAAGGCGAAGAGTGGGGTTGGGCTTGAAGCCATAGTATTTTTATAG   60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1  CCGGAGCTCACGGTTCAAGTCAAGGCGAAGAGTGGGGTTGGGCTTGAAGCCATAGTATTTTTATAG   60

Qy         61  AATTAATGGAAAACGCAGAAAAGACATCACAAAACCAAGAAGACTTTGGAAAATGAAGCCTA      120
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61  AATTAATGGAAAACGCAGAAAAGACATCACAAAACCAAGAAGACTTTGGAAAATGAAGCCTA      120

Qy        121  GGAGAAAATTTAGAAGAGACGAATTATTTGCATAAGGACACGGGAGGACCAGCATGCTAA      180
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121  GGAGAAAATTTAGAAGAGACGAATTATTTGCATAAGGACACGGGAGGACCAGCATGCTAA      180

Qy        181  AAAGACCTGTTGCTTTTGCATTGCACCAAAACAGCCCATGCCCATGCTGATGAATTTGACTGCCCTT      240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181  AAAGACCTGTTGCTTTTGCATTGCACCAAAACAGCCCATGCCCATGCTGATGAATTTGACTGCCCTT      240

Qy        241  CAGAACTTCAGCACACACAGGAACTCTTCCCACAGTGGCACTTGCCCAATTAAAATAGCTG      300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241  CAGAACTTCAGCACACACAGGAACTCTTCCCACAGTGGCACTTGCCCAATTAAAATAGCTG      300

Qy        301  CTATTATAGGACATCTCTCGACTTTTTCTTTACACTCCTTCTGAGGGGCATATCAAC      360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301  CTATTATAGGACATCTCTCGACTTTTTCTTTACACTCCTTCTGAGGGGCATATCAAC      360

Qy        361  CAACTTCCCATCAACAATATTTTATAAAATTCCAAATCCTGGTCATCAACAAAGTCTTGC      420
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361  CAACTTCCCATCAACAATATTTTATAAAATTCCAAATCCTGGTCATCAACAAAGTCTTGC      420

Qy        421  CAATGGTTTCCATCACTCTCTTTGGCATTGTGTTTGGTTTTGGATAGTGGATGT      480
               |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421  CAATGGTTTCCATCACTCTCTTTGGCATTGTGTTTGGTTTTGGATAGTGGATGT      480

Qy        481  TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGGATGT      540
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481  TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGGATGT      540

Qy        541  TAACAAGAAAGCAGTTGGGCTTCCAGTTTCTTTTGGCTATACTGCATGCAATTTATA      600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541  TAACAAGAAAGCAGTTGGGCTTCCAGTTTCTTTTGGCTATACTGCATGCAATTTATA      600

Qy        601  GTCGTCTTACCCAAATGAGGCGATCCTACAGATACAAGTTGCTAAAACTGGGCATATCAAC      660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601  GTCGTCTTACCCAAATGAGGCGATCCTACAGATACAAGTTGCTAAAACTGGGCATATCAAC      660

Qy        661  AGGTCCAACAAAAATAAAGAAGATGCCTGATTGAGCATAATGTTTGGAGAATGAGATTT      720
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661  AGGTCCAACAAAAATAAAGAAGATGCCTGATTGAGCATAATGTTTGGAGAATGAGATTT      720

Qy        721  ATGTGTCTCTGGGAATGTGGGATTGGCAATACTGGCCTCGTTGGCTGTTGGCATCTATTC      780
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721  ATGTGTCTCTGGGAATGTGGGATTGGCAATACTGGCCTCGTTGGCTGTTGGCATCTATTC      780

Qy        781  CATCTGTGAGTGACTCTTTGACATGGAGAGAATTCACTATATTCAGAGCAAGCTAGGAA      840
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781  CATCTGTGAGTGACTCTTTGACATGGAGAGAATTCACTATATTCAGAGCAAGCTAGGAA      840

Qy        841  TTGTTTCCCTTCTACTGGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG      900
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841  TTGTTTCCCTTCTACTGGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG      900

Qy        901  ATATAAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTTCCTTCCAA      960
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901  ATATAAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTTCCTTCCAA      960

Qy        961  TTGTTGTGTCCTGATATTTAAAAGCATAACTACTATTCCTCGCCAACTTTTAAATGAGGAAGAAGGA      1020
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961  TTGTTGTGTCCTGATATTTAAAAGCATAACTACTATTCCTCGCCAACTTTTAAATGAGGAAGAAGGA      1020

Qy       1021  AGATTAGACATGGTTGGGAAGACGTTCACCAAAAATTAACAAAACTGAGATATGTTCCCAGT      1080
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021  AGATTAGACATGGTTGGGAAGACGTTCACCAAAAATTAACAAAACTGAGATATGTTCCCAGT      1080
```

RESULT 10
US-10-144-678A-878
; Sequence 878, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144,678A
; CURRENT FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-144-678A-878

  Query Match   100.0%; Score 1195; DB 6; Length 1195;
  Best Local Similarity   100.0%; Pred. No. 1.1e-281;
  Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy   61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAGAGAACTTTGGAAAATGAAGCCTA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAGAGAACTTTGGAAAATGAAGCCTA 120

Qy   121 GGAGAAAATTAGAAGAAGACGATTATTTGCATAAGGAACACAGGGAGGAGACCAGCCATTA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGAGAAAATTAGAAGAAGACGATTATTTGCATAAGGAACACAGGGAGGAGACCAGCCATTA 180

Qy   181 AAAGACCTGTCGTTTGCATTTGCACCAAAACACCCACTGCTGATTGATGAATTGACTGCCCTT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AAAGACCTGTCGTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTGACTGCCCTT 240

Qy   241 CAGAACTTCAGCACACACAGGAACTCTTCCACAGTGGCACTTGCCAATTAAAAATAGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CAGAACTTCAGCACACACAGGAACTCTTCCACAGTGGCACTTGCCAATTAAAAATAGCTG 300

Db   241 CAGAACTTCAGCACACACAGGAACTCTTCCACAGTGGCACTTGCCAATTAAAAATAGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   301 CTATTATAGCACATCCTGCAGACTTTCTTCTTCTCTCTGAGCGGGCACTTGCCAATTAAAATAGCTG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTATTATAGCACATCTCGAGACTTTCTTCTTCTCTCTGAGCGGGCACTTGCCAATTAAAATAGCTG 360

Db   301 CTATTATAGCACATCTCGAGACTTTCTTCTTCTCTCTGAGCGGGCACTTG 360
          ...

Db   361 CAAACTTCCCATCAACAATATTTTTATAAAAATTCCAATCCTTGGTCATCAACAAAGTCTTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy   481 TCCAACTTCATAATGAACCAAGTATAAGAAGAGTTCCACAATGGGTTGGGATGGAGATGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TCCAACTTCATAATGAACCAAGTATAAGAAGAGTTCCACAATGGGTTGGGATGGAGATGT 540

Qy   541 TAACAAGAAAAGCAGAGTTTGGGCCTTCTCCAGTTTCTTTTTTTGCTGGTACTGCATGCCAATTTATA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TAACAAGAAAAGCAGAGTTTGGGCCTTCTCCAGTTTCTTTTTTTGCTGGTACTGCATGCCAATTTATA 600

Qy   601 GTCTGTCTTACCCAATGAAGGCGGATCCTTACAGATACAAGTTGCTAAACTGGGCCATATCAAAC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTCTGTCTTACCCAATGAAGGCGGATCCTTACAGATACAAGTTGCTAAACTGGGCCATATCAAAC 660

Qy   661 AGGTCCAACAAAATAAAGAAGACGCATGGCATGACGAATGATGAAGGAGATT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 AGGTCCAACAAAATAAAGAAGACGCATGGCATGACGAATGATGAAGGAGATT 720

Qy   721 ATGTGTCTCTCTGGGAATTGTGGGGATTGGCAATTACTGGCCTCCTGTTGGCTGTGACATCTATTC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATGTGTCTCTCTGGGAATTGTGGGGATTGGCAATTACTGGCCTCCTGTTGGCTGTGACATCTATTC 780

Qy   781 CATCTGTGAGTGACTCTTTGACATGGAGAGAGAATTTCAACTATATTATTCAGAGCAAGCTAGGAA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 CATCTGTGAGTGACTCTTTGACATGGAGAGAGAATTTCAACTATATTATTCAGAGCAAGCTAGGAA 840

Qy   841 TTGTTTCCCTTCTACTGGGGCACAAATACACGGCATTGTTGCCTGGAATAAGTGGATAG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TTGTTTCCCTTCTACTGGGGCACAAATACACGGCATTGTTGCCTGGAATAAGTGGATAG 900

Qy   901 ATATAAAACAAATTGTATGGTATACACCCTCCAACTTTTATGGATAGTGCTGTTTTCCTTCCAA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 ATATAAAACAAATTGTATGGTATACACCCTCCAACTTTTATGGATAGTGCTGTTTTCCTTCCAA 960

Qy   961 TTGTGTGTCCTGATATTAAAAGCATACTATCCTGCCATGCTTGAGGAAGAAGAGATACTGA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TTGTGTGTCCTGATATTAAAAGCATACTATCCTGCCATGCTTGAGGAAGAAGAGATACTGA 1020

Qy   1021 AGATTAGACATGGTTGGGGAGACGTCACCAAAAATTAACAAAAACTGAGATATGTTCCAGT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 AGATTAGACATGGTTGGGGAGACGTCACCAAAAATTAACAAAAACTGAGATATGTTCCAGT 1080

Qy   1081 TGTAGAATTACTGTTTACACACATTTTGTTCAAATATTGATTATTATTTATCACCAACATT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TGTAGAATTACTGTTTACACACATTTTGTTCAAATATTGATTATTATTTATCACCAACATT 1140

Qy   1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195

RESULT 11
US-10-294-025-878
; Sequence 878, Application US/10294025
; Publication No. US20030185830A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

```
;
;  TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.427C29
;  CURRENT APPLICATION NUMBER: US/10/294,025
;  CURRENT FILING DATE: 2002-11-12
;  NUMBER OF SEQ ID NOS: 1038
;  SOFTWARE: FastSEQ for Windows Version 3.0
;
;  SEQ ID NO 878
;  LENGTH: 1195
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-294-025-878

Query Match           100.0%;  Score 1195;  DB 6;  Length 1195;
Best Local Similarity 100.0%;  Pred. No. 1.1e-281;
Matches 1195;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy     1  CCGAGACTCACGGTCAAGCTTAAGGCGAAGAGAGTGGGTGGCTGAAGCCATACTATTTATAG  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  CCGAGACTCACGGTCAAGCTTAAGGCGAAGAGAGTGGGTGGCTGAAGCCATACTATTTATAG  60

Qy    61  AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA  120

Qy   121  GGAGAAAATTTAGAAGAAGACGATTATTTTGCATTAGACGACACGGGAGAGAACCAGCATGCTAA  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  GGAGAAAATTTAGAAGAAGACGATTATTTTGCATTAGACGACACGGGAGAGAACCAGCATGCTAA  180

Qy   181  AAAGACCTGTGCTTTTGCATTCCACCAAACAGCCCATGCTGATGAATTTGACTGCCCCTT  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  AAAGACCTGTGCTTTTGCATTCCACCAAACAGCCCATGCTGATGAATTTGACTGCCCCTT  240

Qy   241  CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG  300

Qy   301  CTATTATATAGCATCTCTGACTTTTCTTTACACTCTTCTCTGAGGGGAAGTAATTCACCCTTTAG  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  CTATTATATAGCATCTCTGACTTTTCTTTACACTCTTCTCTGAGGGGAAGTAATTCACCCTTTAG  360

Qy   361  CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC  420

Qy   421  CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG  480

Qy   481  TCCAACTTCATAATGGAACAACTATATAAGAAGTTTCCACATATTGGTTGGATAAGTGGATGT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  TCCAACTTCATAATGGAACAACTATATAAGAAGTTTCCACATATTGGTTGGATAAGTGGATGT  540

Qy   541  TAACAAGAAAGCAGTTTGGGCCTTCTCCAGTTTCTTTTTTGCTCGTGTTACTGCAATTTATA  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  TAACAAGAAAGCAGTTTGGGCCTTCTCCAGTTTCTTTTTTGCTCGTGTTACTGCAATTTATA  600

Qy   601  GTCTGTCTTACCCAATGAGCGATCCTACGATACAAGTTGCTAAACTGGGCATATCAAC  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  GTCTGTCTTACCCAATGAGCGATCCTACGATACAAGTTGCTAAACTGGGCATATCAAC  660

Qy   661  AGGTCCAACAAAATAAGAAGATGCCTGGATTGAGCATGACATCTATTC  720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  AGGTCCAACAAAATAAGAAGATGCCTGGATTGAGCATGACATCTATTC  720

Qy   721  ATGTGTCTCTGGGAAATTCGTGGGAAATGGCAATACTGGCTCTGTTGGCTCTGTGACATCTATTC  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  ATGTGTCTCTGGGAAATTCGTGGGAAATGGCAATACTGGCTCTGTTGGCTCTGTGACATCTATTC  780

Qy   781  CATCTGTGAGTGACTCTTTGACATGGAGAGAGCAAGCTAGGAA  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  CATCTGTGAGTGACTCTTTGACATGGAGAGAGCAAGCTAGGAA  840

Qy   841  TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG  900
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RESULT 12
US-10-393-590-35
;  Sequence 35, Application US/10393590
;  Publication No. US2003019065 6A1
;  GENERAL INFORMATION:
;  APPLICANT: WANG, YIXIN
;  TITLE OF INVENTION: BREAST CANCER PROGNASTIC PORTFOLIO
;  FILE REFERENCE: CDS 268 US NP
;  CURRENT APPLICATION NUMBER: US/10/393,590
;  CURRENT FILING DATE: 2003-03-21
;  PRIOR APPLICATION NUMBER: 60/368,789
;  PRIOR FILING DATE: 2002-03-29
;  NUMBER OF SEQ ID NOS: 100
;  SOFTWARE: PatentIn version 3.1
;
;  SEQ ID NO 35
;  LENGTH: 1195
;  TYPE: DNA
;  ORGANISM: human
US-10-393-590-35

Query Match           100.0%;  Score 1195;  DB 6;  Length 1195;
Best Local Similarity 100.0%;  Pred. No. 1.1e-281;
Matches 1195;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy     1  CCGAGACTCACGGTCAAGCTTAAGGCGAAGAGAGTGGGTGGCTGAAGCCATACTATTTATAG  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  CCGAGACTCACGGTCAAGCTTAAGGCGAAGAGAGTGGGTGGCTGAAGCCATACTATTTATAG  60

Qy    61  AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA  120

Qy   121  GGAGAAAATTTAGAAGAAGACGATTATTTTGCATAAGACGACACGGGAGAGAACCAGCATGCTAA  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  GGAGAAAATTTAGAAGAAGACGATTATTTTGCATAAGACGACACGGGAGAGAACCAGCATGCTAA  180

Qy   181  AAAGACCTGTGCTTTTGCATTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  AAAGACCTGTGCTTTTGCATTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT  240

Qy   241  CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG  300

Qy   301  CTATTATATAGCATCTCTGACTTTTCTTTACACTCTTCTCTGAGGGGAAGTAATTCACCCTTTAG  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  CTATTATATAGCATCTCTGACTTTTCTTTACACTCTTCTCTGAGGGGAAGTAATTCACCCTTTAG  360

Qy   361  CAACTTCCCATCAACAATATTTTTATAAAATTCAAATCCTGGTCATCAACAAAGTCTTGC  420
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RESULT 13
US-10-393-567-35
Sequence 35, Application US/10393567
Publication No. US20030194733A1
GENERAL INFORMATION:
APPLICANT: WANG, YIXIN
TITLE OF INVENTION: CANCER DIAGNOSTIC PANEL
FILE REFERENCE: CDS 269 US NP
CURRENT APPLICATION NUMBER: US/10/393,567
CURRENT FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: 60/368,667
PRIOR FILING DATE: 2002-03-29
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patentin version 3.1
SEQ ID NO 35
LENGTH: 1195
TYPE: DNA

ORGANISM: human
US-10-393-567-35

Query Match 100.0%; Score 1195; DB 6; Length 1195;
Best Local Similarity 100.0%; Pred. No. 1.1e-281;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db   961 TTGTTGTTCCTGATATTTAAAAAGCATACTATTCCTGCCATGCTTGAGGAGAAGATACTGA 1020
Qy 1021 AGATTAGACATGGTTGGGAGACGTCACCAAAATTAACAAAAACTGAGATATGTTCCCAGT 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAAACTGAGATATGTTCCCAGT 1080
Qy 1081 TGTAGAATTACTGTTTACACACATTTTGTTCAATATTGATATATTTATCACCAACACATT 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 TGTAGAATTACTGTTTACACACATTTTGTTCAATATTGATATATTTATCACCAACATT 1140
Qy 1141 AGGTCCAACAAAAATAAAGAAGAAGATGCCTGGATTGAGCAGTGAGTTTGGAGAATGGAGATTT 1195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 AGGTCCAACAAAAATAAAGAAGAAGATGCCTGGATTGAGCAGTGAGTTTGGAGAATGGAGATTT 1195
Qy 1141 TCAAGTTTGTATTTGTTAATAAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 TCAAGTTTGTATTTGTTAATAAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195

RESULT 14
US-10-394-087-35
Sequence 35, Application US/10394087
Publication No. US20030194734A1
; GENERAL INFORMATION:
; APPLICANT: Jatkoe, Tim
; TITLE OF INVENTION: SELECTION OF MARKERS
; FILE REFERENCE: CDS 265 US NP
; CURRENT APPLICATION NUMBER: US/10/394,087
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/368,790
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 35
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: human
US-10-394-087-35

Query Match   100.0%; Score 1195; DB 6; Length 1195;
Best Local Similarity 100.0%; Pred. No. 1.1e-281;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGGAGAGTGGGGTGGCCATACTATTTTATAG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGGAGAGTGGGGTGGCCATACTATTTTATAG 60
Qy   61 AATTAATGGAAAGCGAGAAAAGACATCACAAAACCAAGAGAGAACTTTGGAAAATGAAGCCTA 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AATTAATGGAAAGCGAGAAAAGACATCACAAAACCAAGAGAGAACTTTGGAAAATGAAGCCTA 120
Qy   121 GGAGAAATTTAGAAGAAGACGATTATTTCCATAAGGACACGGGAGGAGAGACCAGCACATGCTAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGGAGAGACCAGCACATGCTAA 180
Qy   181 AAAGACCTGTGCTTTTGCATTGGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AAAGACCTGTGCTTTTGCATTGGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
Qy   241 CAGAACTTCAGCACACAGGAACTCTTTCCACAGTGGCCACTTGCCAATTAAAATAGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CAGAACTTCAGCACACAGGAACTCTTTCCACAGTGGCCACTTGCCAATTAAAATAGCTG 300
Qy   301 CTATTAATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGGAAGTAATTCACCCTTTAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTATTAATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGGAAGTAATTCACCCTTTAG 360
Qy   361 CAACTCCCATCAACAACATATTTTTATAAAATTCCAATCCTGGTCGTCATCAACAAAGTCTTGC 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CAACTCCCATCAACAACATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
Qy   421 CAATGGTTTCCATCACTCTCCTTGGGCCATTGGTGTTGGATAAGTGCAGGCAATTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CAATGGTTTCCATCACTCTCCTTGGGCCATTGGTGTTGGATAAGTGCAGGCAATTG 480
Qy   481 TCCAACTTCATAATGGAACCAAGTATATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TCCAACTTCATAATGGAACCAAGTATATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Db   481 TCCAACTTCATAATGGAACCAAGTATATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   541 TAACAAGAAAAGCAGTTGGGCTTCTCAGTTCTCTTTTTTGCTGCTTTGCTACTGGCAATTTATA 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TAACAAGAAAAGCAGTTGGGCTTCTCAGTTCTCTTTTTTGCTGCTTTGCTACTGGCAATTTATA 600
Qy   601 GTCTGTCTTACCCAATGAAGGGCATCCTACAGATACAAGATCAGTTGCTAAACTGGGCATATCAAC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTCTGTCTTACCCAATGAAGGGCATCCTACAGATACAAGATCAGTTGCTAAACTGGGCATATCAAC 660
Qy   661 AGTCCAACAAAATAAAGGAAGAAGATGCCTGGATTGAGCAGTGAGTTTGGAGAATGGAGATTT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 AGTCCAACAAAATAAAGGAAGAAGATGCCTGGATTGAGCAGTGAGTTTGGAGAATGGAGATTT 720
Qy   721 ATGTGTCTTCTGGGAATTGTTGGGAATTGGGCAATACTGGCCTCTGTTGGGCGTTGGTGACATCTATTC 780
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATGTGTCTTCTGGGAATTGTTGGGAATTGGGCAATACTGGCCTCTGTTGGGCGTTGGTGACATCTATTC 780
Qy   781 CATCTGTGAGTGACTCTTTGACATGGAGAGAGAATTTCACTATTCACAGAGCAAGCTAGGAA 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 CATCTGTGAGTGACTCTTTGACATGGAGAGAGAATTTCACTATTCACAGAGCAAGCTAGGAA 840
Qy   841 TTGTTTCCCTTCTACTCGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TTGTTTCCCTTCTACTCGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
Qy   901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATTAGTGCTGTTTCCTTCCAA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATTAGTGCTGTTTCCTTCCAA 960
Qy   961 TTGTTGTTCCTGATATTTAAAAAGCATACTATTCCTGCCATGCTTGAGGAGAAGATACTGA 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TTGTTGTTCCTGATATTTAAAAAGCATACTATTCCTGCCATGCTTGAGGAGAAGATACTGA 1020
Qy 1021 AGATTAGACATGGTTGGGAGACGTCACCAAAATTAACAAAAACTGAGATATGTTCCCAGT 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAAACTGAGATATGTTCCCAGT 1080
Qy 1081 TGTAGAATTACTGTTTACACACATTTTGTTCAATATTGATATATTTATCACCAACACATT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 TGTAGAATTACTGTTTACACACATTTTGTTCAATATTGATATATTTATCACCAACATT 1140
Qy 1141 TCAAGTTTGTATTTGTTAATAAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
          ||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 TCAAGTTTGTATTTGTTAATAAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195

RESULT 15
US-10-295-027-713
Sequence 713, Application US/10295027
Publication No. US20030223250A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C
; APPLICANT: Glynne, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-0125000US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15

; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Patentin Ver. 2.1
; NUMBER OF SEQ ID NOS: 1386
;
; SEQ ID NO 713
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-295-027-713

Query Match   100.0%; Score 1195; DB 6; Length 1195;
Best Local Similarity 100.0%; Pred. No. 1.1e-281;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 CCGAGACTCACGGTCAAGCTGCAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATATTTTATAG 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CCGAGACTCACGGTCAAGCTGCAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATATTTTATAG 60

Qy   61 AATTAATGGAAAGCAGAGAAAAGACATCACAAAACCAAGAGAAGAGAACTTTGGAAAATGAAGCCTA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AATTAATGGAAAGCAGAGAAAAGACATCACAAAACCAAGAGAAGAGAACTTTGGAAAATGAAGCCTA 120

Qy   121 GGAGAAATTTAGAAGAGACGATTATTTGCATAAGGACACCGGAGAGAGACCAGCATGCTAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGAGAAATTTAGAAGAGACGATTATTTGCATAAGGACACCGGAGAGAGACCAGCATGCTAA 180

Qy   181 AAAGACCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAAATTTGACTGCCCTT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AAAGACCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAAATTTGACTGCCCTT 240

Qy   241 CAGAACTTCAGCACACACAGGAACTCTTTTCCACAGTGACACTTGCCAATTAAAAATAGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CAGAACTTCAGCACACACAGGAACTCTTTTCCACAGTGACACTTGCCAATTAAAAATAGCTG 300

Qy   301 CTATTATATAGGCATCTCTGACTTTTCTTCTTTCACTCCTTCTGAGGGAGTAATTCACCCTTTAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTATTATATAGGCATCTCTGACTTTTCTTCTTTCACTCCTTCTGAGGGAGTAATTCACCCTTTAG 360

Qy   361 CAACTTCCCATCAACAATATTTTATAAAATTCCAATCCTGGTCATCACAAAGTCTTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CAACTTCCCATCAACAATATTTTATAAAATTCCAATCCTGGTCATCACAAAGTCTTGC 420

Qy   421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGGTGTGTAGCAGCAAATTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGGTGTGTAGCAGCAAATTG 480

Qy   481 TCCAACTTCATTAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TCCAACTTCATTAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy   541 TAACAAGAAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTTGCTGTACTGCATGCAATTTATA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TAACAAGAAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy   601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACCAAGTTGCTAAACTGGGCATATCAAC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACCAAGTTGCTAAACTGGGCATATCAAC 660

Qy   661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCACATGAGTGTTTGGAGAATGGAGATTT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCACATGAGTGTTTGGAGAATGGAGATTT 720

Qy   721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGGCTCTGTTGGGCTGTGACATCTATTC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGGCTCTGTTGGGCTGTGACATCTATTC 780

Qy   781 CATCTGTAGTGAGTGACTCTTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 CATCTGTAGTGAGTGACTCTTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy   841 TTGTTTCCCTTCTTACTGGGCACAATACACGGCCATTGATTTTTGCCTGGAATAAGTGGATAG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TTGTTTCCCTTCTTACTGGGCACAATACACGGCCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy   901 ATATAAAACAATTTGTATGGTATACACCTCCAAACTTTATGATAGCTGTTTCCTTCCTCCAA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 ATATAAAACAATTTGTATGGTATACACCTCCAAACTTTATGATAGCTGTTTCCTTCCTCCAA 960

Qy   961 TTGTTGTCCTGATATATTTAAAAGCATACTATTCCTGCCATGCTTGAGAGAAGGATACTGA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TTGTTGTCCTGATATATTTAAAAGCATACTATTCCTGCCATGCTTGAGAGAAGGATACTGA 1020

Qy   1021 AGATTAGACATGGTTGGGAGACGTCACCAAAAATTAACAAAAACTGAGATATGTTTCCCAGT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 AGATTAGACATGGTTGGGAGACGTCACCAAAAATTAACAAAAACTGAGATATGTTTCCCAGT 1080

Qy   1081 TGTAGAATTACTGTTTACACACATTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TGTAGAATTACTGTTTACACACATTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy   1141 TCAAGTTTGTATTTGTTTAATAAAATGATTTATTCAAGGAAAAAAAAAAAAAAAA 1195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TCAAGTTTGTATTTGTTTAATAAAATGATTTATTCAAGGAAAAAAAAAAAAAAAA 1195

Search completed: December 5, 2005, 07:54:08
Job time : 1120.59 secs

OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
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Run on: December 6, 2005, 16:30:04 ; Search time 948 Seconds
                                              2957.088 Million cell updates/sec

Title: US-10-750-262-2
Perfect score: 1790   (without alignments)
Sequence: 1 MESRKDITNQEELWMKPRR...........IRHGWEDVTKINKTEICSQL 339

Scoring table: BLOSUM62
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                Ygapop 10.0 ;   Ygapext 0.5
                Fgapop   6.0 ;   Fgapext 7.0
                Delop   6.0 ,   Delext   7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
 9: /cgn2_6/ptodata/1/pubpna/US0D_PUBCOMB.seq:*
-MAXLEN=200000000 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -YGAPEXT=0.5
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-FGAPOP=6 -FGAPEXT=7 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Published_Applications_NA_Main:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	1790	100.0	1177	8	US-10-696-639-15	Sequence 15, Appli
2	1790	100.0	1193	6	US-10-165-044-1	Sequence 1, Appli
3	1790	100.0	1193	7	US-10-408-009-1	Sequence 1, Appli
4	1790	100.0	1193	8	US-10-857-785-1	Sequence 1, Appli
5	1790	100.0	1193	8	US-10-856-109-1	Sequence 1, Appli
6	1790	100.0	1193	8	US-10-830-899-2	Sequence 2, Appli
7	1790	100.0	1193	8	US-10-753-195-1	Sequence 1, Appli
8	1790	100.0	1193	9	US-10-752-421-1	Sequence 1, Appli

9	1790	100.0	1193	9	US-10-861-662-2	Sequence 2, Appli
10	1790	100.0	1195	3	US-09-759-143-878	Sequence 878, Appl
11	1790	100.0	1195	3	US-09-780-669-878	Sequence 878, App
12	1790	100.0	1195	3	US-09-822-827-878	Sequence 878, App
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15	1790	100.0	1195	5	US-09-012-896-878	Sequence 878, App
16	1790	100.0	1195	5	US-10-011-095-1	Sequence 1, Appli
17	1790	100.0	1195	5	US-10-010-667A-1	Sequence 1, Appli
18	1790	100.0	1195	5	US-10-205-823-396	Sequence 396, Appl
19	1790	100.0	1195	6	US-10-144-678A-878	Sequence 878, App
20	1790	100.0	1195	6	US-10-294-025-878	Sequence 878, App
21	1790	100.0	1195	6	US-10-393-590-35	Sequence 35, Appl
22	1790	100.0	1195	6	US-10-393-567-35	Sequence 35, Appl
23	1790	100.0	1195	6	US-10-394-087-35	Sequence 35, Appl
24	1790	100.0	1195	6	US-10-295-027-713	Sequence 713, Appl
25	1790	100.0	1195	6	US-10-295-027-1130	Sequence 1130, Ap
26	1790	100.0	1195	8	US-10-643-795A-16	Sequence 16, Appl
27	1790	100.0	1195	6	US-10-643-795A-42	Sequence 42, Appl
28	1790	100.0	1195	9	US-10-750-262-1	Sequence 1, Appli
29	1790	100.0	1195	9	US-10-948-515-16	Sequence 16, Appl
30	1790	100.0	1195	6	US-10-948-518-42	Sequence 42, Appl
31	1790	100.0	1195	9	US-10-956-157-1811	Sequence 1811, Appl
32	1790	100.0	1195	9	US-10-956-157-7046	Sequence 7046, Ap
33	1790	100.0	1195	9	US-10-858-887-1	Sequence 1, Appl
34	1790	100.0	1195	9	US-10-631-467-428	Sequence 428, App
35	1790	100.0	1195	9	US-11-051-454-396	Sequence 396, App
36	1790	100.0	1195	9	US-10-425-114-16445	Sequence 16445, A
37	1790	100.0	1201	7	US-09-814-353-19910	Sequence 19910, A
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40	1732.5	96.8	1365	8	US-10-830-899-6	Sequence 16, Appl
41	1732.5	96.8	1365	8	US-10-861-662-6	Sequence 42, Appl
42	1724	96.3	1354	8	US-10-723-467-1811	Sequence 5120, Ap
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ALIGNMENTS

RESULT 1
US-10-696-639-15
; Sequence 15, Application US/10696639
; Publication No. US20050037439A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corporation
; APPLICANT: Bourner, Maureen J.
; TITLE OF INVENTION: DIFERENTIALLY EXPRESSED GENES INVOLVED IN CANCER, THE
; TITLE OF INVENTION: POLYPEPTIDES ENCODED THEREBY, AND METHODS OF USING THE SAME
; FILE REFERENCE: 01040/1
; CURRENT APPLICATION NUMBER: US/10/696,639
; CURRENT FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/422,176
; PRIOR FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 3114
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 1177
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-696-639-15

Alignment Scores:
Pred. No.:   1.63e-195
Score: 1790.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 8

US-10-750-262-2 (1-339) x US-10-696-639-15 (1-1177)

Length:	1177
Matches:	339
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

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; APPLICANT: Agensys, Inc.
; APPLICANT: Rene S. Hubert
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas Saffran
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Steven Chappell Mitchell
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits

; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF

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Alignment Scores:
Pred. No.:
Score:                    1.666e-195      Length:       1193
Percent Similarity:       1790.00         Matches:      339
Best Local Similarity:    100.00%         Conservative: 0
Query Match:              100.00%         Mismatches:   0
                          100.00%         Indels:       0
DB:                       6               Gaps:         0
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Alignment Scores:
Pred. No.:

US-10-408-009-1	1.66e-195 Length: 1193

RESULT 3
US-10-408-009-1
Sequence 1, Application US/10408009
Publication No. US20040072196A1
GENERAL INFORMATION:
APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Stephen C. Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 511582001603
CURRENT APPLICATION NUMBER: US/10/408,009
CURRENT FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 09/455,486
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1193
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (64)...(1083)
US-10-408-009-1

Score:	1790.00	Matches:	339
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:		Gaps:	0

US-10-750-262-2 (1-339) x US-10-408-009-1 (1-1193)

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Db  244  CTTCAGCACAGCACAGGAACTCTTTCCACAGTGCCACTTGCCACTTAAAATAGGCTGCTGCTGCT 303

Qy   81  IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValAlaValIleHisProLeuAlaThr 100
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Db  304  ATAGCATCTCTGACTTTTCTTTACACTCTTCTCAGAGTAAGTAATTCACCCTTTAGCAACT  363

Qy  101  SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleLeuAspAsnLeuValLeuProMet 120
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Db  364  TCCCATCAACAATAATTTTATAAAATTCCAATCCTGTCATCAACAAGTGTTGCCATG  423

Qy  121  ValSerIleThrLeuLeuAlaLeuValAlaTyrLeuProGlyValIleLeuAlaAlaValAlaGln 140
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Db  424  GTTTCCATCACTCTCTTGGCATTGGTTACCTGCGTGATAGCAGCAAGTGTCCAA  483

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Db  484  CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTGGATTAAGTGGATGTTAACA 543

Qy  161  ArgLysGlyPheGlyLysLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu 180
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Db  544  AGAAAGCAGTTTGGGAAGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 603

Qy  181  SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200
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Db  604  TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 663

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Db  664  CAACAAAATAAAGAAGATGCCTGGATTGAGGAGCATATTGATGATGTTACTAGGATGGAAATTTATGTG 723

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Db  724  TCTCTGGGAATTGTGGGGATTGGCAATACTCGGCTCTGTTGGCCTGTGACCATCTTATTCCATCT 783

Qy  241  ValSerAspSerSerLeuThrTrpTyrThrProProThrPheMetIleLeuAlaValPheLeuProIleLeuVal 260
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Db  784  GTGAGTGACTCTTTGACATGGAGAAATTCACTATATTCAGAGGAAGCTGTTTTCCTTCAAATTGTT 843

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Db  844  TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 903

Qy  281  LysGlnPheValTrpTyrThrProProThrPheMetIleLeuAlaValPheLeuProIleVal 300
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Db  904  AAACAAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 963

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Db   1024 AGACATGGTTGGGGAAGACGTCACCAAAAATTAACAAAAACTGAGATATGTTCCCAGTTG 1080
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RESULT 4
US-10-857-785-1

; Sequence 1, Application US/10857785
; Publication No. US20040219162A1
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; APPLICANT: Stephen C. Mitchell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 5115820001607
; CURRENT APPLICATION NUMBER: US/10/857,785
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: US 09/455,486
; PRIOR APPLICATION NUMBER: 1999-12-06
; PRIOR APPLICATION NUMBER: US 09/323,873
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: US 60/087,520
; PRIOR APPLICATION NUMBER: 1998-06-01
; PRIOR APPLICATION NUMBER: US 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)...(1083)
US-10-857-785-1

Alignment Scores:
Pred. No.:
Score: 1790.00
Percent Similarity: 100.00%   Matches: 1193
Best Local Similarity: 100.00%   Conservative: 0   Mismatches: 0
Query Match: 100.00%   Indels: 0   Gaps: 0
DB: 8

US-10-750-262-2 (1-339) x US-10-857-785-1 (1-1193)

```
Qy     1 MetGluSerArgLysAspIleThrAsnGlnGluLeuTrpLysMetLysProArgArg 20
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    64 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 123

Qy    21 AsnLeuGluGlnHisAspTyrLeuHisLysAspThrGlyThrSerMetLeuLysArg 40
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   124 AATTTAGAGCAGCACGATTATTTGCATAAGGACACGGGAACCAGCATGCTAAAAAGA 183

Qy    41 ProValLeuLeuHisLeuHisSerLeuHisThrAlaHisAlaAspGluPheAspCysProSerGlu 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   184 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 243

Qy    61 LeuGlnHisThrGlnLeuPheProGlnTrpHisLeuProIleLeuTyrIleLeuAlaAlaIle 80
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   244 CTTCAGCACACACAGAAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTGTATT 303

Qy    81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   304 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 363

Qy   101 SerHisSerGlnGlnTyrPheTyrLysValIleLeuProIleLeuAsnLysValLeuProMet 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   364 TCCCATCACACAATATTTTTATAAAATTCCAATCCTGGTCATCACAACAAAGTCTTGCCAATG 423

Qy   121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaIleAlaIleGln 140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db   424 GTTTCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 483

Qy   141 LeuHisAsnGlyThrLysTyrLysGlySPheProHisTrpLeuAspGlyTrpMetLeuThr 160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   484 CTTCATAATGGAACCAAGTATAAGAAAGGTTTCCACATTGGTTGGATAGAATGGTGTTAACA 543

Qy   161 ArgLysGlnPheGlyLeuLeuSerPhePheAlaValLeuHisAlaIleTyrSerLeu 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   544 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTGCTGTACTGCATGCAATTTATAGTCTG 603

Qy   181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   604 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATACAGTC 663

Qy   201 GlnGlnAsnLysGluAspAlaAlaTrpIleGluHisAlaAspValTrpArgMetGluIleTyrVal 220
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   664 CAACAAAATAAGAAGGATGCCTGGATTGAGCATGCAGTGGTTTGGAGAATGGAATTTAIGTG 723

Qy   221 SerLeuGlyIleValGlyLeuLeuAlaIleLeuAlaLeuAlaValThrSerIleLeuProSer 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   724 TCTCTGGGAATTGTGGGATTGCAAATACTGGCTCTTGCATGTGGTGACATCTATTCCATCT 783

Qy   241 ValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerLysLeuGlyIleVal 260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   784 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 843

Qy   261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   844 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 903

Qy   281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   904 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 963

Qy   301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLysIle 320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   964 GTCCTGATAATTTAAAAGCATTACTATTCCTGCCATGCTTGAGGAAGAAGATTAGAAGATT 1023

Qy   321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1024 AGACATGGTTGGGGAAGACGTCACCAAAAATTAACAAAAACTGAGATATGTTCCCAGTTG 1080
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RESULT 5
US-10-856-109-1

; Sequence 1, Application US/10856109
; Publication No. US20040219591A1
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; APPLICANT: Stephen C. Mitchell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 5115820001606
; CURRENT APPLICATION NUMBER: US/10/856,109
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: US 09/455,486
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 09/323,873
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: US 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: US 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS

LOCATION: (64)....(1083)

US-10-856-109-1
US-10-856-109-1

Alignment Scores:
Pred. No.:
Score: 1790.00   Length: 1193
Percent Similarity: 100.00%   Matches: 339
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: Indels: 0
                          1.66e-195   Gaps: 0

US-10-750-262-2 (1-339) x US-10-856-109-1 (1-1193)

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Qy   1 MetGluSerArgLysAspIleThrAsnGlnGluLeuTrpLysMetLysProArgArg  20
Db  64 ATGGAAAGCAGAAAAGACATCACAAAACCAAGAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 123

Qy  21 AsnLeuGluGluAspAspTyrLeuHisLysAspThrGlyThrSerMetLeuLysArg  40
Db 124 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGGAGAAGACCAGCATGCTAAAAAGA 183

Qy  41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu  60
Db 184 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 243

Qy  61 LeuGlnHisThrGlnGluLeuPheProGlnThrPHisLeuProIleLysIleAlaAlaIle  80
Db 244 CTTCAGCACACACAGGAACTCTTCCACAGTGGCACTTGCCCAATTAAAATAGCCTGCTATT 303

Qy  81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValValIleHisProLeuAlaThr 100
Db 304 ATAGCAATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAAATTCACCCTTTAGCAACT 363

Qy 101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleLeuPheLeuProMet 120
Db 364 TCCCATCAACAACATATTTTATAAAATTCCAATCCTGGTCATCAACAACAAAGTCTTGCCAATG 423

Qy 121 ValSerIleThrLeuLeuLeuValAlaLeuValTyrLeuProGlyValIleAlaLeuAlaLeuValGln 140
Db 424 GTTTCCATCACTCTTCTGCTAGTTGCTTTACCTGGCGTGATTGCACAAAGTGTCCAA 483

Qy 141 LeuHisAsnGlyThrLeuTyrLysSerProHisIleTrpLeuAspLysTrpMetLeuThr 160
Db 484 CTTCATAATGGAACCAAGTATAAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 543

Qy 161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu 180
Db 544 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTGCTGTACTGCACGCAAATTTATAGTCTG 603

Qy 181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200
Db 604 TCTTACCCAATGAGGAGGTCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 663

Qy 201 GlnGlnAsnLysGluAspAlaTrpIleGluGlnSerLysLysGlyIleVal 220
Db 664 CAACAAAATAAAGAAGATGCCTGGATTGAGCAATGAGTTTTAGGAATTGTG 723

Qy 221 SerIleGlyIleIleValGlyLeuAlaIleLeuLeuAlaLeuAlaValThrSerIleProSer 240
Db 724 TCTATTGGGATTATTGTGGGATTGGCAATACTGCTTGCACTAGCTGTTACCTCCATCCT 783

Qy 241 ValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerLysLeuGlyIleVal 260
Db 784 GTGAGTGACTCTTTGACAATGGAGAATTTCACTATAATTCAGAGCAAGCTAGGAATTGTT 843

Qy 261 SerLeuLeuGluGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
Db 844 TCCCTTCTACTGGGCACAATAACACGCATTGATTTTTGCCTGGAATAACTGGATAGATATA 903

Qy 281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300
Db 904 AAACAATTTGTAGGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 963
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Qy 301 ValLeuIlePheLysSerIleLeuPheLeuArgLysSerLysLeuLeuIle 320
Db 964 GTCCTGATATTTAAAAGCATACTATTCCTGCCATCCTTGAGGAAGAAGATACTTGAAGATT 1023

Qy 321 ArgHisGlyTrpGluAspValThrIleLysTyrIleIleCysSerGlnLeu 339
Db 1024 AGACATGGTTGGGAAGACGTCACCAAAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1080
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RESULT 6
US-10-830-899-2
; Sequence 2, Application US/10830899
; Publication No US20040253232A1
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Etessami, Soudabeh
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Perez-Villar, Juan
; APPLICANT: Meyrick Morrison, Karen Jane
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Faris, Mary
; APPLICANT: Gudas, Jean
; APPLICANT: Raitano, Arthur B.
; TITLE OF INVENTION: Antibodies and Molecules Derived
; TITLE OF INVENTION: therefrom that Bind to STEAP-1 Proteins
; FILE REFERENCE: 51158-20016.26
; CURRENT APPLICATION NUMBER: US/10/830,899
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: 09/323,873
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 10/010,667
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 10/011,095
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 10/236,878
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 09/455,486
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)....(1085)
US-10-830-899-2

Alignment Scores:
Pred. No.:
Score: 1790.00   Length: 1193
Percent Similarity: 100.00%   Matches: 339
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: Indels: 0
                          1.66e-195   Gaps: 0

US-10-750-262-2 (1-339) x US-10-830-899-2 (1-1193)

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Qy   1 MetGluSerArgLysAspIleThrAsnGlnGluLeuTrpLysMetLysProArgArg  20
Db  66 ATGGAAAGCAGAAAAGACATCACAAAACCAAGAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy  21 AsnLeuGluGluAspAspTyrLeuHisLysAspThrGlyThrSerMetLeuLysArg  40
Db 126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGGAGAAGACCAGCATGCTAAAAAGA 185

Qy  41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu  60
Db 186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy  61 LeuGlnHisThrGlnGluLeuPheProGlnThrPHisLeuProIleLysIleAlaAlaIle  80
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RESULT 7
US-10-753-195-1

; Sequence 1, Application US/10753195
; Publication No. US20050004349A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Rene S. Hubert
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas Saffran
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Steven Chappell Mitchell
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 51158-20016.02
; CURRENT APPLICATION NUMBER: US/10/753,195
; CURRENT FILING DATE: 2004-01-06

; PRIOR APPLICATION NUMBER: US/10/165,044
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: US 60/091,183
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 09/323,873
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: US 09/455,486
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: US 09/455,486
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: WO 99/62941
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: PCT/US00/33040
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.1

SEQ ID NO 1
; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)...(1191)
US-10-753-195-1

Query Match: 8
DB:

US-10-750-262-2 (1-339) x US-10-753-195-1 (1-1193)

Alignment Scores:
Pred. No.:
Score: 1.66e-195
Score: 1790.00   Length: 1193
Percent Similarity: 100.00%   Matches: 339
Best Local Similarity: 100.00%   Conservative: 0
Query Similarity: 100.00%   Mismatches: 0
Query Match: 8   Indels: 0
                                                 Gaps: 0

Qy   1 MetGluSerArgLysAspIleThrAsnGlnHisGluLeuTrpLysMetLysProArgArg 20
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGAAAGCAGAAAAGATATCACAAATCAGCATGAACTCTGGAAAATGAAGCCTAGGAGA 20

Qy   21 AsnLeuGluGluAspAspTyrLeuHisGlyAspThrGlyThrSerMetLeuLysArg 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   64 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 123

Qy   41 ProValLeuLeuHisLeuGlnThrAlaHisGluAspGluPheSerProSerGlu 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   124 CCTGTGCTTTTGCATCTGCAGACAGCCCATGAAGATGAATTTTCACCCTCAGAA 183

Qy   61 LeuGlnHisThrGlnLeuPheProGlnTrpHisLeuProIleLysIleAlaIleAlaIle 80
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   184 CTTCAGCACACACAGGACTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 243

Qy   81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleLeuProLeuAlaThr 100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   244 ATAGCAACTCTCGACTTTCTTTACACTCTTCTGAGGGAAGTAAT 303

Qy   101 SerHisGlnGlnThrTyrPheTyrLysAspAspTyrLeuHisGlyAspThrGlyThr 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   304 TCCCATCAACAAACATATTTTTATAAAGATGACTATTTA 363

Qy   121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln 140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   364 GTTTCCATCACTCTTCTTGGCATTGGTTACCTGGCAGCAAATTGTCCAA 423

Qy   141 LeuHisAsnGlyTyrPheTyrLysLysPheProHisIleTrpLeuAspLysTyrMetLeuThr 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   424 GTTTCCATCACTCTTCTTGGCATTGGTTACCTGGCAGCAAATTGTCCAA 483

Qy   161 ArgLysGlnPheGlyLeuLeuSerPhePheAlaValLeuLeuHisAlaIleLeuTyrSerLeu 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   484 CTTCATAATGGAACCAAGTATATAAGAAGTTTCCACATTGGTTGGATAAGGTGAGTGTAACA 543

Qy   181 SerLeuGlnPheGlyLeuLeuSerPhePheAlaValLeuLeuHisAlaIleLeuTyrSerLeu 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   544 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATCCAATTTATAGTCTG 603

Qy   201 GlnGlnAsnLysGluGlyLysAlaTrpIleGlyUhiSerAspValTrpArgMetGluIleLeuTyrVal 220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   604 CAACAAAATAAAGAAGGAAAATGGCCTGGAATGGCATGAGTTTGGAGAATGGAATTTATAGTCTG 605

Qy   241 ValSerAspSerLeuThrArgGluPheHisTyrIleGlnSerLeuGlyIleIleVal 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCCAAGCTAGGAGTGTT 845

Qy   261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   846 TCCCTTCTACTGGGCCAATACACGCATTGATTTTGCCTGGAATAAGTGGATAGATATA 905

Qy   281 LysGlnPheGluValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   906 AAACAAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy   301 ValLeuIlePheHisLysSerIleLeuProCysLeuArgGlyLysGlyIleLeuLeuLysIle 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   966 GTCCTGATATTTAAAAGCATAACTATTCCCTGCCTCAGGGAAGGAAGATACTGAAGAATT 1025

Qy   321 ArgHisGlyIleTyrProGluAspThrLysIleLeuAsnIleCysSerSerGlnLeu 339
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1026 AGACAATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082

...4154-4.rnp.m

RESULT 8

US-10-752-421-1

; Sequence 1, Application US/10752421
; Publication No. US20050063975A1

GENERAL INFORMATION:
    APPLICANT: Daniel E. Afar
    APPLICANT: Rene S. Hubert
    APPLICANT: Arthur B. Raitano
    APPLICANT: Douglas C. Saffran
    APPLICANT: Stephen C. Mitchell
    TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS EXPRESSED IN HUMAN CANCERS AND USES THEREOF
    FILE REFERENCE: 511582001612
    CURRENT APPLICATION NUMBER: US/10/752,421
    CURRENT FILING DATE: 2004-01-05
    PRIOR APPLICATION NUMBER: US 09/455,486
    PRIOR FILING DATE: 1999-12-06
    PRIOR APPLICATION NUMBER: US 09/323,873
    PRIOR FILING DATE: 1999-06-01
    PRIOR APPLICATION NUMBER: US 60/087,520
    PRIOR FILING DATE: 1998-06-01
    PRIOR APPLICATION NUMBER: US-60/091,183
    PRIOR FILING DATE: 1998-06-30
    NUMBER OF SEQ ID NOS: 47
    SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1
    LENGTH: 1193
    TYPE: DNA
    ORGANISM: Homo sapiens
    FEATURE:
    NAME/KEY: CDS
    LOCATION: (64)...(1083)

US-10-752-421-1
    LOCATION: (64)...(1083)

US-10-750-262-2 (1-339) x US-10-752-421-1 (1-1193)

Alignment Scores:
    Pred. No.:
    Score: 1.66e-195
    Percent Similarity: 190.00
    Best Local Similarity: 100.00%
    Percent Similarity: 100.00%
    Query Match: 100.00%
    DB: 9

    Length: 1193   Matches: 339
    Score: 190.00   Matches: 339
                               Conservative: 0
                               Mismatches: 0
                               Indels: 0
                               Gaps: 0

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Qy     1 MetGluSerArgLysAspAlaIleThrAsnGlnLeuLeuTrpLysMetLysProArgArg 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    64 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 123

Qy    21 AsnLeuGluGluAspAspTyrLeuHisLysAspAspProThrGlyThrSerMetLeuArg 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   124 AATTTAGAAGAAGACGATTATTTGCATAAGGACGACCCGACTGGTACAAGTATGCTG 183

Qy    41 ProValLeuGluHisGluHisAlaHisAlaAspAspProPheLeuProSerGlu 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   184 CCTGTGCTTTTGCATTGCACCAAACAGCCCATGCTGATGAAATTTGACTGCCCTTCAGA 243

Qy    61 LeuGlnHisHisThrGlnLeuGlnLeuPheProGlnThrTrpHisLeuProIleLysAlaAlaAlaIle 80
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   244 CTTCAGCACACAGCACCAGAACTCTTCCCACAGTGGCACTTCCAATTAAAATAGCTGCTATT 303

Qy    81 IleAlaSerLeuThrPhePheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   304 ATAGCACTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 363

Qy   101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleLeuAsnLysValLeuProMet 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   364 TCCCATCAACAATATTTTTATAAAATTCCAAATCCTGGTCATCAACAAAGTCTTGCCAATG 423

Qy   121 ValSerIleThrLeuLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaAlaIleValGln 140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   424 GTTTCCATCACTCTTCTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 483

Qy   141 LeuHisAlaAsnGlyThrArgTyrArgLysSerPheProHisTrpLeuAspAspValTrpMetLeuThr 160
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   484 CTTCATGCAAATGGAACCAAAGTATAAGAAGTTTCCACATTGGTTGGATGATGTTAACA 543

Qy   161 ArgLysGlnGlnPheGlyLeuLeuSerPhePheGlnAlaValLeuHisAlaIleTyrSerLeu 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   544 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTGGCTGTACTGCCATGAATTTATAGTCTG 603

Qy   181 SerTyrProMetArgArgSerTyrArgTyrLysSerLeuLeuAsnTrpAlaTyrGlnGlnVal 200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   604 TCTTACCCAATGAGGCGGCCATCCTACAGATATAAGAGTTTGCTAAACTGGGCATATCAACAGGTC 663

Qy   201 GlnGlnAsnLysGlyLysAspAlaIleThrIleGluHisAlaAspValTrpProLysMetGluIleTyrVal 220
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   664 CAACAAAATAAAGGAGCATCCTGGATTGAGCATGCAGATGTTTGGAATGGAGATTTATGTG 723

Qy   221 SerLeuGlyIleValGlyLeuValAlaIleLeuLeuAlaValThrSerIleProSer 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   724 TCTCTCGGAATTGTGGGATTGGCAATACTGCTCGTGACATCTATTCCATCT 783

Qy   241 ValSerAspSerLeuThrThrArgGluPheHisHisTyrIleGlnSerLysLeuGlyIleVal 260
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   784 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATTATATTCAGAGCAAGCTAGGAATTGTT 843

Qy   261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   844 TCCCTTCTACTGGGCACAATACACGGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 903

Qy   281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaLeuValAlaPheLeuProLeuVal 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   904 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTCTGGTTTTTCCTTCAAATTGTT 963

Qy   301 ValLeuIlePheLysLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLeuLysIle 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   964 GTCCTGATATTTAAAAAGCATACTATTCCTGCCATGCTTGAGGAGAAGAAGATACTGAAGATT 1023

Qy   321 ArgHisGlyTyrProGluAspValThrLysThrGlyIleCysSerGlnLeu 339
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1024 AGACATGGTTGGGAAGACGTCACCAAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1080
```

RESULT 9

US-10-861-662-2

; Sequence 2, Application US/10861662
; Publication No. US20050086707A1

GENERAL INFORMATION:
```
APPLICANT: Jakobovits, Aya
APPLICANT: Etessami, Soudabeh
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Perez-Villar, Juan
APPLICANT: Meyrick Morrison, Karen Jane
APPLICANT: Jia, Xiao-Chi
APPLICANT: Faris, Mary
APPLICANT: Gudas, Jean
APPLICANT: Raitano, Arthur B.
TITLE OF INVENTION: Antibodies and Molecules Derived
      therefrom that Bind to STEAP-1 Proteins
FILE REFERENCE: 51158-20016.26
CURRENT APPLICATION NUMBER: US/10/861,662
CURRENT FILING DATE: 2004-06-04
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 10/010,667
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 10/011,095
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 10/236,878
PRIOR FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 09/455,486
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 103
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2
LENGTH: 1193
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (66)...(1085)
```

```
Alignment Scores:
Pred. No.:
Score:                     1.66e-195
Percent Similarity:        1790.00
Percent Identity:          100.00%
Best Local Similarity:     100.00%
Query Match:               100.00%
DB:                        9

US-10-750-262-2 (1-339) x US-10-861-662-2 (1-1193)

Length:          1193
Matches:         339
Conservative:    0
Mismatches:      0
Indels:          0
Gaps:            0
```

```
Qy    1 MetGluSerArgLysAspIleThrAsnGlnGluLeuTrpLysMetLysProArgArg 20
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy   21 AsnLeuGluGluValAspAspTyrLeuHisLysAspSerThrGlyGluThrSerMetLeuLysArg 40
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  126 AATTTAGAAGAAGAAGACGATTATTTGCATAAGGACAGCACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy   41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluAspProSerGlu 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGTCTGATGAATTTGACTGCCCTTCAGAA 245

Qy   61 LeuGlnHisThrGlnGluLeuPheProGlnThrProHisLeuProIleLeuLysGluIleAlaAlaIle 80
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db  246 CTTCAGCACACACAGGAACTCTTCCCACAGACTCCACACTTACCTATT 305

Qy   81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleIleHisProLeuAlaThr 100
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db  306 ATAGCACATCTGACTTTCTTTACACTCTTCTTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy  101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleLeuAspSerValLeuProMet 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCATCAACAAAGTCTTGCCAATG 425

Qy  121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGlnGln 140

Db  426 GTTTCCATCACTCTCTTGGCAATTGTGTTTACCTGCTGCAGGTGTGTGATAGGCAGCAATTGTCCAA 485

Qy  141 LeuHisAlaAsnGlyTyrLysTyrLysSerPheProHisTrpLeuAspThrTrpMetLeuThr 160
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db  486 CTTCATGCTAATGGAACCAAGTATAAGAGTTTCCCACATTGGTTGGATACATGGATGTTAACA 545

Qy  161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu 180
        |||||||||||||||||||||||||||||||||||||||||||||||
Db  546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy  181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200
        |||||||||||||||||||||||||||||||||||||||||||||||
Db  606 TCTTACCCAATGAGGCGGTCGTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy  201 GlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArgMetGluIleTyrVal 220
        |||||||||||||||||||||||||||||||||||||||||||||||
Db  666 CAACAAAATAAAGAAGATGCCTGGATAGAACATGATGTTTGGAGAATGGAAATTTATGTG 725

Qy  221 SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSer 240
        |||||||||||||||||||||||||||||||||||||||||||||||
Db  726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy  241 ValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerLysLeuGlyIleVal 260
        |||||||||||||||||||||||||||||||||||||||||||||||
Db  786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy  261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
        |||||||||||||||||||||||||||||||||||||||||||||||
Db  846 TCCCTTCTACTCGGGACAATACACGCCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy  281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300
        |||||||||||||||||||||||||||||||||||||||||||||||
Db  906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTTCCTTCCAATTGTT 965

Qy  301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLysIle 320
        |||||||||||||||||||||||||||||||||||||||||||||||
Db  966 GTCCTGATATTTAAAAGCATACTACTTCCTGCCATGCTTGAGGAAGAAGATAATCTGAAGATT 1025

Qy  321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339
        |||||||||||||||||||||||||||||||||||||||||||||
Db 1026 AGACATGGTTGGGAGGATGTCACCAAAATTAACAAAACTGAAATATGTTCCCAGTTG 1082
```

RESULT 10

US-09-759-143-878
Sequence 878, Application US/09759143
Patent No. US20020022248A1

GENERAL INFORMATION:
```
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqui
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
      DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 878
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LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-878

Alignment Scores:
Pred. No.:
Score: 1.67e-195   Length: 1195
Percent Similarity: 100.00%   Matches: 339
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: Indels: 0
                                            Gaps: 0

US-10-750-262-2 (1-339) x US-09-759-143-878 (1-1195)

```
Qy      1  MetGluSerArgLysAspIleThrAsnGlnGluLeuTrpLysMetLysProArgArg   20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  ATGGAAAGCAGAAAAGACATCACAAACCAAGAGAAACTTTGGAAAATGAAGCCTAGGAGA  125

Qy     21  AsnLeuGluGluAspAspThrTyrLeuHisGlyAspThrGlyThrSerMetLeuLysArg   40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    126  AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGAGCACCAGCATGCTAAAAAGA  185

Qy     41  ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAlaAspGluPheAspCysProSerGlu   60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    186  CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA  245

Qy     61  LeuGlnHisThrGlnGluLeuPheProGlnTrpHisLeuProIleLysIleAlaAlaIle   80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    246  CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT  305

Qy     81  IleAlaSerLeuThrPheLeuTyrThrLeuLeuLeuArgGluValIleAlaIleHisAlaThr  100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    306  ATAGCATCTCGACTTTTCTTTCACATCTTTGACTGTGGGAGAAGTAATTCACCCTTTAGCAAACT  365

Qy    101  SerHisGlnGlnThrTyrPheTyrIleProIleLeuGluValIleLeuProMet  120
           ||||||||||||||||||||||||||||||||||||||||||
Db    366  TCCCATCAACAATATTTTATAAAATTCCAATCCTGGGTCATCAACAAAGTCTTGCCAATG  425

Qy    121  ValSerIleThrLeuLeuValThrLeuTyrLeuProGlyValIleAlaAlaAlaValGln  140
           ||||||||||||||||||||||||||||||||||||||||||
Db    426  GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA  485

Qy    141  LeuHisAsnGlyThrLysTyrLysGlySerPhePheProHisLeuTrpMetLeuThr  160
           ||||||||||||||||||||||||||||||||||||||||||
Db    486  CTTCATAATGGAACCAAGTATAAAGGAAGTTTCCCATTGGGATAAGTGGATGTTAACA  545

Qy    161  ArgLysGlnPheGlyValGlyLeuGlyLeuSerPhePheProPheAlaValLeuHisAlaAlaIleTyrSerLeu  180
           ||||||||||||||||||||||||||||||||||||||||||
Db    546  AGAAAGCAGTTTGGGGCTTCCACGTTTCTTTTTGCTGTACTGCATGCAATTTACAGTCTG  605

Qy    181  SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal  200
           ||||||||||||||||||||||||||||||||||||||||||
Db    606  TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC  665

Qy    201  GlnGlnAsnLysGlyGluAspAlaIleTrpIleGluLeuTyrTyrVal  220
           ||||||||||||||||||||||||||||||||||||||||||
Db    666  CAACAAAATAAAGAAGGAGATGCCATGATTGGGATTGAGCTATATTATGTG  725

Qy    221  SerLeuGlyIleLeuValAlaIleLeuLeuAlaValThrSerIleLeuProSer  240
           ||||||||||||||||||||||||||||||||||||||||||
Db    726  TCTCTGGGAATTGTGGCTATTCTGCTTGCTGTCACCTCATTCCATCT  785

Qy    241  ValSerAspSerLeuThrArgGluHisIleTyrIleGlnSerArgLeuGlyIleVal  260
           ||||||||||||||||||||||||||||||||||||||||||
Db    786  GTGAGTGACTCTTTGACATGGAGAATTCACTATATTCAGAGCAAGGCTAGGAATTGT  845

Qy    261  SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle  280
           ||||||||||||||||||||||||||||||||||||||||||
Db    846  TCCCTTCTACTGGGCACAATACAGCACATTGATTTTTGCCTGGAATAAGTGGATAGATATA  905

Qy    281  LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal  300
           ||||||||||||||||||||||||||||||||||||||||||
Db          (...)
```

RESULT 11
US-09-780-669-878
; Sequence 878, Application US/09780669
; Patent No. US2002005197A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqui
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-878

Alignment Scores:
Pred. No.:
Score: 1.67e-195   Length: 1195
Percent Similarity: 100.00%   Matches: 339
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: Indels: 0
                                            Gaps: 0

US-10-750-262-2 (1-339) x US-09-780-669-878 (1-1195)

```
Qy      1  MetGluSerArgLysAspIleThrAsnGlnGluLeuTrpLysMetLysProArgArg   20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  ATGGAAAGCAGAAAAGACATCACAAACCAAGAGAAACTTTGGAAAATGAAGCCTAGGAGA  125

Qy     21  AsnLeuGluGluAspAspThrTyrLeuHisGlyAspThrGlyThrSerMetLeuLysArg   40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    126  AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGAGCACCAGCATGCTAAAAAGA  185

Qy     41  ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAlaAspGluPheAspCysProSerGlu   60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    186  CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA  245

Qy     61  LeuGlnHisThrGlnGluLeuPheProGlnTrpHisLeuProIleLysIleAlaAlaIle   80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    246  CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT  305
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Alignment Scores:

US-09-822-827-878

; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens

; SOFTWARE: FastSEQ for Windows Version 3.0
; NUMBER OF SEQ ID NOS: 982
CURRENT FILING DATE: 2001-03-28
CURRENT APPLICATION NUMBER: US/09/822,827
NUMBER OF SEQ ID NOS: 982
FILE REFERENCE: 210121.534C1
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
GENERAL INFORMATION:
Patent No. US20020081680A1
Sequence 878, Application US/09822827

RESULT 12

Pred. No.:	1.67e-195
Score:	1790.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	3

Length:	1195
Matches:	339
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-10-750-262-2 (1-339) x US-09-822-827-878 (1-1195)

[Sequence alignment data follows, pairing query (Qy) and database (Db) rows of protein/DNA sequence with alignment bars. The alignment begins with MetGluSerArgLysAspPileThrArgAsnGlnGluGlnLeuTrpLysMetLysProArgArg / ATGGAAAGCAGAAAAGACATCACAAACCACAAGGAACACTTTGGAAAATGAAGCCTAGGAGA (positions 1–20 / 1–125) and continues through the full sequence.]

US-10/750,262-2.rspom

Qy 321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1026 AGACATGGTTGGGAAGACGTCACCAAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082

RESULT 13
US-09-895-793-878

; Sequence 878, Application US20020192763A1
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSEQ for Windows Version 3.0
;
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-895-793-878

US-10-750-262-2 (1-339) x US-09-895-793-878 (1-1195)

Alignment Scores:
Pred. No.:

Score: 1790.00
Percent Similarity: 100.00%
Percent Identity: 100.00%
Query Match: 100.00%
Best Local Similarity: 100.00%
DB: 3

Length: 1195
Matches: 339
Mismatches: 0
Conservative: 0
Indels: 0
Gaps: 0

Db:

Qy   1 MetGluSerArgLysSerArgIleThrAsnGlnEluGluLeuTrpLysMetLysProArg 20
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Db   1 ATGGAAAAGCAGAAAAAGACAATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 20

Qy   21 AsnLeuGluGluAspAspThrTyrLeuHisLysAspPheGluThrGlyThrSerMetLeuLysArg 40
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   66 ATGGAAAAGCAGAAAAAGACAATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy   41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGlyPheAspCysProSerGlu 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 126 AATTTAGAAGAAGACGATTATTTGCATAAGGACAGACAGCAGCAACTGTAAAAAAGA 185

Qy   61 LeuGlnHisThrGlnGluLeuPheProGlnThrHisLeuProIleLeuSerIleAlaIle 80
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 186 CCTGTGCTTTTGCATTTGCACCAAACAGCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy   81 IleAlaSerLeuLeuThrPheLeuuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy 306 ATAGCACTCTCGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAAACT 365
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Qy 101 SerHisGlnHisTyrPheTyrLysIleProIleLeuVallIleAsnLysLysValLeuProMet 120
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Db 366 TCCCATCAACAAAATATTTTTATAAAAAAAATTCCAAATCCTGGTCATCAACAACAAGTCTTGCCAATG 425

Qy 121 ValSerIleThrLeuLeuAlaLeuValTyrLeuGlyProGlyValIleAlaAlaIleValGln 140
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Db 426 GTTTCCATCACTCTTCTTGCCATTGTTTACCTCGGCCAGGGTGTGATAGCAGCAATTGTCCAA 485

Qy 141 LeuHisLeuAsnGlyThrLysLysTyrLysLysSPhePheAlaValLeuHisAlaIleTyrSerLeu 160
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 486 CTTCATAATGGAACCAAGAAGTATAAGAAGTTTCCACATTGGTTGGATATTAAGAATGGAGATGTTAACA 545

Qy 161 ArgLysGlnPheGlyTyrLeuLeuSerPhePheAlaValLeuHisAlaIleTyrSerLeu 180
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Db 546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy 181 SerTyrProMetArgArgSerTyrArgTyrLysSleLeuAsnTrpAlaLeuTyrSerLeu 200
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Db 606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGATTTTGGTTGGCTTATACTCTCT 665

Qy 201 GlnGlnAsnLysGlyAspAlaTrpIleGluLeuHisAspValTrpArgMetGluIleTyrVal 220
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Qy 221 SerLeuGlyIleValGlyIleLeuAlaIleLeuValAlaValThrSerIleProSer 240
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Db 726 TCTCTCGGGAATTGTGGGCATTGCAATACTGGCTCTGTTGGCAGTACATCTATTCCATCT 785

Qy 241 ValSerAspSerLeuTrpArgGluPheHisSerTyrIleLeuGlnSerLysLysGlyIleVal 260
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Db 786 GTGAGTGACTCTTTGACATGGAGAGAATTCCACTATATTCAGAGCAAGCTAGGAAATTGGT 845

Qy 261 SerLeuLeuLeuGlyIleThrIleHisIleAlaLeuLeuPheAlaLeuTrpAsnLysSerTrpIleAspIle 280
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Db 846 TCCCTTCTTACTCGGGCCACAAATACACGCATTGATTTTTGCCTGGAAATGGATGGAGATATA 905

Qy 281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValAlaPheLeuLeuProIleVal 300
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Qy 301 ValLeuIlePheLysSerIleLeuLeuPheLeuProCysGluArgLysLysLeuLeuLysIle 320
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Db 966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGCAGAAGAAACTACTGAAGATT 1025

Qy 321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339
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Db 1026 AGACATGGTTGGGAAGACGTCACCAAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082

RESULT 14
US-09-895-814-878

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; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.

; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
Query Match: US-09-895-814-878
DB:

US-10-750-262-2 (1-339) x US-09-895-814-878 (1-1195)

Alignment Scores:
Pred. No.:
Score: 1.67e-195   Length: 1195
           1790.00   Matches: 339
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 3   Indels: 0
DB: Gaps: 0

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Qy    1  MetGluSerArgLysAspIleThrArgAsnGlnGluLeuTrpLysMetLysProArgArg  20
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Db    1  ATGGAAAGCAGAAAAGACATCACAAGAAACCAAGAGCTTTGGAAAATGAAAGCCTAGAGA  125

Qy   21  AsnLeuGluGlyAspAspTyrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg  40
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  126  AATTTAGAGAGAGACGATTAATTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA  185

Qy   41  ProValLeuLeuHisLeuHisGlnThrHisLaHisAlaAspProGluPheAspCysProSerGlu  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  186  CCTGTGCTTTTGCATTTGCACCAAACAGCCCATCCTGATGAATTTGACTGCCCTTCAGAA  245

Qy   61  LeuGlnHisThrGlnLeuGluPheProGlnTrpHisLeuProIleuIleAlaAlaIle  80
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  246  CTTCAGCACACACAGGAGACTCTTTCCCACAGTGCCACTTGCCAATTAAAATAGCTGCTATT  305

Qy   81  IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr  100
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Db  306  ATAGCACTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT  365

Qy  101  SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeuProMet  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  366  TCCCATCAACAATAATTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTTCTTGCCAATG  425

Qy  121  ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaLaAlaIleValGln  140
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  426  GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTAGCACGCAAATTGTCCAA  485

Qy  141  LeuHisAsnGlyThrLysTyrLysSerPheProHisTrpLeuAspLysTrpMetLeuThr  160
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Db  486  CTTCATACAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA  545

Qy  161  ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu  180
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Db  546  AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTGCTGTACTGCATGCAATTTATAGTCTG  605

Qy  181  SerTyrProMetArgArgSerTyrArgTyrLysGlyLeuLeuAsnTrpAlaTyrGlnIleVal  200
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  606  TCTTACCCAATGAGGCGGATCCTACAGATACAAGTTGCTAAACTGGGCCATATCAACAGGTC  665

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Db  666  CAAACAAAATAAAGAAAGAAGTGCCTGGACATGAGCATGATGTTTGGAGAATGGAGATTTATGTG  725

Qy  221  SerLeuGlyIleValGlyLeuValAlaIleLeuLeuAlaLeuAlaValThrSerIleProSer  240
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Db  726  TCTCTCGGGAATTGTGGGTATTGGCAATACTGGCTCTTGTTGGCGCTGACATCTAATTCCATCT  785
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; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hepler, William T.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Wang, Aijun
; APPLICANT: Li, Samuel X.
; APPLICANT: Carter, Darrick
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Day, Craig H.
; APPLICANT: Stolk, John A.
; APPLICANT: Retter, Marc W.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Xu, Jiangchun
; GENERAL INFORMATION:

RESULT 15
US-10-012-896-878
; Sequence 878, Application US/10012896
; Publication No. US20020183251A1

US-10-012-896-878
Db

; APPLICANT: Houghton, Raymond L.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-878

Alignment Scores:
Pred. No.:
Score: 1.67e-195   Length: 1195
           1790.00   Matches: 339
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 5   Indels: 0
DB: Gaps: 0

US-10-750-262-2 (1-339) x US-10-012-896-878 (1-1195)

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Qy  241  ValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerLysLeuGlyIleVal  260
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Db  786  GTGAGTGACTCTTTGACATGGAGAGAAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT  845

Qy  261  SerLeuLeuLeuGlyThrLeuHisIleAlaLeuIlePheAlaTrpAsnLysThrPheIle  280
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  846  TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATGGATGATATA  905

Qy  281  LysGlnPheValTrpIleTyrThrProProThrPheMetIleAlaLaValPheLeuProIleVal  300
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Db  906  AAACAAATTGTATGGATATACACCTCCAACTTTTATGATAGCTGTTTTTCCTTATGTT  965

Qy  301  ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysGlyIleLeuLysIle  320
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  966  GTCCTGATATTTAAAAGCATACTAATTCCTGCCATGCTTGAGGAAAGAAGACTACTGAAGATT  1025

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ub-1U-/5U-2U2-2.rnpdm

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Db  126  AATTTAGAAGAAGACGCATCATACTTGCATAAGGATGACACGGGATATGAAACCAGCATGCTTAAAAAGA  185

Qy   41  ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu  60
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Qy   61  LeuGlnHisThrGlnGluLeuPheProGlnThrHisLeuProLeuLysIleIleAlaAlaIle  80
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Db  306  ATAGCATCTTCTGACTTTTTGTACACTCTTCTGGGAAGTAATTCACCCTTTAGCAACT  365

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Db  366  TCCCATCAACAATATTTTTATAAAAATCCTGGTCATCAACAAGTCTTGCCAATG  425

Qy  121  ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleAlaValGln  140
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Qy  141  LeuHisAsnGlyThrLysTyrTyrLysLysSerPheProHisTrpLeuAspLysTrpMetLeuThr  160
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Qy  161  ArgLysGlnPheGlyLeuLeuSerPhePheProAlaValLeuHisAlaAlaIleTyrSerLeu  180
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Qy  201  GlnGlnAsnGlyGluAspIleAlaTrpIleGluHisAspValTrpArgMetGluIleTyrVal  220
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Qy  221  SerLeuGlyTyrIleValGlyLeuAlaIleLeuLeuAlaLeuAlaValThrSerIleProSer  240
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Qy  241  ValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerLysLeuGlyIleVal  260
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Qy  261  SerIleLeuLeuGlyThrArgIleHisAlaLeuIlePheAlaTrpAsnLysSerIleAspIle  280
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Qy  281  LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  906  AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT  965

Qy  301  ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysLeuLeuLysIle  320
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Qy  321  ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerSerGlnLeu  339
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Job time : 959 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 6, 2005, 16:29:58 ; Search time 159 Seconds
                                                   (without alignments)
                                                   663.545 Million cell updates/sec

Title: US-10-750-262-2
Perfect score: 1790
Sequence: 1 MESRKDITNQEELWKMKPRR..........IRHGWEDVTKINKTEICSQL 339

Scoring table:
                BLOSUM62
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Searched: 3289935 seqs, 15561033 residues

Total number of hits satisfying chosen parameters: 6579870

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 200000000

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
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-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
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       10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	107	6.0	3137	6	US-10-793-626-3842	Sequence 3842, Appli
2	99.5	5.6	2622	6	US-10-750-185-48126	Sequence 48126, A
3	99.5	5.6	2803	6	US-10-750-185-29256	Sequence 29256, A
4	93.5	5.2	819	6	US-10-793-626-1307	Sequence 1307, Ap
5	92.5	5.2	3263	6	US-10-793-626-3595	Sequence 3595, Ap
6	90.5	5.1	1179	6	US-10-793-626-3305	Sequence 3305, Ap
7	90.5	5.1	1564	7	US-11-110-977-1	Sequence 1, Appli
8	89.5	5.0	1515	6	US-10-467-657-2439	Sequence 2439, Ap

9	87.5	4.9	340000	7	US-11-102-978-3	Sequence 3, Appli
c 10	87	4.9	3083	6	US-10-793-626-4225	Sequence 4225, Ap
c 11	87	4.9	3301	6	US-10-793-626-4209	Sequence 4209, Ap
c 12	87	4.9	4071	6	US-10-793-626-3381	Sequence 3381, Ap
c 13	86	4.8	1068	6	US-10-467-657-4965	Sequence 4965, Ap
c 14	85.5	4.8	1138	6	US-10-750-185-36689	Sequence 36689, A
c 15	85.5	4.8	1462	6	US-10-750-185-37763	Sequence 37763, A
c 16	85	4.7	660	7	US-10-793-626-2205	Sequence 2205, Ap
c 17	85	4.7	1368	6	US-11-074-176-237	Sequence 237, Appli
18	85	4.7	1517	6	US-10-750-185-26344	Sequence 26344, A
c 19	85	4.7	2557	6	US-10-793-626-3829	Sequence 3829, Ap
c 20	85	4.7	3146	6	US-10-793-626-4281	Sequence 4281, Ap
c 21	84	4.7	3646	6	US-10-793-626-4070	Sequence 4070, A
22	84	4.7	963	6	US-10-750-185-27964	Sequence 27964, A
c 23	83.5	4.7	1470	6	US-10-793-626-2631	Sequence 2631, Ap
c 24	83.5	4.7	3304	6	US-10-793-626-4182	Sequence 4182, Ap
c 25	83.5	4.7	4142	6	US-10-793-626-3523	Sequence 3523, Ap
c 26	83	4.6	819	6	US-10-467-657-7791	Sequence 7791, Ap
27	83	4.6	1636	7	US-11-102-240-77	Sequence 77, Appli
28	83	4.6	1915	7	US-11-068-686-3	Sequence 3, Appli
29	83	4.6	1917	6	US-11-074-176-221	Sequence 221, Appli
30	82	4.6	3109	6	US-10-793-626-3708	Sequence 3708, Ap
c 31	82	4.6	3149	6	US-10-793-626-3902	Sequence 3902, Ap
32	81.5	4.6	2007	6	US-10-750-185-45307	Sequence 45307, A
33	81.5	4.6	2721	6	US-10-485-517-51	Sequence 51, Appl
34	81.5	4.6	3514	6	US-11-082-389-401	Sequence 401, Appl
35	81.5	4.6	1020	6	US-10-750-185-44589	Sequence 44589, A
36	81	4.5	2419	6	US-10-793-626-1693	Sequence 1693, Ap
37	81	4.5	3075	7	US-11-055-822-507	Sequence 507, App
38	81	4.5	3075	7	US-11-055-822-593	Sequence 593, App
39	81	4.5	3806	6	US-10-750-185-49215	Sequence 49215, A
40	81	4.5	4105	6	US-10-793-626-4166	Sequence 4166, Ap
c 41	81	4.5	4105	6	US-10-750-185-45307	Sequence 45307, A
c 42	80	4.5	1406	7	US-10-750-185-38622	Sequence 38622, A
c 43	80	4.5	360	7	US-11-174-150-17	Sequence 17, Appl
c 44	80	4.5	1347	6	US-10-467-657-677	Sequence 677, App
45	80	4.5	3976	6	US-10-750-185-60435	Sequence 60435, A
	80	4.5	5099	6	US-10-821-234-193	Sequence 193, App

ALIGNMENTS

RESULT 1
US-10-793-626-3842

; Sequence 3842, Application US/10793626
; Publication No. US2005025547BA1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 3842
; LENGTH: 3137
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3842

Alignment Scores:
Pred. No.:   0.179
Score: 107.00
Percent Similarity: 44.07%
Best Local Similarity: 23.70%
Query Match: 5.98%

Length:	3137
Matches:	64
Conservative:	55
Mismatches:	94
Indels:	58
Gaps:	17

DB:

US-10-750-262-2 (1-339) x US-10-793-626-3842 (1-3137)

RESULT 2

Sequence 48126, Application US/10750185

Publication No. US20050260603A1

GENERAL INFORMATION:

APPLICANT: MMI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31

PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 48126
LENGTH: 2622
TYPE: DNA
ORGANISM: Bovine
US-10-185-48126   1986880404440
DB:

Alignment Scores:

Pred. No.:	1.02
Score:	99.50
Percent Similarity:	36.57%
Best Local Similarity:	21.04%
Query Match:	5.56%

Length:	2622
Matches:	65
Conservative:	48
Mismatches:	95
Indels:	101
Gaps:	13

US-10-750-262-2 (1-339) x US-10-750-185-48126 (1-2622)

[Sequence alignment — protein and DNA comparison between Query (Qy) and Database (Db) sequences, displayed in paired rows with match bars]

Db   2038 -----GCAGCTTTTGTGTATCTCAAACCACCTTCCGTTTTGCACCTTGACCAAGGGAAAG 2092
          ||||||:|:::   :::
Qy   293 --IleAlaValPheLeuProIleValValLeuIleLeuPheLysSerIleLeuPheLeuPheLeuProC 312
Db   2093 TGTCATCCCTGTTTTATACCATTGTGGTGTCCCAATGTTAAATACCACTGATATAT------A 2146
Qy   312 ysLeuArgLysIleLeuLys 319
          ||||:|| :::||
Db   2147 GTTTGAGGAAACAAGGATGTCAAA 2169

RESULT 3
US-10-185-29256
Sequence 29256, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: KERR, Richard
; APPLICANT: DeNISE, Sue K.
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29256
; LENGTH: 2803
; TYPE: DNA
; ORGANISM: Bovine
US-10-185-29256 1986680686697

Alignment Scores:
Pred. No.:
Score: 1.13
Percent Similarity: 99.50
Percent Identity: 34.15%
Best Local Similarity: 20.33%
Query Match: 5.56%
DB: 6

Length: 2803
Matches: 75
Conservative: 51
Mismatches: 100
Indels: 143
Gaps: 18

US-10-750-262-2 (1-339) x US-10-185-29256 (1-2803)

Qy   17 LysProArgArgAsnLeuGluGlnAsp----------------------AspTyrLeuHisLys 30
          ::: |||
Db   1251 AGGAAACAGAAGACCTAGAGGAGATCTAAATCAGCTCATGGAATGATCCCTTAGA---AspTyrLeuHisLys 1307

Qy   31 AspThrGlyGluThrSerMetLeuLysArgProValLeuLeuHisLeuHisGlnThrAla 50
          ||| :::
Db   1308 --GGGAGGGTATTCAGAGCTG- 1325

Qy   51 HisAlaAspGluPheAspCysProSerGluLeu 61
          |||
Db   1326 ------------TGTTCCAGCTCCTTGTGACAGGAGAGGGCTCTTCCAAAA 1367

Qy   62 GluHisThrGlnLeuPheProGlnTrpHisLeuProIleLeuLysSerIleAlaAlaIleIle 81
          |||||
Db   1368 GACCACACACA-------ACTTGGACTTTAGAA- 1394

Qy   82 AlaSerLeuThrPheLeuThrLeuArgGluValIleHisProLeuAlaThrSer 101
          |||
Db   1395 ------------ACAATTGTTGGAAAAAAATATGAGGCAACTACCACAC 1436

Qy   102 HisGlnGlnTyrPheLysIleProIleLeuValIleAsnLysValLeuProMetVal 121
          |||||
Db   1437 CATCAGTCACAGTTTTAT------------AGCAAA 1460

Qy   122 SerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleLeuValGlnLeu 141
          :::::|||
Db   1461 ------------CTTTTA 1460

Db   1461 TTTGCAACTTTGTGGCAGAAGAAGCCTTCCTGCACGAAACTCATGGCTGCAGAGAATATATTAA 1520
          ||
Qy   142 HisAsnGlyThrLysTyrIleLysPhePorHisTrpLeuAspLysTrpMetLeuThrArg 161
          :::|||:::   :::||||||
Db   1521 TGTTCTGTTCGCAAG------------------------GAATGTGTGGATCGCTTACTGATGTCAAGA 1565

Qy   162 LysGln----------------------PheGlyLeuLeu 167
          ||||::: ||
Db   1566 AAAGAAAATGGAACGGGGCAAAAAGAAAAGAAATGTCAGGGGATTATTTATCATTAACTTTCC 1625

Qy   168 SerPhePhePheAlaValLeuHis------------------AlaIleTyr 178
          ||| :::
Db   1626 CTCTTCTTTGTCCCTGTTACTCCATCGGTTATTAATCTCACAATGTCGGTCTTAGCG 1685

Qy   179 SerLeuSerTyrProMetArgArgSerTyrArgTyrrLys------------------ 191
          |||:::   :::
Db   1686 TCTCGTCCAACACATTAATTAAGGAAGTACTACGGACCAAAGTATACCAGGCCATCATAGA 1745

Qy   192 -----LeuLeuAsnTrpAlaTyrGlnGlnValGlnGlnAsnLysGluAspAlaTrpIle--- 209
          :::   :::
Db   1746 GAGAGGGATAAGAAAATTGTTTCTACCTTCGTTTTCTCAGAGACAAGCGAACACAAGAAAAACA 1805

Qy   210 GluHisAspValTrpArg------------------MetGluIle 218
          ||| :::
Db   1806 CAACGAGCTTGCTCGGCGCCCCACAAGCAACCAGTCGCCGTGGTAAAGGTAGTGATTGGGAGT 1865

Qy   219 TyrValSerLeuGlyIleValGlyLeuValAlaIleLeuLeuAlaLeuAlaValThrSerIle 238
          |||:::||| :::::|||
Db   1866 TACTTTCAGTCTCGGCTACACAGAGGGTTTCCCTGGTGGCT---CAGCGCGGGTAAAGAATCTG 1922

Qy   239 ProSerValSerAsp------------------SerLeuThrTrpArgGluPheHisTyrIleGln 254
          ||||| :::
Db   1923 CCTTCAGTCAGCAGGAGACCCAGGGGCTCAGTCCCTGGGCTGGGGAAGAC------CCTCTGGAG 1976

Qy   255 SerLysLeuGlyIleValSerLeuLeuLeu------------------ 264
          :::
Db   1977 AAAGGAATGGGAGAACCTACTCCAGTAATTCTTGAGTGGGAGGTTGCGTGGGCAGCAGTAACGGCC 2036

Qy   265 -----GlyThrIleHisAlaLeuIlePheAlaLeuTrpAspAsnLysTrpIleLysGln 282
          :::   :::
Db   2037 TGGAGGGCCTACAGTCCACGGGGGTCCCAAAGAGTTGGATGAAAGAGTCGGACACTACTGAG 2096

Qy   283 PheValTrpTyrThrProProThrPheMetIleAlaLysValPheLeuProIleValValLeu 302
          :::   :::||||||
Db   2097 CGACTAACACTTCACTTCACTTCTGGTCTTG 2123

Qy   303 IlePheLysSerIleLeuPheLeuPro 311
          :::|||::|||||||
Db   2124 GTTGACAGAGAAGTCTTTTCTGACTTCCC 2150

RESULT 4
US-10-793-626-1307
Sequence 1307, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU348OUS
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1307
; LENGTH: 819
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-1307

```
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; APPLICANT: KIMMERLY, WILLIAM JOHN
; GENERAL INFORMATION:
; Publication No. US2005025547BA1
; Sequence 3595, Application US/10793626
US-10-793-626-3595/c
RESULT 5
```

Alignment Scores:

Pred. No.:
Score: 0.878
Percent Similarity: 93.50
Best Local Similarity: 39.47%
Query Match: 23.31%
                             5.22%

Length: 819
Matches: 62
Conservative: 43
Mismatches: 82
Indels: 79
Gaps: 16

US-10-750-262-2 (1-339) x US-10-793-626-1307 (1-819)

```
Qy   64  ThrGlnGluLeuPheProGlnTrp------HisLeuProIleLysIleAlaAlaIleIle  81
         |||||              :::     :::     ::::::   |||
Db  202  ACACAACAGGCACCACCAATGGTTGTATCATTTTCATTTAAGTTTAAGTTGTTGTGAT  261

Qy   82  AlaSer------LeuThrPheLeuTyrThrLeuLeuArgGluValIleLeuHisProLeu  98
         |||                 |||:::     :::        :::::
Db  262  GCTCAAGGTCTCAATAATTAGTTATATCTTTTTAAAATCCATCAAATCTGTAATAAAATG  321

Qy   99  AlaThrSerHisGlnLeuGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeu  118
            |||||||               |||||:::
Db  322  ---ATGAAGCAACAATGG---

Qy  119  ProMetValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaAlaIle  138
         |||||||:::                 :::|||||
Db  361  AAAAATTGTAAAGTTGGGATT-----GTTCGTATAATTTATTTATTACTTTATTAATGCGGGGTG  414

Qy  139  ValGlnLeuHisAsnGlyThrLeuTyrLysPheProHisTrpLeuAspLysTrpMet  158
         :::            |||                 :::
Db  415  ATT------GGAACA------TCATTACCTAACATATTA---AGTTATCAT  450
```

(remaining alignment rows continue)

US-10-750-262-2 (1-339) x US-10-793-626-3595 (1-3263)

Alignment Scores:

Pred. No.:
Score: 9.4
Percent Similarity: 92.50
Best Local Similarity: 38.59%
Query Match: 20.13%
                             5.17%

Length: 3263
Matches: 60
Conservative: 55
Mismatches: 91
Indels: 92
Gaps: 15

```
; FILE REFERENCE: PU348OUS
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3595
; LENGTH: 3263
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3595
```

```
Qy    279 AspIle-----------------LysGlnPheValTrpTyrThrProProThrPheMetIleAla 294
          :::                                             |||:::
Db    924 TAGTAAAATTACTACTTAGAAAATATGAAACGTAAAAATTAACTGTTTCGTATTTAGT 865
          |||||||||
Qy    295 ValPheLeuProIleValVal-----------------LeuIlePheLysSerIleLeuPheLeu 310
          |||:|||               |||||||:|||
Db    864 TTATATCTGAAATTAAAAGTAGGGCTTTAGATTTAAATATTCAGGGAGGTGACATTTCTA 805
Qy    311 ProCysLeuArgLysLysIleLeuLysIle-ArgHisGlyTrpGluAspVal 327
          |||           |||||                      |||:|||
Db    804 TGGCAGAAAAAATTATTATTGTTGTCGGTGAGGGACTACGTGGTTCTGATGTC 753
```

RESULT 6
US-10-793-626-3305

Sequence 3305, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMBERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO:3305
LENGTH: 1179
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic

US-10-793-626-3305

Alignment Scores:
Pred. No.:
Score: 3.43
Percent Similarity: 90.50
Best Local Similarity: 40.56%
Query Match: 6

Length:	1179
Matches:	56
Conservative:	45
Mismatches:	75
Indels:	73
Gaps:	15

US-10-750-262-2 (1-339) x US-10-793-626-3305 (1-1179)

```
Qy    39 LysArgProValLeuLeuHisLeuHisGlnThrAlaHisAlaAsp-----GluPheAsp 56
         |||               ||||||                        |||
Db   541 AAAGAAGATGAAATTGTCACATCCAAAATCAAACACCTCGTTCATCTAGTATTGAATCACAA 600

Qy    57 CysProSerGluLeuGlnHisThrGlnGlyLeuPheProGlnThrProHisLeuProIleLeuLys 76
         |||                   |||||:::||||
Db   601 ACTGGCTCAAGCGTCATAAGACCTCGTGAGGTTTTAAA-----TATCTGATGATTACA 654

Qy    77 IleAlaIleAlaIleIleAla---SerLeuThrPheLeuValTyrThrLeuArgGluValIle 95
         ::::|||                  :::|||
Db   655 TTTTTAGTGCTGGTTGCTAATTCGTAACATTCGTGTT----- 696

Qy    96 HisProLeuAlaThrSer-----HisGlnGlnTyrPheTyrLysIleProIleLeuVal 113
         |||                    |||:::   ::|||||||||:|||
Db   697 AATCCATTAATTTATCCAATGACATGAAAATGTCTTTGTCTTAGCACTACTGTT 756

Qy   114 IleAsnLysValLeuProMetValSerIleThrLeuLeuAlaLeuValTyrLeuProGly 133
         :::||::                            |||
Db   757 ---AATGGTGTAGCAGGTGGTGTGATTGGTACTCA 795

Qy   134 ValIleAlaAlaIleLeuValGlnLeuHisAsnGlyThrLysTyrLysPheProHisTrp 153
         |||||:::                 |||       |||       |||
Db   796 GTTTTTATCT----------------------------------- 804

Qy   154 LeuAspLysTrpMetLeuThrArgLysGlnPheGlyLeuLeuSerPhe---PhePheAla 172
         |||||:::                               :::|||      |||
Db   805 ---GATAAGTTT-----------ACTAGTAAGCGTTGGTTAATAATTTCGATTCAATATATTATA 855
```

```
Qy   173 ValLeuHisIleAlaIleTyrSerLeuSerTyrPro-------------------MetArgArgSer 187
         :::::                              |||:::             |||
Db   856 ATAATGATGAATAATTCTTAACTTATATTATTATTACCAGAACAGGAATTAGTTGGCTTA 915

Qy   188 TyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnAsnLysGluAspAla 207
         :::       ||||||   |||:::||||||       |||:::
Db   916 TTTAGTGTGAAATTAATGGCTTATAGTGAGTACGACAAAATCCAGCTATTCAAAGTGGTATTATTGAA 975

Qy   208 TrpIleGluHisAspVal-----TrpArgMetGluIleTyrValSerLeu 222
         |||:::           |||      |||
Db   976 CACGTTCGAAGGAGATACAAGCCAAGTGATGAGTTGGAATATGTCG------AGTCTC 1026

Qy   223 ---------------GlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaVal 235
                        |||||||||:::||||||||||:::||
Db  1027 AATGCCGGTATTGGCGTTGGCGGAAATCCGTAGGTGGACTCGTTATGACACATTTATCAGTG 1086

Qy   236 ThrSerIleProSerValSerAspSerLeuThrTrpArgGluPheHisGlyTyrIleGlnSer 255
         |||                                                     |||
Db  1087 GAATAGTTACT-----------------------------------TATACTAGTGCA 1110

Qy   256 LysLeuGlyIleValSerLeuLeuLeu 264
         :::|||||:::||||||:::
Db  1111 TTGATAGGTTTAATTAGTCTTATCATT 1137
```

RESULT 7
US-11-110-977-1

Sequence 1, Application US/11110977
Publication No. US20050260682A1
GENERAL INFORMATION:
APPLICANT: Charmley, Patrick R.
APPLICANT: Smith, Ryan C.
APPLICANT: Argonza-Barrett, Rhodora H.
APPLICANT: Fitzgibbon, Matthew P.
APPLICANT: Wang, Kai P.
TITLE OF INVENTION: Compositions and Methods for Diagnosing or Treating Psoriasis
FILE REFERENCE: CECH118764
CURRENT APPLICATION NUMBER: US/11/110,977
CURRENT FILING DATE: 2005-04-19
PRIOR APPLICATION NUMBER: US/10/112,645
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 60/280,514
PRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1564
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (314)..(1138)
OTHER INFORMATION:

US-11-110-977-1

Alignment Scores:
Pred. No.:
Score: 5.26
Percent Similarity: 39.91%
Best Local Similarity: 18.42%
Query Match: 7

Length:	1564
Matches:	42
Conservative:	49
Mismatches:	75
Indels:	62
Gaps:	8

US-10-750-262-2 (1-339) x US-11-110-977-1 (1-1564)

```
Qy   134 ValIleAlaAlaIleLeuValGlnLeuHisAsnGlyThrLysTyrLysPheProHisTrp 153
         |||||:::                 |||       |||       |||
Db   286 GTGTTGAGTAAAACAGACCAAGTTGGATCATGGGAATTCAGAGGTCATGCCCCTCCGG 345

Qy   154 LeuAspLysTrpMetLeuThrArgLysGlnPheGlyLeuLeuSerPhePhePheAlaVal 173
         |||:::                                       :::|||:::
Db   346 ----------AACCTTCTTTTTATTATTGGTCTTG 372
```

```
Qy   174 LeuHisAlaIleTyrSerLeuSerTyrProMetArgArgSerTyrArgTyrLysLeuLeu 193
                                                     ||||
Db   373 GTG----------------------------------------GTGTACAAAGAGTAT 390

Qy   194 AsnTrpAlaThrGlnIleTyrValGlnIleGlnAsnLysGluAspAlaTrpIleGluHisAspVal 213
             |: |::|  |||:||  ::|||||:  ||||::||||  |||||  |:|:::|||||:
Db   391 TCTGAAGTATAATCTGCAAAAAGCAAAAGCGAACCTGCTTGGTTCCAAAACATTATT 450

Qy   214 -TrpArgMetGluIleTyrArgValSerLeuGlyTyrIleValGlyLeuAlaIleLeuLeuAlaLeuLeu 233
          ::  ||| ||||  |:|  :||:||||||  ||||:||  |||||:|||||||:|:|||
Db   451 CTATCGGATTGGAAATTTGGAGGGAATTACAATAGTTGGCGCTTAACTGGCCATGGC 510

Qy   233 uAlaValThrSerIleProSer------------------------ 240
          |||||
Db   511 TGGGGAGCAGTTATTCCTGGAGGGCCCATCTGAGTGTTATAATGACTATAAACAGGTCA 570

Qy   241 -ValSerAspSerLeuThrTrpArgGluPhe------HisTyrIleGlnSerLysLeuGl 258
          |:::  ||::  |||:  |||||||  ::||    |||::||||:||||:||||:
Db   571 CTGGAATCAACTCCTGGGCTGGCATCATTTCACCACGTATTTCTTCTTTGGGCTGTTGGG 630

Qy   258 yIleValSerLeuLeuLeuGlyThrIleHisAlaLeuIleHisAlaTrpAsnLysTrp-- 277
          |||:|  ||  |::::|||  |||||||:|||:|||:|||||||||:|:||||
Db   631 TGTGGCAGATATCTTACGTTCTGTGTTCCTTTACCAAGTTAAT 690

Qy   278 --------IleAspIleLysGlyGlnPheValTrpTyr----------ThrProProThrPh 291
                  |||:  |||  |||||:||||||||  |:|    |||||||||:|
Db   691 GTTGTCAAAATGCCTTATTTGTGGAGGGCCTTATCTTCTTACAACCACTCAATGGCCGGGA 750

Qy   291 eMetIleAlaLeuValPheLeuPro------IleValValLeuIlePhe----------- 304
          ||:|||||||:  ||||  ||:    |||||||||||
Db   751 AATGCTGGACACTTTGGTGCACCAGCTGCCTGGTTTTCGTCTTTCTTCTGACAGGCCTTCGT 810

Qy   305 ------------LysSerIleLeuPheLeuProCysLeuArgLysLysIll 317
                    |||  |||  |||::  ||||  ::|
Db   811 TGCCCTCCTAGAGTTCCTTGTTCGGACAACAATGTACTTCTCGGACGTCAAGTCT 870

Qy   317 eLeuLysIleArgHisGlyTrp 324
          |||  :::|||  ||||
Db   871 CATTCTGCTTCAGGGGAGCTGG 892
```

```
RESULT 8
US-10-467-657-2439
    Sequence 2439, Application US/10467657
;    Publication No. US20050260581A1
;    GENERAL INFORMATION:
;    APPLICANT: CHIRON SpA
;    APPLICANT: FONTANA Maria Rita
;    APPLICANT: PIZZA Mariagrazia
;    APPLICANT: MASIGNANI Vega
;    APPLICANT: MONACI Elisabetta
;    TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
;    FILE REFERENCE:
;    CURRENT APPLICATION NUMBER: US/10/467,657
;    CURRENT FILING DATE: 2003-08-11
;    PRIOR APPLICATION NUMBER: GB-0103424.8
;    PRIOR FILING DATE: 2001-02-12
;    NUMBER OF SEQ ID NOS: 9218
;    SOFTWARE: SeqWin99, version 1.04
;    SEQ ID NO 2439
;    LENGTH: 1515
;    TYPE: DNA
;    ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2439

Alignment Scores:
Score:                    6.56         Length:       1515
Pred. No.:                89.50        Matches:        85
Percent Similarity:       36.86%       Conservative:   51
Best Local Similarity:    23.04%       Mismatches:    133
Query Match:              5.00%        Indels:        133
                          6            Gaps:           19

US-10-750-262-2 (1-339) x US-10-467-657-2439 (1-1515)
```

```
Qy    19 ArgArgAsnLeuGluGluAspAspTyrLeuHisIleLysAspAspThrGlyGluThrSerMetLeu 38
           |||::|||  ||||  |||  :::||||||:|||||  ||:|
Db   252 CGGCAAAACCTTTTTTCAGACGGC------------- 275

Qy    39 LysArgProValLeuLeuHis----------LeuHisGlnThrAlaHisAlaAspGluPheAsp 56
           ::||  ||||||:|||||  ||||  |||::||||||:||:|||:|||::
Db   276 AATCACCCTGCCTTTGTCACATCCCCGCCATTGTCAGCTGTTTCAGCTGTGAC 335

Qy    57 CysProSerGluLeu------------------GlnHisThrGlnGluLeu-PheProGl 70
           |||    ||||  |||||:  |||||||  |||:
Db   336 CTTCCGCGGCTCGAAGAGATTTGGGGCGACAGTGATGATGATTATGAGCCTGCTTCCTCGGCT 395

Qy    70 nTrpHisGluProIleLysIleAlaAlaAlaIleIleAlaSerLeuThrPheLeuTyrThrLe 90
              |:||:|||  :::|||||||||||:||||||:|::|||||||::||:
Db   396 CGCCTACCTTGCCCGTCGAGGGCGGCACTCAAAGCATCAGCCTGTTCTAC-- 444

Qy    90 uLeuArgGluValIleLeuHisProLeuAlaThrSerHisGlnThrTyrPheTyrLysIlePr 110
              |:|||||:|||||||||::||||||||:|::||||||||||||:||||:||:|:
Db   445 -----GAAGAAGTCAGCCTGTTCCTTGGGCAAAAGCCGCTGAAACCTTTTTTCC 495

Qy   110 oIleLeuValIleLeuAsnLysValLeuProMetVal------SerIleThrLeuLeuHisAla-- 128
           |  ||||:|||:||:|||||||||  |:|||:|    :::||||:  |||:||::|
Db   496 ----GCCATCCTCCCACAGCTCAAACCCGCGAGCAGCAGCGGTGTTACTGACCCT 551

Qy   128 uValTyrIleu---------------------ProGlyValIleAlaAl 137
           |  |:|||||                     |||||||||||  |
Db   552 GCAATGGTCGGGTGAATTGGGGCGGCGTATCCATTGTGAACTACCCACTTTTACCACTGC 611

Qy   137 aIleValGlnLeuHisAsnGlyThrLysThrGlyLysPheProHisTrpLeuLysTr 157
           ||||  |  ||:|||||||:|||  |:||  ||:||:|  |::|:|||::|::
Db   612 CATTTTCCAAGAATACGAA--AATGTCCTACAACAACAATACCCGCCTGCTTCCGC 668

Qy   157 pMetLeuThrArgLysGlnPheGlyTyrLeuLeuLeuSerPhePhePheAlaValLeuHisAla-- 176
           |  :::|||::|||||||||  :||  |||||||||||  |:|||||||||:  ||||||:
Db   669 TGTTTTGACG---GCGGTGTGCGGCCATCGTCGTATTGGGAGAAAGCATATTTCGCGGCAA 725

Qy   177 ------IleTyrSerLeuSerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAs 194
                 |||::||||  |||  |||  ||:||||||||  :||  :||::|||||||:
Db   726 AGCCAAGAATTTACCACAGCGGCAAAAGGCGTTGCCCGTCGTCCTTATCCGTCAAAACCCTC-- 783

Qy   194 nTrpAlaThrGlnIleTyrGlnIleGlnAsnLysGluAspAlaTrpIleGluHisAspVal 214
           ||:||  |||::|||:|||||||  ::|||||||
Db   784 ----AAACTGCCCGGTCAGATCGGCGGCGAATTGTTTT 815

Qy   214 pArgMetGluIleTyrArgValSerLeuGlyTyrIleVal---------GlyLeuAlaIleLeuLeuAl 231
           :||  :||||  :::||||::|  ||||||:||:||    ||||||:|||||::
Db   816 TTTAAGCAGCTGTTGATTACCGGCATTATTATCCCGTATTGATACATTG 872

Qy   231 aLeuLeuAlaValThrSer------------IleProSerValSerAspSerLeuThrTr 247
           |||||||||  |  |:|    :::|||||::  ||||||:|
Db   873 GATGATGGTCGGCACTTCCGGCACAATCGCGCTCGTTATCCGTATTGATGCC- 924

Qy   247 pArgGluPheHisTyrIleGlnSer---LysLeuGlyIleLeuValSerLeuLeuLeuGlyTh 266
           ||  ::|||::||||:|||  |||  ||||:|:|||::||:  :::
Db   925 ----TTTATCCTTCCTTAAGCGTATCGGATTTGGACTAT 971

Qy   266 rIleHisAlaLeuIlePheAlaLeuTrp------------AsnLysTr 277
           |||:|||||  ||:|||||:|||||  |||||
Db   972 ATTAATGGCCTTGCCCCTTGTTGTTGGGCATCAGTTCGTTAACCGTTG 1031

Qy   277 pIleAspIleLysGlyGlnPheValTrpTyrThrProProThrPheMetIleAlaLeuValPheLe 297
           |||:||  |::|||  |::||||||  :|||||  ::|||||:|  |:
Db  1032 GATAGACAGGCTGCCGGTTTTTTACGCAGCCGCGTCCCGGGTTTGGGTTATCGCCATCCTT 1091

Qy   297 uPro----------IleValValLeuIl 303
           ||:          |||||||||||::||:
Db  1092 GGTTTATTTCAGCATACAACTACACCCCTGCGGTTTACCAAAACCTTTACCAGTGCTCATCCT 1151

Qy   303 ePheLysSerIleLeuPheLeuPro------------CysLeuArgLysLysIleLeuLy 319
           :||||  ||||:|||||||  ||:    :::||::||:|
Db  1152 TGCCTATTTCATGCTTTACCTGCGGATGGACGACTTCCTTGGACA 1211
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Qy   319 sIleArgHisGlyTyrGluAspVal 327
          ||| ||| ||| |||
Db   1212 ACTCCCAAAGGGATGGAAACAGGTC 1236

RESULT 9

US-11-102-978-3
; Sequence 3, Application US/11102978
; Publication No. US20050142A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Technology Transfer Office
; APPLICANT: University of Utah Research Foundation
; TITLE OF INVENTION: Diagnosis and Treatment of Herpes Simplex Virus Disease
; FILE REFERENCE: 0274-5537.1US
; CURRENT APPLICATION NUMBER: US/11/102,978
; CURRENT FILING DATE: 2005-04-11
; PRIOR APPLICATION NUMBER: PCT/US2003/033152
; PRIOR FILING DATE: 2003-10-18
; PRIOR APPLICATION NUMBER: 60/419,576
; PRIOR FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
;
; SEQ ID NO 3
; LENGTH: 340000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: (56948)..(57115)
; OTHER INFORMATION: C21orf34 exon
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (80006)..(81089)
; OTHER INFORMATION: Gene VDAC2P; voltage-dependent anion channel isoform 2 pseudogene
; FEATURE:
; NAME/KEY: exon
; LOCATION: (167308)..(167438)
; OTHER INFORMATION: C21orf34 exon
; FEATURE:
; NAME/KEY: exon
; LOCATION: (216732)..(216833)
; OTHER INFORMATION: C21orf34 exon

US-11-102-978-3

Alignment Scores:
Pred. No.:
Score: 4.23e+04
Percent Similarity: 87.50
Best Local Similarity: 37.54%
Query Match: 22.92%
DB: 4.89%

US-10-750-262-2 (1-339) x US-11-102-978-3 (1-340000)

Qy   57 CysPro-SerGluLeuGlnHisThrGlnLeuPheProGlnTrpHisLeuProLeuy 76
         ||||| |||| || ||| |::||
Db 183992 TGTCCACTCCAGAATTATTTTTGACAAGTTTTCTTTCTTGGAAATTTTAATTGAT 184051

Qy   76 sIleAlaIleAlaIleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHi 96
         ::|| ||||| |||| ||||| |||::|
Db 184052 TCTCATCGCC--ACTTCAAATGTTTATTTTCTTACTTACTTTGTTACACATTGTATTG-- 184106

Qy   96 sProLeuAlaThrSerHisGlnTyrPheTyrLysIleProIleLeuValIleAsnLy 116
         ::| :::||| |||||
Db 184107 --------------------------ATGTTATTTCTTGCTCTTCCAA 184129

Qy   116 sValLeuProMetVal----------SerIleThrLeuLeuAlaLeuValTyrLeuProGlyVa 134
         |::|| |||| |||||||
Db 184130 AATCCTAGCACATGCTTATTTTTGGAGTTATTCTGAAACCGCTCTATTATTT-------- 184178

Qy   134 lIleAlaIleValGln--LeuHisAsnGlyThrLysTyrLys---------- 148
         ||||||| ||||||
Db 184179 ----TCATGTCTTCTGGAATAACTTCACTGAATGGTTGTTTTAAAATTTTGCTGGGTGCCT 184234

'''   ...   ...   Page 7

Qy   149 ------LysPheProHisTrpLeuAspLysTrpMet------LeuThr-----ArgLy 162
               :||::| |||||| |::|
Db 184235 TTTTATATCATTCTCTCATGGCTTAGAATTTGGTTTCAGGCTTAACTGGAATGAGAAG 184294

Qy   162 r-----GlnPheGlyLeuLeuSerPhePheGlnPheAlaValLeuHisAlaIleTyrSerIle 180
              :::||||| ::||:| :| ||||||
Db 184295 GAATTTAAAAATTCTTCTCTCTCTCATTGCTAGCCCTTCCTGCCAATTCCTATTGTCT 184354

Qy   180 uSer--------------------TyrProMetArgArgSerTyrArgTyrLysLeuLe 193
         |||| ::|||::|| ||::|
Db 184355 TAGTTGTTGGCTCTGTACCCTCTCGTTTCCCAGTC------TATAATCTCTG 184399

Qy   193 uAsnTrpIleAlaTyrGlnGlnnValGlnGlnAsnLysGluAspAlaIleGluHisAspVa 213
         ::| ::||| ||||| |||||
Db 184400 CTAATGGGGATATCAAAAACCTAGTC-ACTAAATCAAAGAGCAGTCTGTCCCAGGATGT 184457

Qy   213 l-------Trp-----------ArgMetGluIleTyrValSerIle 222
         | ||| ||||| |||||
Db 184458 GACTGTGAGATTATGGCTCGCTTTGCTTTCCCAAGAAACCAGCTCTATCCAAGCCG 184517

Qy   222 uGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSerVal 242
         ::|||| |||||
Db 184518 TGGCCTCCAGGAAAAGGAGGGTGTTAGTCAGTTGT----------- 184559

Qy   242 rAspSerLeuThrTrpArg----------------------------- 248
         |:::|||| |||
Db 184560 CTCTTGTTCTTACCTTCAGGTTTTAAATCAGTAGAAGCTTGGCACTGATTATTACTCCCTGTGG 184619

Qy   249 ------------GluPheHisTyrIleGlnSerLysGlyIleValSerLeuLeuLeuLeu 264
                     |||||::|| ||||::|
Db 184620 GACACATGTGGCCATCCAGTTACTTTGCAGATACAAGATTGGCTTGCTT---CTCATCT 184676

Qy   264 uGlyThrIleHisIleAlaLeuIlePheAlaValPheLeuProIleValLeuIlePheVa 284
         :|| ||| ||| |||::|
Db 184677 AGACACCATC--- 184686

Qy   284 lTrpTyrThrProThrPheMetIleAlaValPheLeuProIleValLeuIlePh 304
         ||| :|| ||| ||||::|
Db 184687 -TGGTGCCAGTGTACCTCACTTGTGTTATAGTTTATTCTGGTATGTTTATTCTTGTTT 184745

Qy   304   e 304
                 |||||
Db 184746 T 184746

RESULT 10
US-10-793-626-4225/c
; Sequence 4225, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 4225
; LENGTH: 3083
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
;
US-10-793-626-4225

Alignment Scores:
Pred. No.:
Score: 37.9
Percent Similarity: 87.00
Best Local Similarity: 32.58%
Query Match: 22.66%
                            4.86%

Length: 3083
Matches: 80
Conservative: 35
Mismatches: 103
Indels: 135

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DB: US-10-750-262-2 (1-339) x US-10-793-626-4225 (1-3083)          Gaps: 6          20

Qy    58 ProSerGluLeuGlnHisThrGlnGluLeuPheProGlnTrp--------------His 72
                                                         :::
Db  2931 CCAAGTTCAATGTTGCATAGAGCAT------------GGATCGAGCCGTATCAATTTCAAT 2884

Qy    73 LeuProIleLysIleAlaAlaIleIleAlaSerLeuThrPheLeuTyrThrLeuLeu--- 91
         |||||||||  :::||                          :::|||
Db  2883 TCACCATTTGCAGATATGGCAAATTTATTAGGTCTTAACTGGTTAGCAAATATTACTTTAT 2824

Qy    92 ---ArgGluValIleHisProLeuAlaThr--- 100
            |||
Db  2823 ATGGAAGCAGTTGTGTCACCCTTTGGTACTGGAGTTTCTTTTGTTGCCGGTTACTGGACGT 2764

Qy   101 ----------SerHisGlnTyrPhe 106
Db  2763 GTGTTACGCGGCTATGGAAGAAAATGGGCATAATTCCTAAATTCTTAGGTAAAATTAATAAA 2704

Qy   107 ---TyrLysIleProIleLeuValIle------AsnLysValLeuProMetValSerIle 123
            |||||                          :::   :::
Db  2703 AAGTATAATATCCCACGTTGTTGCCATTGCATTAAATGCAATAATCAGCATGAATATGGTG 2644

Qy   124 ThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleAlaValGlnLeuHisAsn 143
         |||||||||||||:::|||||||||||||:::||
Db  2643 ACATTGCTTCCGGTGACTGG------GGTACACTAGCTGCGGTTATTTCTACTGCAACA 2593

Qy   144 GlyThrLysTyr--- 152
            |||
Db  2592 TTAGTTGCATATTAACTGGTCCAACTACACGGTTATTTCATTACGTAAAATGGCACCA--- 2536

Qy   153 TrpLeuAspLysTrpTrpMetLeuThrArg--- 165
                                       |||||||
Db  2535 AAAATGACTCGTCCCATTAACTAATATTTAAAGTTAATAATTTATGGCA 2491

Qy   166 LeuLeuSerPhePheAlaValLeuHisAlaIleTyr--- 178
         |||||:::|||||                  :::
Db  2490 CCTTTATCCTTTGTTTTAGCATCATTA------GCTANCTATTGGGGCAAATGTGGCCAACAACA 2434

Qy   179 ---SerLeuSerTyrProMetArgArgSerTyrArgTyrLys 191
            |||
Db  2433 GCAGAAGTTATTTTAATTATTAATTTAGGTTTACCTATTTCTTCTATGATAATAAA 2374

Qy   192 LeuLeuAsnTrpIleAlaTyrGlnInValGlnAsnLysGluAspAlaTrpIleGluHis 211
         |||||||                      :::
Db  2373 ---ATGAATTGGAGAGAATACTAAA---AAACAAATTGGCGGAAGCTTATGGGATT 2326

Qy   212 AspValTrpArgMetGluIleTyrValSerLeuGlyIleValAlaIleLeuAla 231
Db  2325 ATTANCTATCTATTGTTCTGCGCA 2302

Qy   232 LeuLeuAlaValThrSerIleProSerValSerAspSerLeuThrTrpArgGluPheHis 251
                                                           :::
Db  2301 TTCTTTATCATTTATTGGAGTAAAGAGTTCAAA---GGCTTAAATTGG------ATTCAC 2251

Qy   252 TyrIleGlnSerLysLeuGlyIleVal-SerLeuLeuGlyThrIleHisAlaLeuIle 271
         |||||                  :::||||||          :::
Db  2250 TATCCATGGGATTTCTTAGTCATTGTAAATCGTTGCTTTAAATTCTATCAACTAGGTA- 2193

Qy   271 ePheAlaTrpAsnLysTrpIleAspIleLysGlnInPheVal--- 284
                        :::   :::
Db  2192 ---CGACAAGTTACTTTGAAAGTATTATTTCAAGGGTGCCGAACAAGTTG 2146

Qy   285 -------TrpTyrThrProProThrPheMetIleAlaValPheLeuProIleValA 301
                |||
Db  2145 AATAAGAAAATGG--- 2133

Qy   301 lLeuIlePheLysSerIleLeuPheLeuProCysLeuArgGlyLysLysIleLeuLysIleAr 321
                                                :::||||:::|||||
Db  2132 ---GCGATAAGTTGCGTAAAACACGAAAAAAGCGGCTCATAAAGATTGG 2086

Qy   321 gHisGlyTrpGluAspValThrLysIleAsnLysThr 333
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Alignment Scores:
Pred. No.:
Score:                    42.1        Length:        3301
Percent Similarity:      87.00        Matches:         67
Best Local Similarity:  35.71%        Conservative:    38
Query Match:            22.79%        Mismatches:      95
                         4.86%        Indels:          94
                          6            Gaps:           13
DB:
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US-10-750-262-2 (1-339) x US-10-793-626-4209 (1-3301)

```
Qy    73 LeuProIleLysIleAlaAlaIleIleAlaSerLeuThrPheLeuTyrThrLeuLeu-Ar 92
         :::                              :::|||
Db  2526 CTTCCGGTAAAGTGGGCAAAAAATATTGCTAAGTGAGACCTTTGCTAATTAGCATAG 2467

Qy    92 gGluValIleHisProLeuValAlaThrSerHisGlnInTyrPheTyr-----------Ly 108
         :::                                             ::
Db  2466 GTCTCTT--- 2437

Qy   108 sIleProLeuValIleAsnLysValLeuProMetValSerIleThrLeuLeuAlaIle 128
               :::                                     :::
Db  2436 GTTGTCCACAATGGATCCGAGTTTGAGTTTTACCTTATTTAGGGTA---CTTTTAGTACT 2380

Qy   128 uValTyrLeuProGlyValIleAlaAlaIleAlaValGlnLeuHisAsnGlyThrLysTyrLy 148
         |||||||||||||:::||||||||||||
Db  2379 TGTATTTTTAGAAGGATTATTAGCAGCTGATAAATGGAACATGTAATGGGTTAA 2320

Qy   148 sLysPhePheAlaValLeuHisTrpLeuAspLysTrpTrpMetLeuThrArgLysGluLeuGluSe 168
         |||||||||||||                            :::|||||
Db  2319 ACATCTACCACCTAAACAACGTAAAAGCACTTTTT------TATGGCCTATTAGG 2269

Qy   168 rPhePheAlaValLeuHisAlaIleTyrSerLeuSer--- 181
Db  2268 TGCATTCATTTTAGATTAATTAATTAAAGTAATATTATTGCAAACTTCGGTG 2209

Qy   182 ---TyrProMetArgArgSerTyrArgTyrLysLeuLeuAs 194
            |||                       :::
Db  2208 GATTCAGACAGCAGGTCGTGTTTACTTAATCTATATGTCTATTAAA---AATTTATGGCA 2152

Qy   194 nTrpIleAlaTyrGlnInValGlnAsnLysGluAspAlaTrpIleGluHis------- 211
          :::|||                          :::
Db  2151 ATTTTTTCCATCAGTCAAATGAAAAACACCATAAAGAAAACAGGAGCGA 2092

Qy   212 AspValTrpArgMetGluIleTyrVa 220
Db  2091 TGAAACAGGCAACGAAAAAGAGAGTAGGCCCTAAAATCTTTTCGGGACAGATTTAAAGT 2032

Qy   220 lSerLeuGlyIleValGlyLeuAlaIle------LeuAlaLeuLeuAlaVal---Th 236
                                            |||
Db  2031 ----------------------------------LeuAlaLeuLeuAlaVal---Th 236
```

RESULT 12

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Db   2031  TGAATTCGCTGATATCGGCGTTTGCAATTGATTCGATGCTTGCGCCATTAGGCCGT
                  |||||                              |||  :::
Qy    236  rSerIleProSerValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerIy  256
Db   1971  TACATTACCAAAAGTTGGC                    ATACATTTCGGTGTATGGA    1933
Qy    256  sLeuGly-----IleValSerLeuLeuLeuGlyThrIleHisAlaLeuIle-----       271
Db   1932  CTTAGGCCAATTATTGTTAGTTCCTCGGTGGAATGAGATTAGGTGTCATCTGATGAGATT  1873
Qy    272  -------------
Db   1872  TGCAGCAACTTGGTTTGTTGTAGAATTGTGAATAAATATCCAGGACTTGAAGGTGCTGCGT 1813
Qy    272  eAlaTrpAsnGlyTrpIleAspIleLysGlnPheVal-TrpTyrThrProProThrPheM  292
Db   1812  TGCAAATTGTTAGGTGGTAGGTATTAAACTTGTTATAATGGTAC---                1769
Qy    292  erIleAlaValPheLeuProIleValValLeuIlePhe                         304
Db   1768  ------------------TTGCACATCCTGATAATTCGCGGTTT                    1745
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US-10-793-626-3381/c
Sequence 3381, Application US/10793626
Publication No. US20050254578A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3381
; LENGTH: 4071
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence

US-10-793-626-3381

US-10-750-262-2 (1-339) x US-10-793-626-3381 (1-4071)

Alignment Scores:
Pred. No.:

Score:	57.9	
Percent Similarity:	87.00	Length: 4071
Percent Identity:	35.71%	Matches: 67
Best Local Similarity:	22.79%	Conservative: 38
Query Match:	4.86%	Mismatches: 95
		Indels: 94
		Gaps: 13

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Qy     73  LeuProIleGlyLysIleAlaAlaAlaIleIleAlaSerLeuThrPheLeuTyrThrLeu-Ar  92
               |||||| |||||  :::|||  ||||||      |||||||||    ::|
Db   1305  CTTCCGGTAAAGTGGGCAAAAATATTGCTAAGTGAGACCTTTGCTATTAAATTAGGCATAG 1246
Qy     92  gGluValIleHisProLeuAlaThrSerHisGlnGlnTyrPheTyr-------         108
               |||||||||    :::      ||  ||        ::
Db   1245  GTCTCTT-----              TATTTGTTATTTAAACTAAAAGGA          1216
Qy    108  sIleProIleLeuLeuValIleAlaAsnGlyValLeuProMetValSerIleThrLeuLeuAlaIle 128
               |||| :::|||  |||||| :||| :::|||||  |||||||
Db   1215  GTTGTCACAATGGATCCGAGTTGAATTAAGTCAGCTGATAATGCAATTGAATGGGGTAATGGGTTA 1159
Qy    128  uValTyrLeuProGlyValIleValGlnLeuHisAsnGlyThrGlyTyrGly          148
               |||||:||| ||||  :::|||
Db   1158  TGTATTTTAGAGGAATATTAGCAGCTGATAATGCAATTGAATGGGGTAATGGGTTAA     1099
Qy    148  sLysPheProHisTrpLeuAspLysTrpMetLeuThrArgLysGlnPheGlyLeuLeuSe  168
               |||    :::|||||||||
Db   1048  ------------------
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RESULT 13

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Db   1098  ACATCTACCACCTAAACAACGTAAAAAGCACTTTTT-----------TATGGCCTATTAGG  1048
               |||                ::::|||||||||||
Qy    236  rSerIleProSerValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerIy  256
Db    750  TACATTACCAAAAGTTGGC                    ATACATTTCGGTGTATGGA    712
Qy    256  sLeuGly-----IleValSerLeuLeuLeuGlyThrIleHisAlaLeuIle-----       271
Db    711  CTTAGGCCAATTATTGTTAGTTCCTGGTGGAATGAGATTAGGTGTCATCTGATGAGATT    652
Qy    272  -------------
Db    651  TGCAGCAACTTGGTTTGTTGTAGAATTGTGAATAAATATCCAGGACTTGAAGGTGCTGCGT  592
Qy    272  eAlaTrpAsnGlyTrpIleAspIleLysGlnPheVal-TrpTyrThrProProThrPheM   292
Db    591  TGCAAATTGTTAGGTGGTAGGTATTAAACTTGTTATAATGGTAC---                548
Qy    292  erIleAlaValPheLeuProIleValValLeuIlePhe                         304
Db    547  ------------------TTGCACATCCTGATAATTCGCGGTTT                    524
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US-10-467-657-4965
Sequence 4965, Application US/10467657
Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4965
; LENGTH: 1068
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4965

Alignment Scores:
Pred. No.:

Score:	9.9	
Percent Similarity:	86.00	Length: 1068
Percent Identity:	37.09%	Matches: 67
Best Local Similarity:	22.19%	Conservative: 45
Query Match:	4.80%	Mismatches: 112
		Indels: 78

DB: 6   15

US-10-750-262-2 (1-339) x US-10-467-657-4965 (1-1068)

Qy   77 IleAlaAlaIleIleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHis 96
          ||||||
Db   193 ATGTCTTGTGAGGGTGTTTTCCTTGATTTTTGTTGTTGGCATTATTGTTGATTGTCCCT 252

Qy   97 ProLeuAlaThrSerHisGlnGlnTyrPheTyrLysIleProIleLeuVal--------- 113
          :::::
Db   253 ATGCTCGGTCCGGGCAGTTCAATAATTTGGCATCCTGCCCAATTAATCGGTTTTATG 312

Qy   114 IleAsnLysValLeuProMetValSerIleThrLeuLeuAlaLeuValTyrLeu---Pro 132
          :::|||:::|||
Db   313 CAGAACAACGCTGCTGCCGGTGGTTGAAAAATACAATCGGATATCGATCAG 372

Qy   133 GlyValIleIleAlaIleAlaValGlnLeuHisAsnGlyThrLysTyrLysPheProHis 152
          ||||
Db   373 GCATCTATTATTGGCGTCGTTTCAGGCGCCGCATACGGGCGCTTAAGGCG 432

Qy   153 TrpLeuAspLysPheTrpMetLeuThrArgLysGlnProHisGlyLeuLeuSerPhePhePheAla 172
          |||
Db   523 CTGGATTGGCAGCGGGGTGCGTGCCGAAACTGGTTCCGAGGCGGTTTTTGCCGGT 582

Qy   193 LeuAsnTrp--------- 195
          ||||:::|||
Db   466 ATTGTCAGCAGTATCGGCAAACCTGCTCTGCTCCCCCCTTGCTGCTTTAC---TATTTCCTG 522

Qy   196 AlaTyrGlnHisValGlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArg 215
          :::::
Db   583 GCTTATACGCGCAATACGGGGTAATTGAACGAGGTATTGGGCGGTCAG 642

Qy   216 MetGluIleTyrValSerLeuGlyIleVal------------GlyLeuAlaIleAlaLeuALeu 232
          :::|||::::::|||
Db   643 CTTCCTGTGGTCGATGCTTGGTTTACGGTTTGGGGATTGATGCTAGTGCGGACTTG 702

Qy   233 LeuAlaValThrSerIleAlaProSerValSerAspSerLeuThrTrpArgGluPheHisTyr 252
          :::
Db   703 GATTCGGGATTTGCCATCCGGTATCGGTTGCCGGTAATTTGGGTGTTTGTCCCTAT----- 756

Qy   253 IleGlnSerLysLeuGly------IleValSerLeuLeuLeuGlyThrHisIleAlaLeuIle 271
          |||||||:::|||
Db   757 ------------TTGGGGTCCGTTTACGGATTGCTGTCGTTCCACTGTTGCAGCCTTGCTC 804

Qy   272 ------------PheAlaTrpAsnLysTrpIleAspIleLysGlnPheValTrpTyrThrProPro 289
          ::|||:::|||
Db   805 CAGTTCGGTTCGTTCGGAACGGAAATCTTG--------------GCTGTTTGG 843

Qy   290 ThrPheMetIleAlaValPheLeu-----------------ProLeuVal---- 301
          |||
Db   844 GTTTTTGCCGTCGGTCAGTTTCTCGAAAGATTGTTAGGAGAC 903

Qy   302 ---------------LeuIlePheLysSerIleLeuLeuPhe-------- 309
          :::|||
Db   904 CGTATCGGGCTGCTGCTCGGTTTTTTGGCTTAATCTTTTCGCTTTGGGCGGTAACCTTG 963

Qy   310 --------LeuProCysLeuArgLysGlyLysIleLeuLeuLysArg 321
          :::|||:::
Db   964 GGCTTTGTCGGAAATGTTGGCCCGGATTGCCTTTGGGTCGTTAGGCGG 1023

Qy   322 HisGly 323
          |||
Db 1024 GAGGGC 1029

US-10-750-262-2 (1-339) x US-10-750-185-36689 (1-1138)
DB:

Qy   38 LeuLysArgProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCys 57
          |||:::|||
Db   79 CTCCGGAGAGTACTTCAGGTTTTAACCCACTTGACATGGTAAATGGGGATCAAGCTTACTGT 138

Qy   58 ProSerGlyLeuGlnHisThrGlnLeuPheProGlnTrpHisLeuProIleLys--- 76
          :::
Db   139 CTTAATTGAATTACTTTCACTTTGCAATAATTAGCCCTTTCACATATTCCAGTAAACTTA 198

Qy   77 ---------IleAlaAlaIleIleAlaSerLeuThr 85
          :::
Db   199 AAAAGCTTCACTAAAGATATCTCAAATACTCATATAAAGTAGAGTGTTCTTTTCATTGGAT 258

Qy   86 PheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThrSerHisGlnTyr 105
          |||:::
Db   259 TTCATCAAGACTCTTGTG---------TTTATAGATGCA 288

Qy   106 PheTyrLysIleProIleLeuVal-----------AsnLysValLeuProMetVal 121
          :::|||
Db   289 TTTGGCAAAGCATAGATTTTATTTTTGGACTGTTTCCAATGCTCTTTCTCCTAATATT 348

Qy   122 SerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleIleAlaIleAlaValGlnLeu 141
          ::|||
Db   349 TACTGTGTGATCTTGAGTAAG-----------------GCAGCACTGTTCTAATTA 387

Qy   142 HisAsnGlyThrLys-----------------TyrLysPhe 150
          :::|||
Db   388 CAAGATGGTAATAATCTTATCTATAATGAGTTTCTCTATAGGAGAATTCACTGGCCATAGAG 447

Qy   151 ----------ProHisTrpLeuAspLysPheTrpMetLeuThrArgLysGlnProGlyLeu 166
          :::|||
Db   448 TTGACACTCAATCCATCGTGGCTT----------------------- 471

Qy   167 LeuSerPhePheAlaLeuValLeuHisAlaIleTyrSerLeuSerTyrProMetArgArg 186
          |||:::
Db   472 -----TTTTGGTTTGTTTTGTTCTTTCTATATTCTCCTGAGTTCAACATATCACGCT 525

Qy   187 SerTyrArgTyrLysLeu-Leu---AsnTrp 196
          |||:::|||
Db   526 TCAGTAAGATAATAAAAATATATGCATAGCTGGTAGAAAGACACTTCAAGATACAGTTCA 585

Qy   196 --------AlaTyrGlnHisValGlnGlnAsnLysGluAspAlaTrpIleGluHisAsp 212
          :::
Db   585 ... (sequence continues)

Alignment Scores:
Pred. No.:
Score: 12.5   Length: 1138
                        85.50   Matches: 68
Percent Similarity: 36.34% Conservative: 53
Best Local Similarity: 20.42% Mismatches: 122
Query Match: 4.78%   Indels: 91
                        6   Gaps: 12

RESULT 15

US-10-750-185-37763/c:

Sequence 37763, Application US/10750185

Publication No. US2005026603A1

GENERAL INFORMATION:

APPLICANT: MMI GENOMICS, INC.

APPLICANT: DeNise, Sue K.

APPLICANT: KERR, Richard

APPLICANT: ROSENFELD, David

APPLICANT: HOLM, Tom

APPLICANT: BATES, Stephen

APPLICANT: FANTIN, Dennis

TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

FILE REFERENCE: MMI100-2

CURRENT APPLICATION NUMBER: US/10/750,185

CURRENT FILING DATE: 2003-12-31

PRIOR APPLICATION NUMBER: US 60/437,482

PRIOR FILING DATE: 2002-12-31

NUMBER OF SEQ ID NOS: 6922

SOFTWARE: PatentIn version 3.1

SEQ ID NO 37763

LENGTH: 1462

TYPE: DNA

ORGANISM: Bovine

US-10-750-185-37763 1986688107018:

Alignment Scores:

Pred. No.:

Score: 18.3

Percent Similarity: 85.50

Best Local Similarity: 23.00%

Query Match: 4.78%

DB: 6

US-10-750-262-2 (1-339) x US-10-750-185-37763 (1-1462)

	Length:	1462
	Matches:	46
	Conservative:	32
	Mismatches:	78
	Indels:	44
	Gaps:	7

Qy   105 TyrPheTyrLysIlePro-IleLeuValIleAsnLysValLeuProMetValSerIleTh 124
              ||||.|:||| |.||:|||:||:
Db   1426 TATTGGTACTATGGCCCACCTATATGCCATTAACAAAAGTTGTTAGTAGTTT 1367

Qy   124 rLeuLeuAlaLeuValTyrLeuProGlyValIleAlaIleAlaValGlnLeuHisAsnGl 144
              ::: ||||||| |||
Db   1366 TTGGATATTGTCCAATCACCTAGCTACCTGGTTTGCCACCTGTCTAAGTGTTTTCTACTT 1307

Qy   144 yThrLysTyrLysGlyPheProHisTrpLeuAspLysTrpMetLeuThrArgLysGln-- 163
              ||.| ||:|||.||| |||.|::
Db   1306 CTTTAAAGTAGCCAAACTTCTCCCACCCGTTCGTCTCGGGTGGCGAATTCGGTAG 1247

Search completed: December 6, 2005, 18:50:55
Job time : 320 secs

Qy   164 ------------------------PheGlyLeuLeuSerPhePheAlaValLeuHisAlaIl 177
                                         :||:||
Db   1246 TGTGGTACTGGTGCGTTCCTTGGGGTTCTTGGTCCTTACTGTTTTTGAATTATGAAITCAAT 1187

Qy   177 eTyrSerLeuSerThrYrProMetArgArgSerTyrArgTyrLysSerLeuLeuAsn----- Tr 195
              |||.|:||||||||.|| :|| ||| |||
Db   1186 ATATACACTTAGTCATATCTTAACTACACAGCTACAAAAATATATGTAAGAAACTCAACGTG 1127

Qy   195 pAlaTyrGlnGlnValGlnGlnAsnLysGluAspAlaThrProIleGluHisAspValThrPr 215
                                 ||| ||
Db   1126 GTCC----------------------------------TCAGAGTTAAGTAGTGAAAACTCATTTATATCTTCACCA 1091

Qy   215 gMetGluIleTyrValSerLeuGlyIleValGlyLeuValAlaIleLeuLeuLeuLeuAlaVa 235
              || :|:|| ||||
Db   1090 GTTGAATTGTTTTAACTTCATCCAACTTAATCCCTTT---------------CTTCTGTCCCT 1043

Qy   235 lThrSerIle-- 238
              :|||||||:::
Db   1042 GACCTCACTGCCCTCTTTAGTTCTCTCCTTGATGAGACACATCAGGAATTTGCAGTTCAA 983

Qy   239 -ProSerValSerAspSerLeuThrTrpArgGluPheHisIleTyrIleGlnSerLysLeuG 258
                 |||| || :|.||
Db   982 CCCCAGCTCAAAGGATCTCAGCACA------GAGGCCCATAAAAAGAGCCCATGAAAATCGT 929

Qy   258 yIleValSerLeuLeuLeuGlyThrIleHisAla------------LeuIlePheAlaTrp 274
              ||||||||||:::||| ||||:|
Db   928 GAYGTCTTTCCTCCTTCATCATTCATGTCTTCCATCCTTATTAAATAGGTTGG 871

Qy   287 rProProThrPheMetIleAlaValPheLeuProIleValValLeuIleLeuPheLysSer-- 306
              :::||||| :|| |||
Db   885 G----------------------CTCAGTGTATTTCACCTGGTTAAGGTTCTTGAAAATGCCTCAA 929

Qy   307 ------IleLeuPheLeuProCysLeuArgLysGlyLys 316
              ||||:|||||||||:||:||:||||
Db   930 CTGATGAACCCTATGGATTCCCTGTTGTTCACAGAAA 966

Qy   267 eHisAlaLeuIlePheAlaLaTrpAsnLysTrpIleuAspIleLeuGlnPheValTrpTyrTh 287
              |||||||||||||:|| ::|||.||||
Db   826 GCATTT-TTGTTTACTACCATGATTCAGAAAATTCCATGTTTAGGGTTTCATTGGAAAGA 884

Qy   248 -ArgGluPheHisTyrIleGlnSerLysGlyIleValSerLeuLeuLeuGlyThrIl 267
              || ||| |||
Db   766 AGCAGAATTTTTTATGTGTCTCGTAATCCTGAATATTGCAAAAAGAAATCTCCATATTTT 825

Qy   232 uLeuAlaValThrSerIlePheProSerValSerAspSerLeuThrTrp------------ 247
              ||||| |||.|:|||
Db   706 TCTAGTAGTGATTGGTGAGCCCAACTAATCCTGTTCACTGTGTTACTGAGAC 765

Qy   212 pValIlrpArgMetGluIleTyrValSerLeuGlyIleValGlyLeuValAlaIleLeuLeuAlaIle 232
              |||||||::||||:||:||
Db   646 CAICTGGGTGCTGGCGTATCAGTGGGGAATAGGGTTTTATAGCATG 705

Qy   586 TTGATACAIATCAITTCCACATGTACAAGAAAAATAGTTTTAACCAAGCAGTTGCAAAGG 645

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OM protein - nucleic search, using frame_plus_p2n model

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                    GenCore version 5.1.6
                    Copyright (c) 1993 - 2005 Compugen Ltd.

Run on:             December 6, 2005, 16:29:53 ; Search time 200 Seconds
                                                (without alignments)
                                                3012.967 Million cell updates/sec

Title:              US-10-750-262-2
Perfect score:      1790
Sequence:           1 MESRKDITNQEELWKMKPRR..........IRHGWEDVTKINKTBICSQL 339

Searched:           1303057 seqs, 888780828 residues

Scoring table:      BLOSUM62
                    Xgapop   10.0 ; Xgapext   0.5
                    Ygapop   10.0 ; Ygapext   0.5
                    Fgapop    6.0 ; Fgapext   7.0
                    Delop     6.0 ; Delext    7.0

Total number of hits satisfying chosen parameters:   2606114

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_l/USPTO_spool_h/US10750262/runat_06122005_162946_15642/app_query.fasta_1.519 -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCI=0
-DB=Issued_Patents NA  -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCI=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200  -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL  -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :          Issued_Patents NA.*
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                    7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
                    8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
                    9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1790	100.0	1193	3	US-09-455-486-1	Sequence 1, Appli
2	1790	100.0	1195	3	US-09-323-873A-1	Sequence 1, Appli
3	1790	100.0	1195	3	US-09-685-166A-878	Sequence 878, App
4	1790	100.0	1195	3	US-09-679-426-878	Sequence 878, App
5	1790	100.0	1195	3	US-09-759-143-878	Sequence 878, App
6	1790	100.0	1195	3	US-10-010-667A-1	Sequence 1, Appli
7	1790	100.0	1195	3	US-10-012-896-878	Sequence 878, App
8	1782	99.6	1147	3	US-09-949-016-2686	Sequence 2686, Ap
9	1358.5	75.9	3627	3	US-09-323-873A-6	Sequence 6, Appli
10	1358.5	75.9	3627	3	US-09-455-486-4	Sequence 4, Appli
11	1358.5	75.9	3627	3	US-10-010-667A-6	Sequence 6, Appli
12	1071.5	59.9	9073	3	US-09-949-016-14428	Sequence 14428, A
13	905	50.6	592	3	US-09-439-313-342	Sequence 342, App
14	905	50.6	592	3	US-09-352-616A-342	Sequence 342, App
15	905	50.6	592	3	US-09-636-215-342	Sequence 342, App
16	905	50.6	592	3	US-09-685-166A-342	Sequence 342, App
17	905	50.6	592	3	US-09-679-426-342	Sequence 342, App
18	905	50.6	592	3	US-09-759-143-342	Sequence 342, App
19	905	50.6	592	3	US-09-651-236-342	Sequence 342, App
20	905	50.6	592	3	US-09-657-279-342	Sequence 342, App
21	905	50.6	592	3	US-10-012-896-342	Sequence 342, App
22	741	41.4	3884	3	US-09-562-930-10	Sequence 10, Appl
23	741	41.4	2714	3	US-09-562-930-5	Sequence 5, Appli
24	717	40.1	2469	3	US-10-104-047-1185	Sequence 1185, Ap
25	717	40.1	1403	3	US-10-012-896-995	Sequence 995, Appl
26	715	39.9	1886	3	US-10-012-896-1	Sequence 1, Appli
27	713.5	39.9	2118	3	US-09-562-930-1	Sequence 1, Appli
28	651	36.4	1203	3	US-09-562-930-3	Sequence 3, Appli
29	637.5	35.6	4429	3	US-09-544-618-6	Sequence 6, Appli
30	625	34.9	848	3	US-09-455-486-7	Sequence 7, Appli
31	607	33.9	607	3	US-10-012-896-993	Sequence 993, App
32	576	32.2	519	3	US-09-562-930-7	Sequence 7, Appli
33	576	32.2	521	3	US-09-323-873A-7	Sequence 7, Appli
34	497	27.8	1213	3	US-09-083-521-3	Sequence 3, Appli
35	450	25.1	455	3	US-09-621-976-9264	Sequence 9264, Ap
36	400	22.3	366	3	US-09-030-607-215	Sequence 215, App
37	400	22.3	366	3	US-09-439-313-215	Sequence 215, App
38	400	22.3	366	3	US-09-352-616A-215	Sequence 215, App
39	400	22.3	366	3	US-09-232-149A-215	Sequence 215, App
40	400	22.3	366	3	US-09-455-486-7	Sequence 7, Appli
41	400	22.3	366	3	US-09-636-215-215	Sequence 215, App
42	400	22.3	366	3	US-09-159-812-215	Sequence 215, App
43	400	22.3	366	3	US-09-115-453-215	Sequence 215, App
44	400	22.3	366	3	US-09-688-489-215	Sequence 215, App
45	400	22.3	366	3	US-09-679-426-215	Sequence 215, App

RESULT 1
US-09-455-486-1

```
Sequence 1, Application US/09455486
Patent No. 6833438
GENERAL INFORMATION:
APPLICANT:  Daniel E. Afar
APPLICANT:  Rene S. Hubert
APPLICANT:  Arthur B. Raitano
APPLICANT:  Douglas C. Saffran
APPLICANT:  Stephen C. Mitchell
TITLE OF INVENTION:  NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION:  EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE:  129.17-US-I1
CURRENT APPLICATION NUMBER:  US/09/455,486
CURRENT FILING DATE:  1999-12-06
PRIOR APPLICATION NUMBER:  09/323,873
PRIOR FILING DATE:  1999-06-01
NUMBER OF SEQ ID NOS:  34
SOFTWARE:  FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1193
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (64)...(1083)
US-09-455-486-1
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ALIGNMENTS

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Alignment Scores:
Pred. No.:                 1.09e-202
Score:                     1790.00
Percent Similarity:        100.00%         Length:        1193
Best Local Similarity:     100.00%         Matches:       339
                                           Conservative:  0
                                           Mismatches:    0
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Query Match: 100.00%   Indels: 0
DB: 3   Gaps: 0

US-10-750-262-2 (1-339) x US-09-455-486-1 (1-1193)

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Qy   1 MetGluSerArgLysAspIleThrAsnGlnGluGluLeuTrpLysMetLysProArgArg  20
Db  64 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 123

Qy  21 AsnLeuGluGluAspAlaPheTyrLeuHisLysAspThrGlyLysThrSerMetLeuLysSerArg  40
Db 124 AATTTAGAAGAAGACGCATTTTACCTGCATAAAGACACAGGGAAGACCAGCATGCTAAAAAGA 183

Qy  41 ProValLeuLeuHisLeuHisGlnThrAlaHisSerAlaAspSerGluPheAspCysProSerGlu  60
Db 184 CCTGTGCTTTTGCACTTGCACCAAACAGCCCATGCTGATGAAATTTGACTGCCCTTCAGAA 243

Qy  61 LeuGlnHisThrGlnGluLeuPheProGlnThrProHisLeuProIleLeuTyrIleAlaAlaIle  80
Db 244 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 303

Qy  81 IleAlaSerLeuThrProHisLeuTyrThrLeuLeuArgGluValIleIleHisProLeuAlaThr 100
Db 304 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 363

Qy 101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuAsnLysValLeuProMet 120
Db 364 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTTCATCAACAAAGTCTTGCCAATG 423

Qy 121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleLeuAlaAlaIleAlaValGln 140
Db 424 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGCCAA 483

Qy 141 LeuHisLysAsnGlyThrLysTyrLysSerPheProHisIleTrpLeuAspProHisMetLeuThr 160
Db 484 CTTCATAAATGGAACCAAGTATAAGAGTTTCCACATTGGTTGGATGTTAACA 543

Qy 161 ArgLysGlnPheGlyLeuLeuSerPhePheAlaValAlaLeuHisAlaIleTyrSerLeu 180
Db 544 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTGCTGTACTCGCATGCAATTTATAGTCTG 603

Qy 181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200
Db 604 TCTTACCCAATGAGGCGGTCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 663

Qy 201 GlnGlnAsnLysSerLeuGlnAlaTrpIleGluHisAspValProMetGluIleTyrVal 220
Db 664 CAACAAAATAAAAGAGAATGCCTGGAATTGAGTTTGGAGCATGAGATTTATGTG 723

Qy 221 SerLeuGlyIleLeuValAlaIleLeuAlaLeuValAlaThrSerIleProSer 240
Db 724 TCTCTGGGAATTGTGCGATTGGCAATACTGGCCTCTGTTGGCGTGCACATCTATTCCATCT 783

Qy 241 ValSerAspSerLeuThrArgGlyPheHisTyrIleGluGlnSerLysLeuGlyTyrLeuVal 260
Db 784 GTGAGTGACTCTTTGACAAGGGGATTTCACTATATTGAGCAGAAGCTAGGAATTGTT 843

Qy 261 SerLeuLeuLeuGlyThrThrIleHisSerAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
Db 844 TCCCTCTTACTGGGCACAATGCCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 903

Qy 281 LysGlnIlePheValTrpTyrThrProThrPheMetIleLeuAlaValPheLeuProIleVal 300
Db 904 AAACAAATTTGTATGGTATACACCTCCAACTTTATGATAGCTGTTTTCCTTCCAATTGTT 963

Qy 301 ValLeuIlePheLysSerIleLeuLeuProCysLeuArgLysLysIleLeuLeuIle 320
Db 964 GTCCTGATATTTAAAAGCATACTACTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1023

Qy 321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerSerGlnLeu 339
Db 1024 AGACATGGGTTGGGAAGAGCTCACCAAAAATTAACAAAACTGAGAGTAATATGTTCCCAGTTG 1080
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RESULT 2
US-09-323-873A-1

; Sequence 1, Application US/09323873A
; Patent No. 6329503
; GENERAL INFORMATION:
;   APPLICANT: Daniel B. Afar
;   APPLICANT: Rene S. Hubert
;   APPLICANT: Kahan Leong
;   APPLICANT: Arthur B. Raitano
;   APPLICANT: Douglas C. Saffran
;   APPLICANT: Steve Chappell Mitchell
;   TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
;   TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
;   FILE REFERENCE: 129.16USU2
;   CURRENT APPLICATION NUMBER: US/09/323,873A
;   CURRENT FILING DATE: 1999-06-01
;   PRIOR APPLICATION NUMBER: 60/087,520
;   PRIOR FILING DATE: 1998-06-01
;   PRIOR APPLICATION NUMBER: 60/091,183
;   PRIOR FILING DATE: 1998-06-30
;   NUMBER OF SEQ ID NOS: 32
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-09-323-873A-1

Query Match:

US-10-750-262-2 (1-339) x US-09-323-873A-1 (1-1195)

Alignment Scores:
Pred. No.:
Score: 1790.00   Length: 1195
Percent Similarity: 100.00%   Matches: 339
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 3   Mismatches: 0
DB: Indels: 0
                                       Gaps: 0

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Qy   1 MetGluSerArgLysAspIleThrAsnGlnGluGluLeuTrpLysMetLysProArgArg  20
Db  66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy  21 AsnLeuGluGluAspAlaPheTyrLeuHisLysAspThrGlyLysThrSerMetLeuLysSerArg  40
Db 126 AATTTAGAAGAAGACGCATTTTACCTGCATAAAGACACAGGGAAGACCAGCATGCTAAAAAGA 185

Qy  41 ProValLeuLeuHisLeuHisGlnThrAlaHisSerAlaAspSerGluPheAspCysProSerGlu  60
Db 186 CCTGTGCTTTTGCACTTGCACCAAACAGCCCATGCTGATGAAATTTGACTGCCCTTCAGAA 245

Qy  61 LeuGlnHisThrGlnGluLeuPheProGlnThrProHisLeuProIleLeuTyrIleAlaAlaIle  80
Db 246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy  81 IleAlaSerLeuThrProHisLeuTyrThrLeuLeuArgGluValIleIleHisProLeuAlaThr 100
Db 306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy 101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuAsnLysValLeuProMet 120
Db 366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTTCATCAACAAAGTCTTGCCAATG 425

Qy 121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleLeuAlaAlaIleAlaValGln 140
Db 426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGCCAA 485

Qy 141 LeuHisLysAsnGlyThrLysTyrLysSerPheProHisIleTrpLeuAspProHisMetLeuThr 160
Db 486 CTTCATAAATGGAACCAAGTATAAGAGTTTCCACATTGGTTGGATGTTAACA 545

Qy 161 ArgLysGlnPheGlyLeuLeuSerPhePheAlaValAlaLeuHisAlaIleTyrSerLeu 180
Db 546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTGCTGTACTCGCATGCAATTTATAGTCTG 605
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US-09-685-166A-878
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens

SOFTWARE: FastSEQ for Windows Version 3.0
NUMBER OF SEQ ID NOS: 898
CURRENT FILING DATE: 2000-10-10
CURRENT APPLICATION NUMBER: US/09/685,166A
FILE REFERENCE: 210121.427C21
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

APPLICANT: Hepler, William
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Wang, Aijun
APPLICANT: Li, Samuel
APPLICANT: Carter, Darrick
APPLICANT: Vedvick, Thomas S.
APPLICANT: Day, Craig H.
APPLICANT: Stolk, John A.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary R.
APPLICANT: Kalos, Michael D.
APPLICANT: Henderson, Robert A.
APPLICANT: Jiang, Yuqui
APPLICANT: Harlocker, Susan L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Dillon, Davin C.
APPLICANT: Xu, Jiangchun

; GENERAL INFORMATION:
; Patent No. 6630305
; Sequence 878, Application US/09685166A
US-09-685-166A-878

RESULT 3

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Qy  181 SerThrTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaThrGlnGlnVal 200
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Db  606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCAACTCAACAGGTC 665

Qy  201 GlnGlnAsnLysGluAspAlaThrIleGluLeuHisAspAlaThrTyrMetGluIleTyrVal 220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  666 CAACAAAATAAAGAAGATGCCCTGGATTGAGCTACATGACGCATATGAGATTTATGTG 725

Qy  221 SerLeuGlyIleValGlyLeuAlaIleLeuLeuAlaValAlaThrSerIleProSer 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  726 TCTCTCGGGAATTGTGGGACTTGGCCAATACTGGGCTGACATCTATTCCATCT 785

Qy  241 ValSerAspSerLeuThrArgGluThrTrpArgGluTrpLysSerLeuGlyIleVal 260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  786 GTGAGTGACTCTTTGACATGGGAGAATTCACTAATATTCAGAGAGAATTGGAAGATTG 845

Qy  261 SerLeuLeuLeuGlyThrIleHisAlaIleLeuHisProIleLeuAspAsnIle 280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  846 TCCCTTCTACTGGGCACAATACACGCAATTGATTTTTGCCTGAAATAAGTGGATAGAGATA 905

Qy  281 LysGlnPheValIleTrpIleTyrThrProProThrPheMetGluLeuProIleVal 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  906 AAACAATTTGTATGGATATACACCTCCAACTTTTATGAGCTGCCTAAATGTT 965

Qy  301 ValLeuIlePheLysSerIleLeuLeuProCysSerLeuArgLysSerIleLeuLysIle 320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  966 GTCCTGATATTTAAAAAGCATACTATTCCTGCCATGCTTGAGGAGAAGATACTGAAGATT 1025

Qy  321 ArgHisGlyTyrTrpGluAspValThrArgIleAlaAsnLysThrArgIleLeuCysSerGlnLeu 339
         |||||||||||||||||||||||||||||||||||||||
Db 1026 AGACATGGTTGGGAAGACGTCACCAAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082
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Qy   Query Match: 100.00%   Indels: 0
DB: 3   Gaps: 0
US-10-750-262-2 (1-339) x US-09-685-166A-878 (1-1195)

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Qy    1 MetGluSerArgGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleThrTyrSerLeu 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   66 ATGGAAAGCAGAGGAAAAGACATCACAAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy  161 ArgLysGlyIlePheGlyLeuLeuSerPhePheProHisAlaValLeuHisAlaIleThrTyrSerLeu 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  486 CTTCATAATGGAACCAAGTATATAAGAAGTTTCACATTGGATATAAGTGAGTTAACA 545

Qy  141 LeuHisAsnGlyThrLysTyrIleLysSerPheProHisIleTrpLeuAspLysTrpMetLeuThr 160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  426 GTTTCCATCACTCTCTTGGCATTGGTTTAACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy  121 ValSerIleThrLeuLeuAlaLeuValThrTyrLeuProGlyValIleLeuAlaAlaIleValAlaGln 140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  366 TCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy  101 SerHisSerGlnGlnTyrProPheTyrLysIleProIleLeuGluValIleLeuAsnLysValLeuProMet 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  306 ATAGCAATCTCTGACTTTTCTTCCTTACACCTCTTCTGAGGAGAAGTAATTCACCCTTTAGCAACT 365

Qy   81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValValIleIleHisProLeuAlaThr 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCCACTTGCCAATTAAAATAAGTGGTCTATT 305

Qy   61 LeuGlnLeuHisThrGlnGlnLeuLeuHisPheAlaAlaGluPheAspCysProSerGlu 80
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  186 CCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTGACTGCCCTTCAGA 245

Qy   41 ProValLeuLeuGluHisLeuHisSerGlnThrAlaHisIleAlaAspGluPheAspCysProSerGlu 60
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Db  126 AATTTAGAAGAAGACGATTTTTGCATAAGGACACGGGAGGAGGACCATGGCTAAAGAGA 185

Qy   21 AsnLeuGluGlyLeuAspAspPheTyrLeuHisLysGluHisSerAspAspIleThrAsnGlnGluGluLeuTrpLysMetLysProProArgArg 40
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Db   66 AATTTAGAAGAAGACGATTTTTGCATAAGGACACGGGAGGAGGACCATGGCTAAAAGA 125

Qy    1 MetGluSerArgGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleThrTyrSerLeu 20
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Qy  181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaThrGlnGlnVal 200
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Db  606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCAACTCAACAGGTC 665

Qy  201 GlnGlnAsnLysGluAspAlaThrIleGluLeuHisAspAlaThrTyrMetGluIleTyrVal 220
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Db  666 CAACAAAATAAAGAAGATGCCCTGGATTGAGCTACATGACGCATATGAGATTTATGTG 725

Qy  221 SerLeuGlyIleValGlyLeuAlaIleLeuLeuAlaValAlaThrSerIleProSer 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  726 TCTCTCGGGAATTGTGGGACTTGGCCAATACTGGGCTGACATCTATTCCATCT 785

Qy  241 ValSerAspSerLeuThrArgGluThrTrpArgGluTrpLysSerLeuGlyIleVal 260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  786 GTGAGTGACTCTTTGACATGGGAGAATTCACTAATATTCAGAGAGAATTGGAAGATTG 845

Qy  261 SerLeuLeuLeuGlyThrIleHisAlaIleLeuHisProIleLeuAspAsnIle 280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  846 TCCCTTCTACTGGGCACAATACACGCAATTGATTTTTGCCTGAAATAAGTGGATAGAGATA 905

Qy  281 LysGlnPheValIleTrpIleTyrThrProProThrPheMetGluLeuProIleVal 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  906 AAACAATTTGTATGGATATACACCTCCAACTTTTATGAGCTGCCTAAATGTT 965

Qy  301 ValLeuIlePheLysSerIleLeuLeuProCysSerLeuArgLysSerIleLeuLysIle 320
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Db  966 GTCCTGATATTTAAAAAGCATACTATTCCTGCCATGCTTGAGGAGAAGATACTGAAGATT 1025

Qy  321 ArgHisGlyTyrTrpGluAspValThrArgIleAlaAsnLysThrArgIleLeuCysSerGlnLeu 339
         |||||||||||||||||||||||||||||||||||||||
Db 1026 AGACATGGTTGGGAAGACGTCACCAAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082
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RESULT 4
US-09-679-426-878

; Sequence 878, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C20
; CURRENT APPLICATION NUMBER: US/09/679,426
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-679-426-878

Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Percent Identity:
Best Local Similarity:
Query Match:
DB:

1.09e-202
1790.00
100.00%
100.00%
100.00%
3

Length: 1195
Matches: 339
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-10-750-262-2 (1-339) x US-09-679-426-878 (1-1195)

Qy   1 MetGluSerArgLysAspIleThrAsnGlnHisGluLeuTrpLysMetLysProArgArg   20
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Db   1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAGAGAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy   21 AsnGlnGluGluAspAspAspTyrLeuHisLysAspThrGlyThrSerMetLeuLysArg   40
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 126 AATTTAGAAGAAGAACGGATTATTTGCATAAGGACACGGGAGGACCAGCAATGCTAAAAAGA 185

Qy   41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCTTCAGAA 245

Qy   61 LeuGlnHisThrGlnGluLeuPheProGlnTrpHisLeuProIleLeuTyrIleAlaAlaIle   80
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 246 CTTCAGCACACAGCAGAACTCTTTCCACAGTGGCACTTGCCAAATTAAAATAGCCTGCTATT 305

Qy   81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
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Db 306 ATAGCATCTCTGACTTTCTTTACACTCTTCTGAGGGAAGTAAATTCACCCTTTAGCAACT 365

Qy 101 SerHisGlnGlnThrTyrPheTyrLysIleProIleLeuValIleAsnLysValLeuProMet 120
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Db 366 TCCCATCACAACAATATTTTTATAAAATTCCAATCCTGGTTCATCAACAACAAGTCTTGCCAATG 425

Qy 121 ValSerIleThrLeuLeuLeuAlaLeuValTyrLeuProGlyValValIleAlaAlaValGln 140
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Db 426 GTTTCCATCACACTCTTGGCATTGGTTTACCTGCCAGGTGTGATTAGCAGCAATTGTCCAA 485

Qy 141 LeuHisAsnGlyThrLysTyrLysLysPhePheProHisIleTrpLeuAspLysLysTrpMetLeuThr 160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 486 CTTCATAATGGAACCAAGTATAAGAAGAGTTTCCACATTGGGATAAGTGGATGTTAACA 545

Qy 161 ArgLysGlnPheGlyValLeuSerPhePheAlaLeuValAlaLeuHisAlaIleTyrSerLeu 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 546 AGAAAGCAGTTTGGGCTTCTCCAGTTTCTTTTTTGCTGTACTGGCATGCAATCTATAGTCTG 605

Qy 181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200
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Db 606 TCTTACCCAATGAGGCGCTCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy 201 GlnGlnAsnLysGluAspAspAlaTrpIleGluHisAsnValTrpArgMetGluIleTyrVal 220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATAATGTGTGGAGAATGGAGATTTATGTG 725

Qy 221 SerLeuGlyIleValGlyLeuValAlaIleLeuLeuAlaLeuLeuAlaValThrSerIleProSer 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 726 TCTCTGGGAATTGTGGGATTGGTGGCAATACTGCTTGCTGTGACATCTATTCCATCT 785

Qy 241 ValSerAspSerSerLeuThrTrpArgGluHisSerTyrIleGlnSerLysLeuGlyIleVal 260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATACAGAGCAAGCTAGGAATTGTT 845

Qy 261 SerLeuLeuLeuGlyThrIleIleHisSerAlaLeuLeuPheAlaTrpAsnLysTrpIleAspIle 280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGAATA 905

Qy 281 LysGlnPheValIleTrpIleTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 906 AAACAATTTGTAATGGTATACACCCTCCAACTTTTATGATAGCTCGTTTTCCTTCCAAATTGTT 965

Qy 301 ValLeuIleLePheLysSerIleLeuGluProCysLeuArgLysLysLysSerIleLeuLeuLysIle 320
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Db 966 GTCCTGATATTTAAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy 321 ArgHisGlyTrpGluAspValThrLysIleAsnLysLysThrGlnIleLeuCysSerGlnLeu 339
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Db 1026 AGACATGGTTGGGAAGACGTCACCAAAATAATAACAAAAAACTGAGATATGTTCCCAGTTG 1082

RESULT 5
US-09-759-143-878

; Sequence 878, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-759-143-878

Alignment Scores:
Pred. No.:
Score: 1790.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 3

Length: 1195
Matches: 339
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-10-750-262-2 (1-339) x US-09-759-143-878 (1-1195)

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Qy    1 MetGluSerArgLysAspIleThrAsnGlnGluGlnLeuTrpLysMetLysProArgArg  20
Db   66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAGCAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy   21 AsnLeuGluGluAspAlaAspTyrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg  40
Db  126 AATTTAGAAGAAGACGCATTATTTGCATAAGGACACCGGGGAGAGAACCAGCCATGCTAAAAAGA 185

Qy   41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGlnPheAspCysProSerGlu  60
Db  186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy   61 LeuGlnHisThrGlnGluLeuPheProGlnTrpHisLeuProIleLysLysIleAlaAlaIle  80
Db  246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAAGCTGCTATT 305

Qy   81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
Db  306 ATAGCAATCTCTGACTTTCTTTACACTCTTCTGAGGGAAGTAAATTCACCCTTAGCAACT 365

Qy  101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeuProMet 120
Db  366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTACTCAACAAAGTCTTGCCAATG 425

Qy  121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleAlaValGln 140
Db  426 GTTTCCATCACTCTCCTTGGCAGTTGGTTTACCTGCCCAGGTGTGATAGCAGCAATTGTTCCAA 485

Qy  141 LeuHisAsnGlyThrLysTyrLysGlyPheProHisLeuTrpLeuAspArgMetLeuThr 160
Db  486 CTTCATAATGGAACCAAGTATAAGGAGTTTCCACATTGGTTGGATAGAATGGATATTAGTG 545

Qy  161 ArgLysGlnPheGlyLeuLeuSerPhePheProAlaValLeuHisAlaIleLeuTyrSerLeu 180
Db  546 AGAAAGCAGTTGGGCCTTCTCAGTTTCTTTTTCTGTACTGCCATGCAATTTATAGTCTG 605

Qy  181 SerTyrProMetArgArgSerTyrArgTyrLysLeuGlnSerLysLeuGlyIleVal 200
Db  606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCAAACTCAAGACTTTGATACGAGGTC 665

Qy  201 GlnGlnAsnLysGluAspAlaAspTyrIleGluHisAlaAspValTrpAsnLyTyrArgVal 220
Db  666 CAACAAAATAAAGGAAGATGCCTGGAATTGAACATAGTTTGGAACATGGAGATTTATGTG 725

Qy  221 SerLeuGlyValGlyLeuAlaIleLeuValAlaValAlaThrSerIleProSer 240
Db  726 TCTCTGGGAGTTGGGCTTGCAATTACTGGCCTCCTGGTTGCTGTTGCAACAAGTCTTGCCAATG 785

Qy  241 ValSerAspSerLeuThrTrpArgGlnHisTyrIleGlnSerLysLeuGlyIleVal 260
Db  786 GTGAGTGACTCTTTGACATGGAGAATTCACTATATTCAGAGCAAGCTTAGGAGATTGTT 845

Qy  261 SerLeuLeuGlyThrIleHisAlaLeuIlePheAlaLeuIleSerTrpIleAspIle 280
Db  846 TCCCTTCTACTGGGCACAATAACACGCCATGATTTTGCCTGGAATAAAGTGGATAGATATA 905

Qy  281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300
Db  906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy  301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgGlyLysLysIleLeuLysIle 320
Db  966 GTCCTGATTATTTAAAAAGCATACTATTCCTGCCATGCTTGAGGAGAAGAGATACTGAAGATT 1025
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RESULT 6
US-10-010-667A-1

; Sequence 1, Application US/10010667A
; Patent No. 6887975
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Hubert, Rene S.
; APPLICANT: Leong, Kahan
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Saffran, Douglas C.
; APPLICANT: Mitchell, Steve Chappell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 5511582001601
; CURRENT APPLICATION NUMBER: US/10/010,667A
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 09/323,873
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-010-667A-1

Alignment Scores:
Pred. No.:
Score: 1790.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 3

Length: 1195
Matches: 339
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-10-750-262-2 (1-339) x US-10-010-667A-1 (1-1195)

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Qy    1 MetGluSerArgLysAspIleThrAsnGlnGluGlnLeuTrpLysMetLysProArgArg  20
Db   66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAGCAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy   21 AsnLeuGluGluAspAlaAspTyrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg  40
Db  126 AATTTAGAAGAAGACGCATTATTTGCATAAGGACACCGGGGAGAGAACCAGCCATGCTAAAAAGA 185

Qy   41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGlnPheAspCysProSerGlu  60
Db  186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy   61 LeuGlnHisThrGlnGluLeuPheProGlnTrpHisLeuProIleLysLysIleAlaAlaIle  80
Db  246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAAGCTGCTATT 305

Qy   81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
Db  306 ATAGCAATCTCTGACTTTCTTTACACTCTTCTGAGGGAAGTAAATTCACCCTTAGCAACT 365

Qy  101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeuProMet 120
Db  366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTACTCAACAAAGTCTTGCCAATG 425

Qy  121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleAlaValGln 140
```

; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

RESULT 7
US-10-012-896-878
Sequence 878, Application US/10012896
Patent No. 6943236
; GENERAL INFORMATION:

; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-878

US-10-750-262-2 (1-339) x US-10-012-896-878 (1-1195)

Alignment Scores:
Pred. No.:   1.09e-202   length: 1195
Score: 1790.00   Matches: 339
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 3   Gaps: 0

Qy   1 MetGluSerArgGlyAspAspIleThrAsnGlnGluGluLeuTrpLysMetLysProArgArg 20
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   66 ATGGAAAGCAGAGGAGATGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy   21 AsnLeuGluGluLeuAspAsnTyrLeuHisLysAspSerThrGlyGluThrSerMetLeuLysArg 40
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 126 AATTTAGAAGAACGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAGA 185

Qy   41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaLeuAspGluPheGluCysProSerGlu 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy   61 LeuGlnHisThrGlnLeuGluPheProGlnThrTrpHisLeuProIleLeuLysValIle 80
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 246 CTTCAGCACACACAGAGAACTTCCCACAGTGGCACTTCCCATTAAAATAGCTGTAATT 305

Qy   81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuValIleLeuProLeuAlaThr 100
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGGTGATAGCTGGCTGTGCTACT 365

Qy 101 SerHisSerGlnGlnTyrPheTyrLysGlyIleProIleLeuLysValIleLeuProMet 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 366 TCCCATCAACAATATTTTTACAAAGGTATCCCTGGTCATCAACAAAAGTCTTGCCAATG 425

Qy 121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln 140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATTAGCAGCAATTGTCCAA 485

Qy 141 LeuHisAsnGlyThrLysTyrLysGlySerPheProHisTrpLeuAspLysTrpMetLeuThr 160
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 486 CTTCATAATGGAACCAAAGTATATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy 161 ArgLysGlnPheGlyLeuLeuSerPhePheProHisAlaValLeuHisAlaAlaIleTyrSerLeu 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 546 AGAAAGCAGTTTGGGCTTCTCAGTTTTCTTTTGCGTGTACTGCCATGCAATTTATAGTCTG 605

Qy 181 SerTyrProMetArgArgSerTyrArgTyrLysGlyLeuLeuLeuAsnTrpProAlaTyrGlnGlnVal 200
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 606 TCTTACCCAATGAGGCGGATCCTACAGATACAAGTTGCTAAACTGGGCCATATCAACACAGGTC 665

Qy 201 GlnGlnAsnLysGluAspAlaIleTrpIleGluHisSerAspValTrpArgMetGluIleTyrVal 220
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 666 CAACAAAATAAAGAAGAGATGCCTGGAATTGAGCATGTTTGGAGAATGGAGATTTATGTG 725

Qy 221 SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSer 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 726 TCTCTGGGAATTGTGGGAATGGCCAATACTGGCTCTGTTGGCTGTGGCCAATTCAATCTCATCT 785

Qy 241 ValSerAspSerLeuThrLeuThrTrpArgGluPheHisSerTyrIleGlnSerLeuGlyIleVal 260
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 786 GTGAGTGACTCTTTGACATGGAGAGAATTCACTATATTCAGAGCAAGCTAGGAAATGTT 845

Qy 261 SerLeuLeuLeuGlyThrIleHisAlaLeuIleLeuGluAlaTrpAsnLysTrpIleAspAsnIle 280
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 846 TCCCTCTACTGGGCACAATACACGCATTGATTTTTGCCTCGGAATAAGTGGATAGATATA 905

Qy 281 LysGlnPheGlnValTrpArgGlnTyrThrProGluPheMetIleAlaValPheLeuProIleVal 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 906 AAACAATTTGTATCGGTATACACCTCCAACTTTATGATAAGCTGTTTCCTTCAATTGTT 965

Qy 301 ValLeuIleLeuPheLysSerIleLeuPheLeuArgGlyLysSerIleLeuLeuLysIle 320
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 966 GTCCTGATATTTAAAGCATACACTATTCCTGAGGAGAGAAGATACTGAAGATT 1025

Qy 321 ArgHisGlyTrpProGluAspValThrLysIleAsnLysSerThrGluIleCysSerGlnLeu 339
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1026 AGACATGGTTGGGAAGACCTCACCAAAAATAAACAAAAACTGAGATATGTTCCCAGTTG 1082

RESULT 8
US-09-949-016-2686
; Sequence 2686, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2686
; LENGTH: 1147
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2686

Alignment Scores:
Pred. No.:
Score: 1782.00
Percent Similarity: 99.71%
Best Local Similarity: 99.71%
Query Match: 99.55%
DB:

9.12e-202   Length: 1147
               Matches: 338
               Conservative: 0
               Mismatches: 0
               Indels: 1
               Gaps: 0

US-10-750-262-2 (1-339) x US-09-949-016-2686 (1-1147)

```
Qy     1 MetGluSerArgLysAspIleThrAsnGlnGluLeuTrpLysMetLysProArgArg  20
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA  92

Qy    21 AsnLeuGluGluAspAspThrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg  40
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    93 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA  152

Qy    41 ProValLeuLeuHisGlnThrAlaHisAlaAspGlyPheAspCysProSerGlu  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   153 CCTGTGCTTTTGCATTCGACAAACAGCCCATGCTGATGAATTGACTGCCCTTTCAGGA  212

Qy    61 LeuGlnHisThrGlnLeuProGlnTrpHisLeuProIleLysIleAlaAlaIle  80
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   213 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTCCAATTAAAATAGCTGCTATT  272

Qy    81 IleAlaAspSerLeuThrPheLeuTyrThrLeuArgGluValIleHisHisProLeuAlaThr  100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   273 ATAGCAGACTCTCGACTTTCTTTACACTTTCTGAGGGAAGTAATTCACCCTTTAGCCAACT  332

Qy   101 SerHisGlnIleTyrPheTyrLysIleProIleLeuValIleLeuAsnLeuValLeuProMet  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

Db   846 TCCCTTCTACTGGGCACAATACACACCGATTGATTTTGCCTGGAATAAGTGGATAGAATATA 905
Qy   261 SerLeuLeuGlyThrIleHisIleAlaLeuPheAlaLeuTrpProAsnLysTrpIleAspIle 280
Db   906 AAACAGATTTGTATCGGTATACACCTCCAACTTTATGATAGACTGTGTTTCCTTCAATTGTT 965
Qy   301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysLysIleLysIle 320
Db   966 GTTCTCGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTACTGAAGATT 1025
Qy   321 ArgHisGlyTrpGluValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339
Db 1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082

; RESULT 9
US-09-323-873A-6
; Sequence 6, Application US/09323873A
; Patent No. 6329503
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Kahan Leong
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; APPLICANT: Steve Chappell Mitchell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 129.16USC2
; CURRENT APPLICATION NUMBER: US/09/323,873A
; CURRENT FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 3627
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-323-873A-6

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Qy   333 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAAGTGTTGCAATG  392
Db   573 ...
Qy   121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleLeuAlaAlaLeuValGln  140
Db   393 GTTTCCATCACTCCTTGGCATTGGTTTACCTGGTGTTGATAGCAGCAATTGTCCAA  452
Qy   141 LeuHisAsnGlyThrLysTyrLysBlyPheProHisTrpLeuAspLysTrpMetLeuThr  160
Db   453 CTTCATAAATGGAACCAAGTATAAGGATTTCCACATTGGGATAAGTGGATAAGTGGTAAACA  512
Qy   161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu  180
Db   513 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTCGCTGTACTGCATGCAATTTATAGTCTG  572
Qy   181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal  200
Db   573 TCTTACCCAATGAGGCGGATCCTACAGATACAAGTTGCTAAACTGGGCCATATCAACAGGTC  632
Qy   201 GlnGlnAsnLysGluAspAlaTrpIleGluHisAsnAspAlaTrpIleThrGlnValVal  220
Db   633 CAACAAAAATAAAGGAAGATGCCTGGATTGAGCACAATGATGATGAATTGAGAATTATGTG  692
Qy   221 SerLeuGlyIleLeuValGlyLeuAlaIleLeuValAlaLeuAlaValThrSerIleProSer  240
Db   693 TCTCTGGGAAATTGTGGGATTGGCAATACTGGCTCTTGTTGACAATCTATTCCATCT  752
Qy   241 ValSerAspSerLeuThrPheArgGluPheHisIleTyrIleGlnSerLeuGlyGlyVal  260
Db   753 GTGAGTGACTCTTTGACATGGAAGAATTTCACTATATTCAGAGCTTGGGTGGAATGTT  812
Qy   261 SerLeuLeuGlyThrIleHisIleAlaLeuPheAlaLeuTrpProAsnLysTrpIleAspIle  280
Db   813 TCCCTTCTACTGGGCACAATACACACGGATTGATTTTGCCTGGAATAAGTGGATAGATATA  872
Qy   281 LysGlnIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysLysIleLysIle  300
Db   873 AAACAAATTTTGTATCGGTATACACCTCCAACTTTATGATAGCTGTGTTTTCCTTCAATTGTT  932
Qy   301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysLysIleLeuIle  320
Db   933 GTTCTCGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTACTGAAGATT  992
Qy   321 ArgHisGlyTrpGluValThrLysIleAsnLysThrGluIleCysSerGlnLeu  339
Db   993 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG  1049
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Alignment Scores:
Pred. No.:              1.17e-150
Score:                  1358.50                 Length:          3627
Percent Similarity:     29.68%    Percent Identity:  29.68%   Matches:         338
Best Local Similarity:  75.89%                          Conservative:    0
Query Match:            3                               Mismatches:      1
                                                        Indels:          801
                                                        Gaps:            1
DB:
US-10-750-262-2 (1-339) x US-09-323-873A-6 (1-3627)

Qy    1 MetGluSerArgLysAspIleThrAsnGlnGluLeuTrpLysMetLysProArgArg     20
Db    1 ATGGAAAGCAGAAGAGACATCACAAACCAAGAACTTTGGAAAATGAAGCCTAGGAGA    155

Qy   21 AsnLeuGluGluAspAlaProTyrLeuHisLysAspThrGlyThrSerMetLeuLysArg   40
Db  156 AATTTAGAAGAAGACGCGCCATTATTTGCATAAAGGACACAGGGACGAGCATGTTAAAAGA  215

Qy   41 ProValLeuLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu         60
Db  216 CCTGTGCTTTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA         275

Qy   61 LeuGlnHisThrGlnGluLeuProIleLeuHisHisLeuProIleLeuLysIleLeuAlaIle  80
Db  276 CTTCAGCACACACAGGAACTCTTTCCAACACTGGCACTTGCCAATTAAAATAGCTGCTATT    335

Qy   81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleLeuHisProLeuAlaThr  100
Db  336 ATAGCACTCTCGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTAGCAACT    395

Qy  101 SerHisGlnGlnThrTyrPheTyrLysSerProIleLeuLeuValLeuProMet         120
Db  396 TCCCATCAACAATATTTTTATAAATCCAATCCCTGGTCATCAACAAAGTCTTGCCAATG    455

Qy  121 ValSerIleThrLeuLeuValLeuValTyrLeuProGlyValIleLeuAlaAlaIleAlaValGln  140
Db  456 GTTTCCATCACTCTCTTGGCATTGGTTTACTCCGCCAGTGTTGATAGCAGCAATTGTCCAA   515

Qy  141 LeuHisAsnGlyThrLysTyrLysSerPheProHisTrpLeuAspLysTrpMetLeuThr     160
Db  516 CTTCATAATGGAACCAAGTATAAGAGTTTCCCACATTGGTTGGATAAGTGGATGTTAACA    575

Qy  161 ArgLysGlnPheGlyTyrLeuLeuSerPhePheAlaValLeuLeuHisAlaIleTyrSerLeu  180
Db  576 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTGCTGTACTGCATGCAAATTTTATAGTCTG   635

Qy  181 SerTyrProMetArgArgSerTyrAsgTyrLysGlyLeuLeuAsnTrpAlaThrTyrGlnGlnVal  200
Db  636 TCTTACCCAATGAGGCGGCATCCTACAGATACAAAGGTTGCTAAACTGGGCAATTCAACAGGTC  695

Qy  201 GlnGlnAsnLysGlyLuAspAlaLeuTrpIleGluGluHisAlaSpValTrpArgMetGluIleTyrVal 220
Db  696 CAACAAAATAAAGGAAGATGCCTGGATTGAGGAACATGCAGAATGGAGATTTATGTG    755

Qy  221 SerLeuGlyValIleLeuValGlyLeuAlaIleLeuLeuValAlaValAlaThrSerIleProSer  240
Db  756 TCTCTGGGAATTGTGGGATTGGCAATACTGGCCTGTGTTGGCGTGACACTCTTATTCCAAGTCA   815

Qy  241 ValSerAspSerLeuThrTrpArgGluPheHisTyrIle---                       253
Db  816 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATAT-TCAGGTAAATAATATATAAAA    874

Db  935 CATAAAAATAACAAAGTTTTTCAACAGCAAAGATCTTATACTGTTGTTCCAATTAATAAT    994
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Qy ... (additional alignment rows continue with gap markers)

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Db   995 GTGCTCTCCCTGTTGTTTTTCCCTATTGCTTCTAATTAGGACAAGTGTTTCCTAGGACATAAA  1054
Qy   253 ---------------------------------------------------------------  253
Db  1055 TAAAAGGCATTAAAAATATTCTTTGTTTTTTTTTTTTTGTTTGTTTTT               1114
Db  1115 GTTTGTTTTTTTGTGAGATGAAGTCTCGGCTTCTGTTGCCCATGCTGGAGTACACGTGGCACGAT  1174
Db  1175 CTCGGCCTCACTGCAACCTGCGCGCTTCCTGGGGTTCAGGCGGGGATTCTCTTGCCCTTGCCCTCCTG  1234
Db  1235 AGTAGCTGGGATTACAGGCGCCCATCACCATGTCCAGCTAATTTTTGTATTTTAGTAGA  1294
Db  1295 GACAGGGGTTTCCCCATGTTGGCCAGGCTGGTCTCGACTCCTGACCTCAAAATGATCCGCC  1354
Db  1355 CACCTCGGCCTCCCAAAGTGCTGGGATGACAGTGTGAGCCACCACCACTCAGCCTGCTCT  1414
Db  1415 TTCTAATATTTGAAACTTGTTAGACAATTGCTACCCATCTAATGTGATATTTTAGGAAT  1474
Db  1475 CCAATATGCATGGTTTATTATTTCTTAAAAAAAATATTCTTTTACCTGTCACCTGAATTT  1534
Db  1535 AGTAATGCCTTTATGTTACAACTTAGCACTTTCCAGAAACAAAAACTCTCTCCTTGA  1594
Db  1595 AATAATAGAGCTTTTTATCCTACCAAAGATATGCTACTGTGTCTCATTTCAAAGGCTGCTTTTT  1654
Db  1655 CCAGCTTACATTTTATATTACTTACTCCACTTGAAGTTTCTAAATATTCTTGTAATTTTAAA  1714
Db  1715 ACTATCTCAGATTTACTGAGGTTTATCTTCTGGTGGTAGATTATCCATAAGAAGAGTGAT  1774
Db  1775 GTGCCAGAATCACTCTGGGATCCCTTGTCTCGACAAGATTCAAAGGACTAAATTAATTCAG  1834
Db  1835 TCATGAACACTGCCAATTACCGTTTATGGGTAGACATCTTTGGAAAATTTCCACAAGTCA  1894
Db  1895 GACATTCGCAACTATCCCTTCTACAGTCCACACGTATACTCCAACACTTTATTAGGCAT  1954
Db  1955 CTGATTAGTTTGGAAAGTATGCCTCCATCTGAATTAGTCCACTGTGTGGCTAGAGTTGGTA  2014
Db  2015 CAACATTCTCACAGAATTCCTAAATTTTGTTAGGTTCAGCCTGATAACCACTGGAGTTCTT  2074
Db  2075 TGGTCCTCATTAAAATAGCTTTCTTCACACAATTGCTCTGCCCTGTTACACATATGATGAACA  2134
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Qy 254 --GlnSerLysLeuGlyIleVal 260
Db 3215 CTTAATGAACAAATCTTCACCAAATTTGTTTTCTTGTTTGTCGCAAGCAAGCAAGAATTGTT 3274

Qy 261 SerLeuLeuLeuGlyThrIleHisAlaAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
Db 3275 TCCCTTCTACTGGGCACAAATACACGCATTGATTTTGCCTGAATAAGTGGATAGATATA 3334

Qy 281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300
Db 3335 AAACAAATTTGTATGGTGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAAATTGTT 3394

Qy 301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgGlyLysLysLysIleLeuIle 320
Db 3395 GTCCTGATATTTAAAAGCATACTAATTCCTGCCATGCTTGAGGAGAGATACTGAAGATT 3454

Qy 321 ArgHisGlyTrpGluAspValThrLysIleLeuAsnLysLysThrGluIleCysSerGlnLeu 339
Db 3455 AGACAATGGTTGGGAAGAACGTCACCAAAATTAACAAAAAACTGAGATATGTTCCCAGTTG 3511

RESULT 10
US-09-455-486-4
; Sequence 4, Application US/09455486
; Patent No. 6833438
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; APPLICANT: Stephen C. Mitchell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 129.17-US-I1
; CURRENT APPLICATION NUMBER: US/09/455,486
; CURRENT FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/323,873
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 3627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-455-486-4

Alignment Scores:
Pred. No.:   1.17e-150   Length: 3627
Score: 1358.50   Matches: 338
Percent Similarity: 29.68%   Mismatches: 0
Best Local Similarity: 29.68%   Conservative: 1
Query Match: 75.89%   Indels: 801
DB: Gaps: 1

US-10-750-262-2 (1-339) x US-09-455-486-4 (1-3627)

Qy 1 MetGluSerArgLysAspIleThrAsnGlnGluLeuTrpLysProArgArg 20
Db 1 ATGGAAAGCAGAAAAGACATACAAAACCAAGAAGAACTTTGGAAAGCCTAGGAGA

Qy 21 AsnLeuGluGluAspAspTyrLeuHisLysAspThrGlySerMetLeuLysArg 40
Db 156 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAAGCATGCTAAAAAGA 215

Qy 41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluProPheAspCysProSerGlu 60
Db 216 CCTGTGCTTTTGCATCTTGCACCAAACAGCCCATGTCGATGAAATTTGACTGCCCTTCAGAA 275

Qy 61 LeuGlnHisThrGlnIleLeuPheProGlnThrProHisLeuProIleGluLysGluAlaIleIle 80
Db 276 CTTCAGCACACACAGGAACTCTTCCCACAGTGGCACTTGCCATTAAAATAATGCTATT 335

Qy 81 IleAlaSerLeuThrPheLeuTyrThrLeuArgGluValIleIleHisProLeuAlaThr 100

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Db  336 ATAGCATCTCTGACTTTTCTTACACTCTTCTGAGGGAGGTAATTCACCCCTTAGCAAACT  395
Qy  101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleLeuAsnLysValLeuProMet  120
Db  396 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCCAACAAAGTCTTGCAAATG  455
Qy  121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaLeuAlaIleValGln  140
Db  456 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTTGATAGGCAGCAATTGTCAA  515
Qy  141 LeuHisAsnGlyThrLysTyrLysLysPhePheProHisTrpLeuAspLysTrpTrpMetThr  160
Db  516 CTTCATAATGGGACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGTGGATGACA  575
Qy  161 ArgLysGlnPheGlyLeuLeuSerPhePheAlaValLeuLeuAlaLeuIleTyrSerLeu  180
Db  576 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTGCTGTACTGCAGTTTATAGTGTCTG  635
Qy  181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuLeuLeuAsnTrpAlaTyrGlnVal  200
Db  636 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC  695
Qy  201 GlnGlnAsnLysGluAspAlaTrpIleGluHisAspProHisArgMetGluIleTyrVal  220
Db  696 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATCCTCATAGGATGGAGATTTATGTG  755
Qy  221 SerLeuGlyIleLeuValGlyLeuLeuAlaIleLeuLeuAlaLeuValAlaValThrSerIleProSer  240
Db  756 TCTCTGGGAATTCTGGTGGGATTGCTAGCAATACTGCTCGTTGGGCTGTGACAATCTATTCCATCT  815
Qy  241 ValSerArgAspSerLeuThrTrpArgGluPheHisTyrIle-----  253
Db  816 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATAT-TCAGTAAATAATAATATAAAA  874
Qy  253 ------------------------------------------------------------  253
Db  875 TAACCCTAAGAGAGTAAAATCTTCTCTTTTTGTGTTTATGATATAGAATATGTTGACTTTACCC  934
Qy  253 ------------------------------------------------------------  253
Db  935 CATAAAAAATAACAAAGTGTTTCAACAGCAAAGATCTTATACTTGTTCCAAATTAATAAT  994
Qy  253 ------------------------------------------------------------  253
Db  995 GTGCTCTCCTGTGTTGTTTCCCTATTGCTTCTTAATTAGGACAAGTGTTTCCTAGACATAAA  1054
Qy  253 ------------------------------------------------------------  253
Db 1055 TAAAAGGCAATAAAAATATTCTTTGTTTTTTTTTTGTTTTGTTTTTTGTTTTGTTTGTTTT  1114
Qy  253 ------------------------------------------------------------  253
Db 1115 GTTTTGTTTTTTTTGAGATGAAGCTCGCTTCGTTGCCCATGCTGAGTACACAGTGGCACGAT  1174
Qy  253 ------------------------------------------------------------  253
Db 1175 CTCGGCTTCACTGCAACCTGCCGCTCCTGGGTTCAGGCGATTCCTTGCCTTCAGCCTCCCTG  1234
Qy  253 ------------------------------------------------------------  253
Db 1235 AGTAGCTGGGATTACAGGCGCACCCATCACCATGTCCAGCTAATTTTTGTATTTTAGTAGA  1294
Qy  253 ------------------------------------------------------------  253
Db 1295 GACAGGGGTTTCCCATGTTGGCCAGGCTGGTCTCGAATCTCCTGACCTCAAATGATCCGCC  1354
Qy  253 ------------------------------------------------------------  253
Db 1355 CACCTCGGCCTCCCAAAGTGCTGGGATGACAGTGTGAGCCACCACACTCAGCCTGCTCT  1414
Qy  253 ------------------------------------------------------------  253
Db 1415 TTCTAATATTTGAAACTTGTTAGACAATTTGCTACCCATCTAATGTGATGTATTTTAGGAAT  1474
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Qy  253 ------------------------------------------------------------  253
Db 1475 CCAAATATGCAATCGGTTTATTAATTTTCTTAAAAAAATATTCTTTTACCTGTCTGAATTT  1534
Qy  253 ------------------------------------------------------------  253
Db 1535 AGTAATGCCTTTTATTGTTACAACAACTTAGCACTTTCCAGAAACAAAAACTCTCTCCTTGA  1594
Qy  253 ------------------------------------------------------------  253
Db 1595 AATAATAGAGTTTTTATCTACCAAAGATATGCTAGTGTCTCATTTCAAAAGGCTGCTTTTT  1654
Qy  253 ------------------------------------------------------------  253
Db 1655 CCAGCTTACATTTTTATACTTACTCACTTGAAGTTTCTAAATATTCTTGTAATTTTAAA  1714
Qy  253 ------------------------------------------------------------  253
Db 1715 ACTATCTCAGATTTACTGAGGTTTATCTTCTGGTGGGTAGATTATCCATAAGAGAGTGAT  1774
Qy  253 ------------------------------------------------------------  253
Db 1775 GTGCCAGAATCACTCTGGGATCCTTGTCTGCGTCGACAAGGACTAAAATTTAATTCAG  1834
Qy  253 ------------------------------------------------------------  253
Db 1835 TCATGAACACTGCCAAATACCGTTTATGGGTAGAGACATCTTTGGGAAATTCCACAAGGTCA  1894
Qy  253 ------------------------------------------------------------  253
Db 1895 GACATTCGCAAACTATCCCTTCTCACAGTCCACACAGTATACTCCAAACACTTTATTAGGCAT  1954
Qy  253 ------------------------------------------------------------  253
Db 1955 CTGATTAGTTGGGAAAGTATGCCTCCATCTGAATTAGTCCAGTGTGGGCTTAGAGTGTGGTA  2014
Qy  253 ------------------------------------------------------------  253
Db 2015 CAACATTCTCACAGAAATTCCTAATTTGTAGGTTCAGCCTGATAACCACTGGGAGTTCTT  2074
Qy  253 ------------------------------------------------------------  253
Db 2075 TGGTCCTCATTAAATAGCTTTCTTCACACAATTGCTCTGCCTTGTTACACATATGATGAACA  2134
Qy  253 ------------------------------------------------------------  253
Db 2135 CTGCTTTTTAGACTTCATTAGGAATTTAGGACTGCAATCTTGACACACTGAGCCTATTCTAC  2194
Qy  253 ------------------------------------------------------------  253
Db 2195 TATATGTACAATACCTAGCCCCATAATAGGTATACACATACACATTGGTAAAACTAATTTT  2254
Qy  253 ------------------------------------------------------------  253
Db 2255 CAACCAATGACATGACGTATTTTCAACTAGTAACCTAGAAAATGTTTCACTTAAAATCTGAGA  2314
Qy  253 ------------------------------------------------------------  253
Db 2315 ACTGGTTACACTACAAGTTACCTTGGAGATTCATATATGAAAACGCAAAACTTAGCTATTT  2374
Qy  253 ------------------------------------------------------------  253
Db 2375 GATTGTATTCACTGGGACTTAAGAAATCGCCTGAAATAATTGTGAGTTCGATTTGTTCTGG  2434
Qy  253 ------------------------------------------------------------  253
Db 2435 CAGGCTAATGACCATTCCAGTAAAGTGAATAGAGGTCAGAGAGTCGTATAAAAGAGAGTGT  2494
Qy  253 ------------------------------------------------------------  253
Db 2495 TGTCAGAACACCGTTGAGATTACTACTAGGTGAACAACTTATTTTTAAGCAAACTTTATTGTG  2554
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; APPLICANT: Saffran, Douglas C.
; APPLICANT: Mitchell, Steve Chappell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 5115820016.01
; CURRENT APPLICATION NUMBER: US/10/010,667A
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 09/323,873
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 3627
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-010-667A-6

Alignment Scores:
Pred. No.:
Score: 1.17e-150
Percent Similarity: 1358.50   Length: 3627
Percent Identity: 29.68%   Matches: 338
Best Local Similarity: 29.68%   Conservative: 0
Query Match: 29.68%   Mismatches: 1
DB: 75.89%   Indels: 801
                                    3   Gaps: 1

US-10-750-262-2 (1-339) x US-10-010-667A-6 (1-3627)

Qy   1 MetGluSerArgLysAspIleThrAsnGlnGluGluTrpLysMetLysProArgArg 20
         |||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 155

Qy   21 AsnLeuGluGluAspAspTyrLeuHisLysAspThrGlyGluPheMetLeuLysArg 40
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   96 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 215

Qy   41 ProAlaValLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 216 CCTGTGCTTTTGCACTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 275

Qy   61 LeuGlnHisThrGlnIleLeuProGlnTrpHisLeuProIleLeuValIleAlaAlaIle 80
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 276 CTTCAGCACACACAGAAACTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTAATT 335

Qy   81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 336 ATAGCAATCTCTGACTTTTCTTACACTCTTCTGAGGGAAGTAATTCACCCTCTAGCAACT 395

Qy 101 SerHisLeuGlnTyrPheTyrLysIleProIleLeuAsnLysValLeuProMet 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 396 TCCCATCAACAAATATTTTATAAAATTCCAATCCTCGGTCATCACAAAGTCGTTGCCAATG 455

Qy 121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaLeuValGln 140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 456 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTCATAGCAGCAAATGTCCAA 515

Qy 141 LeuHisAsnGlyThrTyrLysTyrLysSerPhePhePheAlaValLeuHisAlaIle 160
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 516 CTTCATAATGGAACCTATAAGTATAAGAGTTTCCACATTGGTTGATAAGTGATGTTAACA 575

Qy 161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 576 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTGCTGTACTGCATGCAATTTATAGTCTG 635

Qy 181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200
         |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db 636 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 695

Qy 201 GlnGlnAsnLysGluAspAlaTrpIleGluHisAspValThrTrpArgMetGluIleTyrVal 220
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Db 253

Qy 216 ... 253

; RESULT 11
; US-10-010-667A-6
; Sequence 6, Application US/10010667A
; Patent No. 6887975
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Hubert, Rene S.
; APPLICANT: Leong, Kahan
; APPLICANT: Raitano, Arthur B.

Qy 321 ArgHisGlyThrProGluAspValThrLysIleAlaAsnLysThrGluIleCysSerGlnLeu 339
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3455 AGACATGGTTGGGAAGAGCTCACCAAAATTAACAAAACTGAGAATATGTTCCCAGTTG 3511

Qy 301 ValLeuIlePheLysSerLeuPheLeuProCysLeuArgLysLysLysIleLeuLeuIle 320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3395 GTCCTGATATTTAAAGATCTTCTGCCATGCTTGAGGAAGAAGAAGATACTGAAGATT 3454

Qy 281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3335 AACAAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 3394

Qy 261 SerLeuLeuLeuGlyThrLeuHisIleAlaLeuIlePheAlaTrpAspAsnLysTrpIleAspIle 280
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3275 TCCCTTCTACTGGGCACAATACACCCATTGATTTTTGCCTGGGATAAGAAGTGGATAGATATA 3334

Qy 254 GlnSerLysLeuGlyIleLeuVal 260
         |||||||||||||||||
Db 3215 CTTATTGAACCAATCTTCACCAATTTGTTTCTTTGGAGACGAAGCTAGGAATTGTT 3274

Qy 253
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Qy 253
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Qy 253
Db 3035 ATTTTGTTCACTTAGACAGCTTGGAGACAAGAAAAATTACCCAAAAAGTAAGGTGAGGGAT 3094

Qy 253
Db 2975 AAATGGTGGAGAAAGAGTAGAAGAAGTTTTTGATCACCTGCCTTCAAAGAAAGGCTGTGA 3034

Qy 253
Db 2915 AATTAAGACAAAATACACAAGAGACAAAGCACAAAAAATAAATATCATAAAGGGGATGAACA 2974

Qy 253
Db 2855 GCAGTGAATCCTGCTATAAGTAAGACTCAGTGACTATCCTGTGAAAACAG 2914

Qy 253
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Qy 253
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Qy 253
Db 2675 TTTAAAACATAGGCCAAGTTCATTCATTCATTATTCATTATTCAAAATCAGAGTGAAT 2734

Qy 253
Db 2615 TTTGTGCACATTGAAAAATTGTTCATATATTATTTCCATGTTATCTGAATATATTTGATTT 2674

Qy 253
Db 2555 TAGTGACAAAGCATCCAATGCAGGCTGAAATGTTTCATCACATCTCTGGATCTCTCTAT 2614

Qy 253
Db 253

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Db    696 CAACAAAATAAAGAAGAATGACGATGACTGGAGTGTTGGAGAGAATTGATGTG 755
Qy    221 |||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    756 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTCGTGTTGGCGTGACATCTATTCCATCT 815
Qy    241 ValSerAspSerLeuThrThrPargGluPheHisTyrIle -----
          816 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTTTATAT-TCAGGTAAAATAATATATAAAA 874
Db    875 TAACCCTAAGGAGGTAAATCTTCTTTTTGTGTTTATGATATAGAATATGTTGACTTTACCC 934
Qy    253 -----
Db    935 CATAAAAAATAACAAATGTTTTCAACAGCAAAGATCTTATACTTGTTCCAATTAATAAT 994
Qy    253 -----
Db    995 GTGCTCTCCTGTTGTTTTTCCCTATTGCTTCTAATTAGGACAAGAGTGTTTCCTAGACATAAA 1054
Qy    253 -----
Db   1055 TAAAAGGCATTAAAATATTCTTTTGTTTTTTTTGTTGTTTATGATATAGTTGTTTTTGTTTTGTTT 1114
Qy    253 -----
Db   1115 GTTTGTTTTTTTGAGATCAAGAGTCTCGCTCTGTTGCCATGCCTCGGAGTTACAGTGGCACGGAT 1174
Qy    253 -----
Db   1175 CTCGGCTCACTGCAACCTGCCGCCTCCCTGGGTTCAGGCGGGCGATTCTTCTTGCCTCAGCCTCCTG 1234
Qy    253 -----
Db   1235 AGTAGCTGGGATTACAGGCGCACCCATCACCACGTGTCCAGCTAATTTTTGTATTTTTTAGTAGA 1294
Qy    253 -----
Db   1295 GACAGGGGTTTTCCCATGTTGGCCAGGCTGGTCTCGATCTCCTGACCTCAAATGATCCGCC 1354
Qy    253 -----
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Qy    253 -----
Db   1415 TTCTAATATTTGAAACTTGTTAGAGCAAATTTGCTACCACCATCTAAATGTGATATTTTAGGAAT 1474
Qy    253 -----
Db   1475 CCAATATGCATGGTTTATTTACAACTTAGCACTTCCAGAAAACAAAAACTCTCCTTGA 1534
Qy    253 -----
Db   1535 AGTAATGCCTTTTATGTTACAACTTAGCACTTCCATTTCAAAAGCTGCTTTTT 1594
Qy    253 -----
Db   1595 AATAATAGAGTTTTTATCTACCAAAAGATATGCTAGTGTCTCATTCAAAGGCTTATAA 1654
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Qy    253 -----
Db   1775 GTGCCAGAATCACTCTGGATCCTTGTGCTGACAAGATTCAAAAGGACTAAAATTTAATTCAG 1834


Qy    253 ----- 253
Db   1835 TCATGAACACTGCCAATTACCGGTTTATGGGTAGACATCTTTGGAAATTTCCACAGGTCA 1894
Qy    253 ----- 253
Db   1895 GACATTCGCAACTATCCCTTCTACATGTCCAACACTTTATTAGGCAT 1954
Qy    253 ----- 253
Db   1955 CTGATTAGTTTGGAAAGTATGCCTCCATCTGAATTAGTCCAGTGTGGCTTAGAGTTGGTA 2014
Qy    253 ----- 253
Db   2015 CAACATTCTCACAGAATTTCCTAATTTTGTAGGTTCAGCCTGATAACCACTGGAGTTCTT 2074
Qy    253 ----- 253
Db   2075 TGGTCCTCATTAAAATAGCTTTCTTCACACATTGCTCTGCCCTGTTTACACATATGAATGACAACA 2134
Qy    253 ----- 253
Db   2135 CTGCTTTTTAGACTTCATTAGGAATTTAGGACTGCATCTTGACAACTGAGCCTATTCTAC 2194
Qy    253 ----- 253
Db   2195 TATATGTACAATAACCTAGCCCATAATAGGTATACAATACACATTTGGTAAAACTAATTTT 2254
Qy    253 ----- 253
Db   2255 CAACCAAATGACATGTATTTTTTCAACTAGTAACCTAGAAATGTTTCACTTAAAATCTGAGA 2314
Qy    253 ----- 253
Db   2315 ACTGGTTACACTACAAGTTACCTTGGAGATTCATTATATGAAAACGCAAACTTAGCTATTT 2374
Qy    253 ----- 253
Db   2375 GATTGTATTCACTGGGACTTAAGAATGCGCCTGAATAATTGTGAGTTCGATTGTTCTGG 2434
Qy    253 ----- 253
Db   2435 CAGGCTAATGACCAATTCCAGTAAAGTGAATAGAGGTCAGAAGTCGTATAAAAGAGGTGT 2494
Qy    253 ----- 253
Db   2495 TGTCAGAACACCGTTGAGATTACATAGGTGAACAACTATTTTTAAGCAACTTTATTGTG 2554
Qy    253 ----- 253
Db   2555 TAGTGACAAAGCATCCCAATGCAGGCTGAAAGTTTCATCACACATCTCTGGATCTCTCTAT 2614
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Db   2615 TTTGTGCGAGACATTGAAAAAAATTGTTCATATTATTCCATGTTATCAGAATATTTGATTT 2674
Qy    253 ----- 253
Db   2675 TTTAAAACATAGGCCAAGTTCATTCACTTCATTATTCAAAATCAGAGTGAAT 2734
Qy    253 ----- 253
Db   2735 CACATTAGTTCGCCTTCACAACTGATAAAGATCACTGAAGTCAAATTGATTTTTGCTATAA 2794
Qy    253 ----- 253
Db   2795 TCTTCAATCTACCTTATATTTAATTGAGAATCTAAAAATGTACAAAATCATTGTGTTGATTCT 2854
Qy    253 ----- 253
Db   2855 GCAGTGATCCTGCTATAAGTAAGACTCAGTCCCTGATTTAGGTATCCCTGTGTGAAAAGCAG 2914
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RESULT 12

Alignment Scores:

Pred. No.:	
Score:	6.24e-116
Percent Similarity:	1071.50
Best Local Similarity:	23.59%
Query Match:	23.59%
DB:	59.86%

Length:	9073	
Matches:	309	
Conservative:	0	
Mismatches:	2	
Indels:	1000	
Gaps:	2	

US-09-949-016-14428

Qy   253   --   253

Db   2915   AATTAAGACAAAAATACACAAGAGACAAAAGCACAAAAAAATAAATATCATAAGGGGATGAACA   2974

Qy   253   --   253

Db   2975   AAATGGGTGGAGAAAGAGTAGACAAAAGTTTTTGATCACCTGCCTTCAAAGAAAGGCTGTGA   3034

Qy   253   --   253

Db   3035   ATTTTGTTCACTTAGACAGCTTGGAGACAAGAAATACCCAAAAGTAAGGTGAGCAGGGAT   3094

Qy   253   --   253

Db   3095   AGGCAAAAAGAGCAGAAAAGATGTGAATGGACATTGTTGAGAAAATGTTAGGAAAAACAAT   3154

Qy   253   --   253

Db   3155   CATAGAAAAGGAGATTTCCAAGCAACAGAGACATATCCAGATGAGGTAGGATGGGGATAAACT   3214

Qy   254   --------------GlnSerLysLeuGlyIleVal   260

Db   3215   CTTAATTGAACCAAATCTTCACCAAATTTGTTTTTCTTTGCAGATCCAAGGCTAGGAATTGTT   3274

Qy   261   SerLeuLeuLeuGlyThrIleHisAlaLeuIleLeuPheAlaTrpAsnLysThrIleAspIle   280

Db   3275   TCCCTTCTTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA   3334

Qy   281   LysGlnPheValTrpTyrTyrThrProProThrPheMetIleAlaValPheLeuProLeuVal   300

Db   3335   AAACAATTTGTATGGTATTACACCTCCAACTTTATGATAGCTGTTTTCCTTCCAAATTGTT   3394

Qy   301   ValLeuIleLeuProLysSerIleLeuLeuPheLeuProCysLeuArgGlyLysLysIleLeuLysIle   320

Db   3395   GTCCTCGATATTTAAAAAGCATACTAATACTATTCCTGCCATGCTTGACGGAAGAAGATACTGAAGATT   3454

Qy   321   ArgHisGlyTyrTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu   339

Db   3455   AGACAATGGTTGGGAAGACGTCACCAAAAATTAACAAAAACTGAGATARGTGTTCCAGTTG   3511

US-10-750-262-2 (1-339) x US-09-949-016-14428 (1-9073)

Qy   29   HisLysAspThrGlyGluThrSerMetLeuLysArgProValLeuLeuHisLeuHisGln   48

Db   3049   CATAAGGACACGGGAGAGAGGAGAGACCCAGCAATGCTAAAAAGAGACCTGTGCTTTTTGCATTTGCAGCAA   3108

Qy   49   ThrAlaHisAlaAspGluPheAspCysProSerGluLeuGlnHisHisThrGlnLeuPhe   68

Db   3109   ACAGCCCATGCTGATGAATTGACTGCTCCCTTCAGCACACACAGGAACTCTTT   3168

Qy   69   ProGlnTrpHisLeuProIleLysIleAlaLeuAlaLeuIleLeuAlaSerLeuThrPheLeuTyr   88

Db   3169   CCACAGTGGCACTTGCCAATTAAAATAGCTGCTATTATAGCAATCTCTGACTTTTCTTTAC   3228

Qy   89   ThrLeuLeuArgGluValValIleIleHisProLeuAlaThrSerHisIleGlnIleTyrProPhe   108

Db   3229   ACTCTTCTGAGGGAAGTAATCAACCCTTTAGCAACTTCCCATCACATAATTTTTATAAA   3288

Qy   109   IleProIleLeuLeuValIleIleAlaAlaLeuValIleAlaValGlnLeuLeuHisAsnGlyThrLeuLeu   128

Db   3289   ATTCCAATCCTGGTTCATCAACAAAAGTTCTTGCCATCACACTCTTCTTGGCATTG   3348

Qy   129   ValTyrLeuProGlyValValIleIleAlaAlaLeuValIleAlaValGlnLeuLeuHisAsnGlyThrLeuLys   148

Db   3349   GTTTACCTGCCAGGTGTGATAGCAATTGCCAACTTCATAATGGAACCAAGTATAAG   3408

Qy   149   LysPheProHisTrpLeuAspGlyTrpMetLeuThrArgGlyLysGlnPheGlyTyrLeuLeuSer   168

Db   3409   AAGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGTTCTTCTCAGT   3468

Qy   169   PhePhePheAlaValAlaLeuAlaIleLeuTyrSerLeuSerTyrProMetArgArgSerTyr   188

Db   3469   TTCTTTTTTGCTGTACTGCCATGCAAATTTATAGTCTGTTCTACCCAATGAGGCCGCATCCTAC   3528

Qy   189   ArgTyrLysLysLeuLeuAsnTrpAlaLaTyrGlnGlnVal   200

Db   3529   AGATACAAGTTGCTAAACTGGGCATATCAACACAGGT-AAGATGACAGTGTTGACACTGTTA   3587

Qy   200   --   200

Db   3588   CTAATAAAAAGTCTAAGTCACCTAACAAAATTAATCATTTCTCATTGTAATATCAATACCC   3647

Qy   200   --   200

Db   3648   CAAACCCTGTTGAAACTCTGTTGTTGAAAAGTCATCTATTTTAAAAATTTTATTATAATTA   3707

Qy   200   --   200

Db   3708   CACTAGGGCTTGGTTGTGTCGGTTTTTATATTGAGAAAATGTTTTTAGGCTGAAATAA   3767

Qy   200   --   200

Db   3768   GGTACAACTTTAGCAACATAAGAAAACATTTGTTCATGGACGAGGGCCATATTTCAAACTT   3827

Qy   200   --   200

Db   3828   CTACCACCCTCACAAGATTACTTTTTTAATAATTGTTGTTCTTCCTCCTTGTTTACCAAATATG   3887

Qy   200   --   200

Db   3888   CATGCACATTACAGTTCTATCCAAGTAAACCATCACAAATAATTATTAGAAAAATTAATAGAT   3947

Qy   200   --   200

Db   3948   TATGGAAGTGTTGCATTCAAGAAAAAAAAGTGATAGCTCCTAGTCATTGTCTTAGAGGA   4007

Qy   200   --   200

Db   4008   ATGCAAAAAAAAAAAAAAAGAAAAGTCATAAAATTTGTGGAGACCTGTTATCAGGGCTTCAT   4067

Qy   200   --   200

Db   4068   AGTAGGCACAGGGAAGAGTGTAGAAGGAGGATTCACATTCAGGAAATAACTGTTGTTTGCA   4127

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Qy    201 ------------------------------------------------GlnGlnAsnLysGluAspAlaTrpIle 209
                                                          |||||||||||||||||||||||
Db   4128 TTTCTTCTTTCTTTTATTTACCTTCTTCGGTAGGTCCAACAAAATAAAGAAGAAGATGCCTGGATT 4187

Qy    210 GluHisAspValTrpArgMetGluIleTyrValSerLeuGlyIleValGlyValGlyLeuAlaIle 229
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4188 GAGCACGATGAGTGTTTGGAGAATGGAGATTTAATGTGTCTCTGGGAATTGTGGGAGTTGGGAGTA 4247

Qy    230 LeuAlaLeuLeuAlaValThrSerIleProSerValSerAspSerLeuThrTrpArgGlu 249
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   4248 CTGGCCTCTTGGCCTGTGACACATCTATTCCATCTGTGAGTGAGTACTCTTTGACATGGAGAGA 4307

Qy    250 PheHisTyrIle------------------------------------------------------ 253
          |||||||
Db   4308 TTTCACTATATTCAGGTAAAATAATATATAAAAATAACCCTAAGAGGTAAATCTTCTTTTG 4367

Qy    253 ------------------------------------------------------------------ 253
Db   4368 TGTTTATGATATAGAATATGTTGACTTACCCATAAAAATAACAAATGTTTTCAACA 4427

Qy    253 ------------------------------------------------------------------ 253
Db   4428 GCAAAGATCTTATACTGTTCCAATTAATAAATGCTCTCCGTGTTGTTTTCCCTATTGCT 4487

Qy    253 ------------------------------------------------------------------ 253
Db   4488 TCTAATTAGGACAAGTGTTTCCTAGACAATAAATAAAGGCATTAAAATATTCTTTGTTTT 4547

Qy    253 ------------------------------------------------------------------ 253
Db   4548 GTTCAGGGCGATTCTCTTGCCTCAGCCTCCTGAGTAGCTGGATTACAGGCGCACCCATCACC 4607

Qy    253 ------------------------------------------------------------------ 253
Db   4608 TTTTTTTTTGTTTGTTGTTTTGTATTTTTGTTGTTTTGTTTTTGAGATGAAAGTCTCGCTC 4667

Qy    253 ------------------------------------------------------------------ 253
Db   4668 TGTTGCCCATGCTGGAGTACAGTGGCGCACGATCTCGGCTCACTGCAAACCTGCCTCCTGG 4727

Qy    253 ------------------------------------------------------------------ 253
Db   4728 ATGTCCAGCTAATTTTTGTATTTTTAGTAGAGACAGGGGTTTTCCCATGTTGGCCAGGCTG 4787

Qy    253 ------------------------------------------------------------------ 253
Db   4788 GTCTCGATCTCCTGACCTCAAATGATCCGCCCACCTCGGCCTCCCAAAGTGCTGGGATGA 4847

Qy    253 ------------------------------------------------------------------ 253
Db   4848 CAGTTGTGAGCCACCACACTCAGCCTGCTCTTTCTACTATTATTGAAACTTGTTAGACAAATT 4907

Qy    253 ------------------------------------------------------------------ 253
Db   4908 TGCCACCCATCTAAGTGATATATTTAGGAATCCAAATATGCATGGTTTATTATTTCTTAAA 4967

Qy    253 ------------------------------------------------------------------ 253
Db   4968 AAAAATATTCTTTTACCTGTCACCTGAAATTAGTAATGCCTTTTAITGTTACACAACTTAG 5027

Qy    253 ------------------------------------------------------------------ 253
Db   5028 CACTTTCCAGAAACAAAAACTCTCTCCTTGAAATAATAGAGTTTTTATCTACCAAAGATA 5087

Qy    253 ------------------------------------------------------------------ 253
Db   5088 TTCTAGTGTCTCATTCAAAGGCTGCTTTTTCCAGCTTACAITTTATTATACTTACTACT 5147

Qy    253 ------------------------------------------------------------------ 253
Db   5148 TGAAGTTTCTAAAATATTCTTGTAATTTTAAAACTATCTCAGATTTACTGAGGTTTATCTT 5207
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Qy    253 ------------------------------------------------------------------ 253
Db   5208 CTGGTGGTTAGATTATCCATAAGAAGACTGATGTGTGCCAGAATCACTCTGGGATCCTTGTCT 5267

Qy    253 ------------------------------------------------------------------ 253
Db   5268 GACAAGATTCAAAGGACTAAAATTAATTCAGTCATGAACACTGCCAATTACCGTTTATGG 5327

Qy    253 ------------------------------------------------------------------ 253
Db   5328 GTAGACATCTTTGGGAAATTTCCACAAGGTCAGACATTCCGCAACTATCCCTTCTACATGTC 5387

Qy    253 ------------------------------------------------------------------ 253
Db   5388 CACACGTATACTCCAACACTTTATTAGGCATCTGATTAGTTTGGAAAGTATGCCTCCATC 5447

Qy    253 ------------------------------------------------------------------ 253
Db   5448 TGAATTAGTTGCCAGTGTGTGGCTTAGAGTTGGTACAACATTCTCAGAGAATTTCCTAAATTTTG 5507

Qy    253 ------------------------------------------------------------------ 253
Db   5508 TAGGTTCAGCCTGATAACCACTGGAGTTCTTTGGTCTCCATTAAATAGCTTTTCTTCACAC 5567

Qy    253 ------------------------------------------------------------------ 253
Db   5568 ATTCCTCTGCCCTGTTACACATATGATGAACACTGCCTTTTTAGACTTCATTAGGAAATTTAG 5627

Qy    253 ------------------------------------------------------------------ 253
Db   5628 GACTGCATCTTGACAACTGAGCCTATTCTACTATATGTACAAATACCTAGCCCATAATAGG 5687

Qy    253 ------------------------------------------------------------------ 253
Db   5688 TATACAATACACATTTGGTAAAACTAATTTCAACCAATGACACGTGTATTTTCAACTAGT 5747

Qy    253 ------------------------------------------------------------------ 253
Db   5748 AACCTAGAAAATGTTTCACTTAAAATCTGAGAACTGGTTACACTACAAGTTACCTTGGAGA 5807

Qy    253 ------------------------------------------------------------------ 253
Db   5808 TTCTATATATGAAAAACGCAAAACTTAGCTATTTGATTGTATTCACTGGGACTTAAGAAATGCG 5867

Qy    253 ------------------------------------------------------------------ 253
Db   5868 CCTGAATAATTGTGAGTTCGATTTGTTCTGGCAGGGTAATGACCAITTCCAGTAAAGTGA 5927

Qy    253 ------------------------------------------------------------------ 253
Db   5928 ATAGAGGTCAGAAGTCGTATAAAAGAGGGTTGTTCAGAACACCGTTGAGATTACATAGGT 5987

Qy    253 ------------------------------------------------------------------ 253
Db   5988 GAACAACTATTTTTAAGCAACTTTATTTGTGTGAGTGACAAAGCAATCCCAATGCAGGCTGA 6047

Qy    253 ------------------------------------------------------------------ 253
Db   6048 AATGTTTCATCACATCTCTGGATCTCTCTATTTGTGCAGACATTGAAAAAATTGTTCAT 6107

Qy    253 ------------------------------------------------------------------ 253
Db   6108 ATTATTTCCATGTTATCAGAATATTTGATTTTTTAAAACATTAGGCCAAGTTCATTCACT 6167

Qy    253 ------------------------------------------------------------------ 253
Db   6168 TCATTATTCATTTATCAAAATCAGAGTGAATCACATTAGTCGGCCTTCACAACTGATAAAG 6227

Qy    253 ------------------------------------------------------------------ 253
Db   6228 ATCACTGAAGTCAAATTGATTTTTGCTATATACTTCAATCTACCTATATTTAATTGAGAA 6287
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Db  6288  TCTAAAATGTACAAATCATTGTGTTGATTCTGCAGGGATCCTGCTATAAGTAAGACTCAG  6347

Qy   253  ------------------------------------------------------------  253

Db  6348  TCCCTTGGATTTTAGGTATCCCTGTGATAAGCAGAAATTAAGACAAATACACAAGAGACAAAAGC  6407

Qy   253  ------------------------------------------------------------  253

Db  6408  ACAAAAAATAAAATACATAAGGGGGATGAACAAAAATGGTGGAGAAAGAGTAGACAAAAGTTT  6467

Qy   253  ------------------------------------------------------------  253

Db  6468  TTGATCACCTGCCTTCAAAGAAAGGCTGTGAAATTTGTTCACTTAGACACAGCTTGGAGACA  6527

Qy   253  ------------------------------------------------------------  253

Db  6528  AGAAATTACCCAAAAGTGAGGAGGATAGGGAAAAAGAGTAGAAAAGATGTGAATGG  6587

Qy   253  ------------------------------------------------------------  253

Db  6588  ACATTGTTGAGAAAATGTATAGGAAAAACAAATCAATAGATTTCCAAGCAACACAGAG  6647

Qy   253  ------------------------------------------------------------  253

Db  6648  CATATCCAGATGATGAGGTAGGATGGGATAAAACTCTTATTGAACCAATCTTCACCAATTTGT  6707

Qy   254  --------GlnSerLysLeuGlyIleValSerLeuLeuLeuGlyThrIleHisAlaIle  270

Db  6708  TTTTCTTTTGCAGAGCAAGCTAGGAAATTGTTTCCCTTCTACTGGGCACAATACACGCATT  6767

Qy   270  uIlePheAlaIleTrpAsnLysThrpIleAspIleLysLysGlnPheValTrpTyrThrProProTh  290

Db  6768  GATTTTTGCCTGGAATAAGTGGATAGTATAAAACAATTTGTATACACTTCCCAAC  6827

Qy   290  rPheMetIleAlaValAlphaLeuPheLeuProIleValAlValLeuLeuPheLysGlnPheIle  310

Db  6828  TTTTATGATAGCTGTTTTTCCTTCCAATTGTTGTCCTGATATTTAAAAAAGCATAATCTATTCCT  6887

Qy   310  uProCysLeuArgLysLysIleLeuArgHisGlyTrpGlnAspValThrLysIl  330

Db  6888  GCCATGCTTGAGGAAGAGATACTGAAGATTAGACAATGGGTTGGGAAGACGTCACCAAAAT  6947

Qy   330  eAsnLysThrGlulleCysSerGlnLeu  339

Db  6948  TAACAAAACTGAGATATTGTTCCCAGTTG  6975
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; ORGANISM: Homo sapien
; US-09-439-313-342

; Alignment Scores:
; Pred. No.:
; Score:                      5.62e-98
; Percent Similarity:         905.00          Length:        592
; Best Local Similarity:      99.42%          Matches:       171
; Query Match:                99.42%          Mismatches:    0
; DB:                         50.56%          Conservative:  0
                              3               Indels:        1
                                              Gaps:          0

US-10-750-262-2 (1-339) x US-09-439-313-342 (1-592)
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Qy     1  MetGluSerArgLysAspAspIleThrArgAsnGlnGluGluLeuTrpLysMetGlyProArg  20
Db   518  ATGGAAAGCAGAAAAAGACGACATCAACAGAAACCAAGAAGAACTTTGGAAAAATGAAGGCCTAGGAGA  459

Qy    21  AsnLeuGluGluAspAspTyrLeuHisLysAspAspThrGlyIleGluHisProLeuAlaThr  40
Db   458  AATTTAGAGAAGACGATTATTTGCATAAGGACACACGGGAGAGAGACCAGCATGCTAAAAAGA  399

Qy    41  ProValLeuLeuHisLeuHisGlnThrAlaHisHisAlaAspGluPheAspProCysProSerGlu  60
Db   398  CCTGTGCTTTTGCATTTGCACCAAAACAGCCCATCGTGATGAATTTGACTGCCCTTCAGAA  339

Qy    61  LeuGlnHisThrGlnLeuGluLeuProGlnIntTrpHisLeuProIleLysIleLeuAlaIleAla  80
Db   338  CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT  279

Qy    81  IleAlaSerLeuThrPheLeuThrTyrThrLeuHisLeuArgGluValIleHisProLeuAlaThr  100
Db   278  ATAGCATCTCTGACTTTTCTTTACACTCTCTGAGGGAGTAATTCACCCTTTAGCACACT  219

Qy   101  SerHisGlnIntTyrPheTyrLysSerIleProIleLeuGluValIleAsnLysGlyValLeuProMet  120
Db   218  TCCCATCAACAATATTTTTATAAAAAGTCCAATCCTGGTCATACAACAAAAGTCTTGCCAATG  159

Qy   121  ValSerIleThrLeuLeuLeuAlaLeuValTyrLeuProGlyValAlIleAlaLeuAlaIleValAlGln  140
Db   158  GTTTCCATCACCTCTTCTTGGCCATTGGTTTACCTGGCTGTGATAGCAGCAATTGTGTCCAA  99

Qy   141  LeuHisIleAsnGlyThrLysTyrLysLysPheProHisTrpLeuAspLysThrTrpMetLeuThr  160
Db    98  CTTCATAATGGAACCAAGTATAAGAAGTTCCCACATTGGTTGGATAAGTGGATGTTAACA  39

Qy   161  ArgLysGlnPheGlyTyrLeuLeuSerPhePhePheAla  172
Db    38  AGAAAGCAGAATTGGGGCTTCCTCAGTTTCTTTTTTTGCT  3
```

; Patent No. 6329505, Application US/0943913
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
;   DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 592
; TYPE: DNA

RESULT 13
US-09-439-313-342/c
Sequence 342, Application US/0943913

Alignment Scores:

RESULT 14
US-09-352-616A-342/c
Sequence 342, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqui
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
;   OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-342

Alignment Scores:

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Pred. No.:                          5.62e-98
Score:                              905.00
Percent Similarity:                 99.42%
Best Local Similarity:              99.42%
Query Match:                        50.56%
DB:                                 3
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US-10-750-262-2 (1-339) x US-09-352-616A-342 (1-592)

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Qy    1 MetGluSerArgLysAspIleThrAsnGlnGluGluLeuTrpLysMetLysProArgArg 20
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  518 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 459

Qy   41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  398 CCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 339

Qy   21 AsnLeuGluGluAspAspTyrrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  458 AATTTAGAAGAAGACGATTATTTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 399

Qy   61 LeuGlnHisThrGlnGluLeuPheProGlnThrPhisLeuProIleLysIleAlaAlaIle 80
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  338 CTTCAGCACACACAGGAAACTCTTTCCACAGTGGCACTTGCCAATTAAATAGCTGCTATT 279

Qy   81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  278 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCACT 219

Qy  101 SerHisGlnGlnTyrrPheTyrrLysIleProIleLeuValIleLeuAsnLysValLeuProMet 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  218 TCCCATCAACAATATTTTTATAAAATTCCAAATCCTGGTCATCAACAAAGTCTTGCCAATG 99

Qy  121 ValSerIleThrLeuLeuAlaLeuValThrTyrLeuProGlyValIleIleAlaAlaIleAlaValGln 140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  158 GTTTCCATCACTCTTCTTGGCATTGGTTTACCTGCGTGTGATAAGCAGCAATTGTCCAA 99

Qy  141 LeuHisAsnGlyThrLysLysTyrrLysLysPhePheProHisTrpLeuAspLysTrpMetLeuThr 160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   98 CTTCATAAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 39

Qy  161 ArgLysGlnPheGlyLeuLeuSerPhePheAla 172
          |||||||||||||||||||||||||||||||
Db   38 AGAAAGCARAATTGGGCTTCTCAGTTTCTTTTTTTGCT 3
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RESULT 15
US-09-636-215-342/c
; Sequence 342, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
```
APPLICANT:  Xu, Jiangchun
APPLICANT:  Dillon, Davin C.
APPLICANT:  Mitcham, Jennifer L.
APPLICANT:  Harlocker, Susan L.
APPLICANT:  Jiang, Yuqui
APPLICANT:  Henderson, Robert A.
APPLICANT:  Kalos, Michael D.
APPLICANT:  Fanger, Gary R.
APPLICANT:  Retter, Marc W.
APPLICANT:  Stolk, John A.
APPLICANT:  Day, Craig H.
APPLICANT:  Vedvick, Thomas S.
APPLICANT:  Carter, Darrick
APPLICANT:  Li, Samuel
APPLICANT:  Wang, Aijun
APPLICANT:  Skeiky, Yasir A.W.
APPLICANT:  Hepler, William
TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE:  210121.42717C17
CURRENT APPLICATION NUMBER:  US/09/636,215
CURRENT FILING DATE:  2000-08-10
NUMBER OF SEQ ID NOS:  852
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; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-636-215-342

Alignment Scores:
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Pred. No.:                          5.62e-98
Score:                              905.00
Percent Similarity:                 99.42%
Best Local Similarity:              99.42%
Query Match:                        50.56%
DB:                                 3
```

US-10-750-262-2 (1-339) x US-09-636-215-342 (1-592)

```
Qy    1 MetGluSerArgLysAspIleThrAsnGlnGluGluLeuTrpLysMetLysProArgArg 20
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  518 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 459

Qy   21 AsnLeuGluGluAspAspTyrrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  458 AATTTAGAAGAAGACGATTATTTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 399

Qy   41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  398 CCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 339

Qy   61 LeuGlnHisThrGlnGluLeuPheProGlnThrPhisLeuProIleLysIleAlaAlaIle 80
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  338 CTTCAGCACACACAGGAAACTCTTTCCACAGTGGCACTTGCCAATTAAATAGCTGCTATT 279

Qy   81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  278 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCACT 219

Qy  101 SerHisGlnGlnTyrrPheTyrrLysIleProIleLeuValIleLeuAsnLysValLeuProMet 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  218 TCCCATCAACAATATTTTTATAAAATTCCAAATCCTGGTCATCAACAAAGTCTTGCCAATG 159

Qy  121 ValSerIleThrLeuLeuAlaLeuValThrTyrLeuProGlyValIleIleAlaAlaIleAlaValGln 140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  338 ... GTTTCCATCACTCTTCTTGGCATTGGTTTACCTGCGTGTGATAAGCAGCAATTGTCCAA 99

Qy  141 LeuHisAsnGlyThrLysLysTyrrLysLysPhePheProHisTrpLeuAspLysTrpMetLeuThr 160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   98 CTTCATAAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 39

Qy  161 ArgLysGlnPheGlyLeuLeuSerPhePheAla 172
          |||||||||||||||||||||||||||||||
Db   38 AGAAAGCARAATTGGGCTTCTCAGTTTCTTTTTTTGCT 3
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Search completed: December 6, 2005, 18:45:28
Job time : 231 secs

OM nucleic - nucleic search, using sw model

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                         GenCore version 5.1.6
                         Copyright (c) 1993 - 2005 Compugen Ltd.

Run on:          December 5, 2005, 03:12:22 ; Search time 320.456 Seconds
                                             (without alignments)
                                             987.688 Million cell updates/sec

Title:           US-10-750-262-1_COPY_66_1082
Perfect score:   1017
Sequence:        1 atggaaagcagaaaagacat..........ctgagatatgttcccagtg 1017

Scoring table:   IDENTITY NUC
                 Gapop 10.0, Gapext 1.0
Searched:        3289935 seqs, 15561033 residues
Total number of hits satisfying chosen parameters:        6579870

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Published_Applications NA_New:*
                 1: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                 2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                 3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                 4: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                 5: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                 6: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                 7: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                 8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
                 9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
                10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	39.2	3.9	1779	6	US-10-750-185-25365	Sequence 25365, A
c 2	37.2	3.7	2464	6	US-10-750-185-39315	Sequence 39315, A
c 3	36	3.5	872	6	US-10-750-185-49060	Sequence 49060, A
c 4	34.2	3.4	1012	6	US-10-750-185-54610	Sequence 54610, A
c 5	34	3.4	3609	6	US-10-750-185-63875	Sequence 63875, A
c 6	34	3.4	1240	6	US-10-750-185-30880	Sequence 30880, A
7	33.8	3.3	1458	6	US-10-821-224-142	Sequence 142, App
c 8	33.8	3.3	2748	6	US-10-750-185-48714	Sequence 48714, A
c 9	33.4	3.3	1840	6	US-10-750-185-38532	Sequence 38532, A
c 10	33.2	3.3	973	6	US-10-750-185-35293	Sequence 35293, A
c 11	33.2	3.3	340000	7	US-11-102-978-3	Sequence 3, Appli
c 12	32.8	3.2	399	7	US-11-108-172-547	Sequence 547, App
c 13	32.8	3.2	1135	6	US-10-750-185-58068	Sequence 58068, A
c 14	32.8	3.2	1765	6	US-10-750-185-54184	Sequence 54184, A
c 15	32.4	3.2	1307	6	US-10-986-501-27	Sequence 27, Appl
c 16	32.4	3.2	1993	6	US-10-750-185-54772	Sequence 54772, Appl
c 17	32.2	3.2	1257	6	US-10-750-185-64012	Sequence 64012, A
c 18	32.2	3.2	1454	6	US-10-750-185-46704	Sequence 46704, A
c 19	32	3.1	1252	6	US-10-750-185-62619	Sequence 62619, A
c 20	32	3.1	3310	6	US-10-750-185-24645	Sequence 24645, A
c 21	32	3.1	4753	6	US-10-750-185-33545	Sequence 33545, A
c 22	31.8	3.1	1370	6	US-10-750-185-57153	Sequence 57153, A
c 23	31.8	3.1	1986	6	US-10-793-626-273	Sequence 273, App
c 24	31.8	3.1	3043	6	US-10-793-626-3478	Sequence 3478, Ap
c 25	31.8	3.1	3165	6	US-10-793-626-3360	Sequence 3360, Ap
c 26	31.8	3.1	3206	6	US-10-750-185-47856	Sequence 47856, A
c 27	31.8	3.1	3636	6	US-10-793-626-4179	Sequence 4179, Ap
c 28	31.8	3.1	4168	6	US-10-793-626-4023	Sequence 4023, Ap
c 29	31.6	3.1	1166	6	US-10-750-185-38045	Sequence 38045, A
c 30	31.6	3.1	1830	6	US-10-750-185-39246	Sequence 39246, A
c 31	31.6	3.1	1838	6	US-10-750-185-52241	Sequence 52241, A
32	31.6	3.1	3001	7	US-11-145-703-175	Sequence 175, App
33	31.6	3.1	3001	7	US-11-145-703-176	Sequence 176, App
c 34	31.6	3.1	150491	7	US-11-112-908-46	Sequence 46, Appl
c 35	31.4	3.1	600	6	US-10-750-185-1485	Sequence 1485, Ap
c 36	31.4	3.1	1407	6	US-10-750-185-44414	Sequence 44414, A
c 37	31.4	3.1	1637	6	US-10-750-185-26752	Sequence 26752, A
c 38	31.4	3.1	2205	6	US-10-750-185-27481	Sequence 27481, A
c 39	31.4	3.1	4176	6	US-10-793-626-4262	Sequence 4262, Ap
40	31.4	3.1	149419	7	US-11-112-908-49	Sequence 49, Appl
41	31.4	3.1	166111	7	US-11-112-908-47	Sequence 47, Appl
42	31.2	3.1	1123	6	US-10-750-185-54609	Sequence 54609, A
43	31.2	3.1	1621	6	US-10-750-185-63586	Sequence 63586, A
c 44	31.2	3.1	2988	6	US-10-750-185-30138	Sequence 30138, A
c 45	31.2	3.1	3194	6	US-10-750-185-48072	Sequence 48072, A
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## ALIGNMENTS

RESULT 1
US-10-750-185-25365
; Sequence 25365, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25365
; LENGTH: 1779
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-25365

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Query Match        3.9%; Score 39.2; DB 6; Length 1779;
Best Local Similarity  54.1%; Pred. No. 0.1;
Matches 80; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Qy   704 TGACACTATTCCATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGA 763
         ||||||  ||||| |||||||  ||||   ||| |||||||||||||| |||||||||||
Db   765 TGACATTAATTCGTCTGTGATTTACTGTTATTCTTACTGTATCGGGTTTAATTATATCATTA 824

Qy   764 GCAAGCTAGGAATTGTTTCCCTTCTPACTGGGCACAAATACACGCATTGATTTTTTGCCTGGA 823
         |||||  |||||||||||||||||| ||||||| ||||||||||| ||||||||| ||||||
Db   825 AAAAGCACATGACACTTAGTCTTTTGCTGTCCAAATAAGATAAAATGATTTGTGTCCTTTGT 884

Qy   824 ATAAGTCGGATAGATATATAAAAACAAATTTGT 851
         |||||     ||||||| |||||||| |||||
Db   885 TAACTTATATTTTTAAAAAACAAATGTTGT 912
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RESULT 2
US-10-750-185-39315/c
; Sequence 39315, Application US/10750185

; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER:
; CURRENT FILING DATE:
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39315
; LENGTH: 2464
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-39315

Query Match 50.6%; Score 37.2; DB 6; Length 2464;
Best Local Similarity 3.7%;
Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

Qy 834 AGATATAAAACAAATTGTATGGGTATACACCTCCAACTTTATGATAGTCGTTTTCCTTCC 893
         ||| ||||| ||| | || | | | ||| | || | || | |||| ||
Db 1748 AGAGAAAGGGAAAATTCTGGAATATAAAATGCCATTCTCGATATATCTGCAGTTCAAT 1689

Qy 894 AATTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATTGCTTGAGGAAGAGATACT 953
        | || | | | ||| ||| | | | | | ||| | || || | | | ||
Db 1688 AACAGCAAGCATGAAATTTGTTCTTCCTTGTCCTATTAAATAGTTAAGAGAGACAAAGA 1629

Qy 954 GGAGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAAACTGAGATATGTTCC 1011
         | ||||| ||| || | |||| || ||||||||| ||| ||||| || | | ||
Db 1628 CAAGATGTTAAACGTGGGTAAAGAAATCATTAAAAAACAAACAAACACAGTGTTTTCC 1571

; RESULT 3
US-10-750-185-49060
; Sequence 49060, Application US/10750185
; Publication No. US200502606603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49060
; LENGTH: 872
; TYPE: DNA
; ORGANISM: Bovine 19866881284640
US-10-750-185-49060

Query Match 3.5%; Score 36; DB 6; Length 872;
Best Local Similarity 51.9%;
Matches 81; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

Qy 316 TTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTC 375
         || | |||| || ||||| | |||| || | | | |||| || | || || ||
Db 57 TATTCTCTTATCCACAACCCACACCTCCAAAACTCTTTCCCATATTTATTTTCATTGGG 116

; Qy 376 TTGGCATTGGTTTACCTGCCAGGTCGTTGGATGACAGCAGAAATGTCCAACTTCATAATGGAACC 435
         |||| ||| || || ||| ||||| ||| ||||| ||| | |||| || | | ||| ||
Db 117 TTTATTTCCATTTCCATACACTCCAGTGACTGACTATAGTAAAAATTTGAGAITTTGTAAGGTAACC 176

Qy 436 AAGTAITAAGAAGTTTCCACAITGTTGGGATAAGTGG 471
        || | || || | ||| |||| || ||| | | | ||
Db 177 AAAAATGAGAAAGGTTGGGAAAATGCTCTATTGCGTGG 212

; RESULT 4
US-10-750-185-54610
; Sequence 54610, Application US/10750185
; Publication No. US200502606603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54610
; LENGTH: 1012
; TYPE: DNA
; ORGANISM: Bovine 19866881259787
US-10-750-185-54610

Query Match 3.4%; Score 34.2; DB 6; Length 1012;
Best Local Similarity 54.3%;
Matches 69; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Qy 235 GCTATTATAGCCATCCTCTGACTTTTCTTTACACTCCTTCTGAGGGAAGTAATTCACCCTTA 294
         | ||||| || | ||| |||||| ||||| |||| || ||||| ||| | || || ||
Db 237 GCAAATAAAACCACACAACATTCTTTTATACTTCAGTTAGAGTGTTACATTGACTTTTTT 296

Qy 295 GCAACTCCCATCAACAACATATTTTTTATAAAATTCCAATCCTGGTCGTCATCAACAAAGTCTTG 354
        | | || |||| | | | || ||||||||| || ||||| | || ||||| | | | |
Db 297 AAAAAITTAGATGAATTATATTTTTGTAAGAGTTTCACTTAAGGAGCATAAAAAAAAGAGCATC 356

Qy 355 CCAATGG 361
         |||||||
Db 357 ACAATGG 363

; RESULT 5
US-10-750-185-63875/c
; Sequence 63875, Application US/10750185
; Publication No. US200502606603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1

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;  SEQ ID NO 63875
;    LENGTH: 3609
;    TYPE: DNA
;    ORGANISM: Bovine
US-10-750-185-63875

Qy   237 TATTATAGCATCTCTGACTTTTCTTTTACACTTCTTTCTGAGGGAAGTAATTCACCCTTTAGC 296
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1979 TATTTTAAGCATTTTTCAAAATTACTTCACAGTCTTTTAAGATCATCATTTAATTGCTGCAT 1920

Qy   297 AACTTCCCATCAACAAATATTTTTATAAAATTCCAATCCTGGTC 339
         ||||||||||||||||||||||||||||||||||||||||||||
Db  1919 AACATTCCATGAAGAGAAAATGTTTTTAACTTACATAAGCAATGTC 1877

Query Match             58.3%;  Score 34.2;  DB 6;  Length 3609;
Best Local Similarity   58.3%;  Pred. No. 4.5;
Matches  60;  Conservative   0;  Mismatches   43;  Indels   0;  Gaps   0;

Db  1919 AACATTCCATGAAGAGAAAATGTTTTTAACTTACATAAGCAATGTC 1877

RESULT 6
US-10-750-185-30880
; Sequence 30880, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;    APPLICANT: MMI GENOMICS, INC.
;    APPLICANT: DeNISE, Sue K.
;    APPLICANT: KERR, Richard
;    APPLICANT: ROSENFELD, David
;    APPLICANT: HOLM, Tom
;    APPLICANT: BATES, Stephen
;    APPLICANT: FANTIN, Dennis
;    TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;    FILE REFERENCE: MMI1100-2
;    CURRENT APPLICATION NUMBER: US/10/750,185
;    CURRENT FILING DATE: 2003-12-31
;    PRIOR APPLICATION NUMBER: US 60/437,482
;    PRIOR FILING DATE: 2002-12-31
;    NUMBER OF SEQ ID NOS: 64922
;    SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30880
;    LENGTH: 1240
;    TYPE: DNA
;    ORGANISM: Bovine   1986688120871
US-10-750-185-30880

Query Match             46.9%;  Score 34;  DB 6;  Length 1240;
Best Local Similarity   46.9%;  Pred. No. 2.9;
Matches 106;  Conservative   0;  Mismatches 120;  Indels   0;  Gaps   0;

Qy   125 TGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCCTTCAGAAACTTC 184
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 TGCTGTTGCTGCTGCTAAGTTCTTCAGTCGTGTCTGTGCGACCCCATAGACTGC 360

Qy   185 AGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAATAGTCGTCTATTATAG 244
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 AGCCCACCAGGCTCCCCATCCTACTTTGCTACTTCCCCAGAATTAAGCTATAGAGCACAGAA 420

Qy   245 CATCTCTGACTTTTCTTTTACACTCTTTCTGAGGGAAGTAATTCACCCTTTAGCCAACTTCCC 304
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CCAACCTGTCCCATTTTTCATGTCCTCCATTCTGAAGCAACTGCTGTTTTCTGAAACTTTTC 480

Qy   305 ATCAACAATATTTTTATAAAAATTCCAATCCTCGGTCATCACAAAGT 350
         |||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AATTGCATCAATATATTCCATTTCTCAAATATTTATCTACACACAGT 526
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```
;    APPLICANT: Andarmani, Susan
;    APPLICANT: Tang, Y. Tom
;    TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
;    FILE REFERENCE: 821A
;    CURRENT APPLICATION NUMBER: US/10/821,234
;    CURRENT FILING DATE: 2004-04-07
;    PRIOR APPLICATION NUMBER: US 60/462,047
;    PRIOR FILING DATE: 2003-04-07
;    NUMBER OF SEQ ID NOS: 1704
;    SOFTWARE: Pt_SEQ_genes Version 1.0
; SEQ ID NO 142
;    LENGTH: 1458
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-10-821-234-142

Query Match             47.1%;  Score 33.8;  DB 6;  Length 1458;
Best Local Similarity   47.1%;  Pred. No. 3.6;
Matches 104;  Conservative   0;  Mismatches 117;  Indels   0;  Gaps   0;

Qy    12 AAAAGACATCACAAACACCAAGAAGAACTTTGAAAAATGAAGCTAGGAGAAATTTAGAAGA 71
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   287 AAGACGCAAGTCCCATGAAGCTGAGGTCTTGAAGCAGCTGGCTGAGAAAACGAGAGCACGA 346

Qy    72 AGACGATTATTTGCATAAGGACACGGGAGAGAGACCAGCCATGCTAAAAAGAACCTGTGCTTTT 131
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   347 GAAAGAAGTGCTTCAGAGGCAATAGAAGAGAACAACACTTCAGTAAAATGGCAGAAGA 406

Qy   132 GCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACAC 191
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   407 GAAACTGACCCACCAAAATGGAAGCTAATAAACAGGAGAGACCGAGAGGCACAAATGGCTGCAA 466

Qy   192 ACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAG 232
         |||||||||||||||||||||||||||||||||||||||||
Db   467 ACTGGAACGTTTGCGAGGAATAAGCACATTGAAGAAG 507

RESULT 8
US-10-750-185-48714
; Sequence 48714, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;    APPLICANT: MMI GENOMICS, INC.
;    APPLICANT: DeNISE, Sue K.
;    APPLICANT: KERR, Richard
;    APPLICANT: ROSENFELD, David
;    APPLICANT: HOLM, Tom
;    APPLICANT: BATES, Stephen
;    APPLICANT: FANTIN, Dennis
;    TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;    FILE REFERENCE: MMI1100-2
;    CURRENT APPLICATION NUMBER: US/10/750,185
;    CURRENT FILING DATE: 2003-12-31
;    PRIOR APPLICATION NUMBER: US 60/437,482
;    PRIOR FILING DATE: 2002-12-31
;    NUMBER OF SEQ ID NOS: 64922
;    SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48714
;    LENGTH: 2748
;    TYPE: DNA
;    ORGANISM: Bovine   1986880696598
US-10-750-185-48714

Query Match             57.7%;  Score 33.3;  DB 6;  Length 2748;
Best Local Similarity   57.7%;  Pred. No. 5;
Matches  79;  Conservative   0;  Mismatches  57;  Indels   1;  Gaps   1;

Qy   789 ACTGGGCCACAATACACGCCATTGATTTTGCCTGGGATAAGTGGATAGATATAAAACAATT 848
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   666 ACTGGATAGGATCGACATGCCATTCTTCTTTCTTTGACTCTCTCTAAATGAGCTTAAGC-ATT 724

Qy   849 TGTATGGTATACACCTCCAACTTTTATGATTAGCTGTTTTCCTTCCAAATTGTTGTCCTGAT 908
         |||||||||  ||              |||||       ||||  ||  |||  |||  ||
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Db   725 TGTATGGCATTTGTCTACAATTAGCATGATGATAGTAGGTAGTAGTACGCTAAAATCTGGGGTAAAT 784
Qy   909 ATTTTAAAAGCATACTAT 925
Db   785 TTCTAAAAACCAAAAACT 801
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RESULT 9
US-10-750-185-38532/c
Sequence 38532, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 38532
; LENGTH: 1840
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-38532
1986688135203T

Query Match   3.3%; Score 33.4; DB 6; Length 1840;
Best Local Similarity   58.6%; Pred. No. 5.3;
Matches   58; Conservative   0; Mismatches 41; Indels   0; Gaps   0;

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Qy   836 ATATAAAACAAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTTCCTTCCAA 895
Db  1252 ATATGAAAATTGTATTGCTTTTGACTTATAACTTTTAATACCTCTTTTTTTTTTTTTCAGA 1193

Qy   896 TTGTTGTCCTGATATTTAAAAGCATACTAATTCCTGCCAT 934
Db  1192 TATCTTTGCTTAACTTCAAAGAATCAGAATTAATCCAAT 1154
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RESULT 10
US-10-750-185-35293
Sequence 35293, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 35293
; LENGTH: 973
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-35293
1986881541753

Query Match   3.3%; Score 33.2; DB 6; Length 973;

Best Local Similarity   57.8%; Pred. No. 4.3;
Matches   59; Conservative   0; Mismatches 43; Indels   0; Gaps   0;

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Qy   870 TTTTATGATAGCTGTTTTTCCTTCCAAATTGTTGTTCCTGATATTTAAAAGCATACTATTCCT 929
Db   844 TTTTTTTAACAGCTTGGTTACAGCTCATAGTTTTTATCAGTAAAACAAAAGGATAGTAGTACACCC 903

Qy   930 GCCATGCTTGAGGAGAGAAGATACTGAAGATTAGACATGGTTG 971
Db   904 CCCAGGCGTGAGGGTGGAGATCCCAAAAGGAGGAGGGCCTGTATG 945
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RESULT 11
US-11-102-978-3/c
Sequence 3, Application US/11102978
; Publication No. US20050250142A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Technology Transfer Office
; APPLICANT: University of Utah Research Foundation
; TITLE OF INVENTION: Diagnosis and Treatment of Herpes Simplex Virus Disease
; FILE REFERENCE: 0274-5537.1US
; CURRENT APPLICATION NUMBER: US/11/102,978
; CURRENT FILING DATE: 2005-04-11
; PRIOR APPLICATION NUMBER: PCT/US2003/033152
; PRIOR FILING DATE: 2003-10-18
; PRIOR APPLICATION NUMBER: 60/419,576
; PRIOR FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; LENGTH: 340000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: (56948)..(57115)
; OTHER INFORMATION: C21orf34 exon
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (80006)..(81089)
; OTHER INFORMATION: Gene VDAC22; voltage-dependent anion channel isoform 2 pseudogene
; FEATURE:
; NAME/KEY: exon
; LOCATION: (167308)..(167438)
; OTHER INFORMATION: C21orf34 exon
; FEATURE:
; NAME/KEY: exon
; LOCATION: (216732)..(216833)
; OTHER INFORMATION: C21orf34 exon
US-11-102-978-3

Query Match   3.3%; Score 33.2; DB 7; Length 340000;
Best Local Similarity   52.1%; Pred. No. 0;
Matches   74; Conservative   0; Mismatches 68; Indels   0; Gaps   0;

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Qy   746 AATTTCACTATATTCAGAGCAAGCTAGGAATTGTTTCCCTTCTACTGGGCACAATACACG 805
Db  9668 AATTAAGATATCATAGGTCAAGTTACACAAATTTACACCTTTTTATTGGTCATAAGTCACA 9609

Qy   806 CATTGATTTTGCCTGGAATAAGTGGATAGATATAAAACAAATTTGTATGGTATACACCTC 865
Db  9608 CAGTAGCATATTTATTTGTCATTTAATTGATTCAAAACCAAAAATATATGTTACCCTT 9549

Qy   866 CAACTTTTATGATAGCTGTTTT 887
Db  9548 CTATTGCTTAAGCCAGGTATTAT 9527
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RESULT 12
US-11-108-172-547/c
Sequence 547, Application US/11108172
; Publication No. US20050260177A1
; GENERAL INFORMATION:
```

; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C15
; CURRENT APPLICATION NUMBER: US/11/108,172
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 10/025,380
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 09/922,217
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 09/833,263
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 09/649,811
; PRIOR FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: US 09/609,448
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/575,251
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/519,444
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 09/504,629
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: US 09/480,321
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: US 09/476,296
; PRIOR FILING DATE: 1999-12-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1130
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 547
; LENGTH: 399
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-108-172-547

Query Match   3.2%;   Score 32.8;   DB 7;   Length 399;
Best Local Similarity   55.8%;   Pred. No. 3.5;
Matches   58;   Conservative   2;   Mismatches   44;   Indels   0;   Gaps   0;

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Qy     5 AAAGCAGAAAAAGACATCACAAAACCAAGAAGAACTTTGGAAAAATGAAGCCTAGGAGAAATT 64
         ||| |||||  | ||| ||     |||| || ||||||||||  ||||| | ||| ||| ||
Db   115 AAAGTAAAAATGTAATAAATTAGAAAAAGTTTGGTAAAATTCAACACCTACGAATGA 56

Qy    65 TAGAAGAAGACGAGTTATTTGCATAAGGACACGGGAGGAGACCAGC 108
         |||||||| | ||| |||||| |  |  |||  | | |||||| ||
Db    55 TAGAACACCAAGAGWRTYTATTAGAAGAAAACTTTTGAGACCTGC 12
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RESULT 13
US-10-185-58068
Sequence 58068, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom

; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58068
; LENGTH: 1135
; TYPE: DNA
; ORGANISM: Bovine   198668381974092
US-10-750-185-58068

Query Match   3.2%;   Score 32.8;   DB 6;   Length 1135;
Best Local Similarity   49;   Conservative   0;   Mismatches   27;   Indels   0;   Gaps   0;

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Qy   443 AGAAGTTTCCACATTGGTTGGGATAAGTGGATTGGTAGTTAACAGAAGAAGCAGTTTGGGCTTCTCA 502
         || |||||||||| |||| ||| ||||   | ||| |||| ||| |||||| |||||||||||| |||
Db   314 ATAAACTTTCACATTTCATCATCATCARAAGGAAAGCAACAAGAAAATATTTTGTGTTTTGGTTA 373

Qy   503 GTTTCTTTTTTGCTGT 518
         ||||||||||| | ||
Db   374 GTTTCTTTTTTTTTTT 389
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RESULT 14
US-10-185-54184
Sequence 54184, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54184
; LENGTH: 1765
; TYPE: DNA
; ORGANISM: Bovine   198668038404477
US-10-750-185-54184

Query Match   3.2%;   Score 32.8;   DB 6;   Length 1765;
Best Local Similarity   64.5%;   Pred. No. 7.8;
Matches   49;   Conservative   0;   Mismatches   27;   Indels   0;   Gaps   0;

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Qy   479 CAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTTGCTGTACTCGCATGCAAATTTATAGTC 538
         |||||| ||||||||||  || |  |||| ||||||||| ||| ||| | ||||||||| |||||
Db    45 CAAGTAAATATTTTGAAGTTCTCATTCATCTACTTCTTTTTCTTTTCTGCATGCCAAGGACAGTG 104
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RESULT 15
US-10-501-27/c
Sequence 27, Application US/10986501
Publication No. US20050244845A1
GENERAL INFORMATION:

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Qy   539 TGTCTTACCCAATGAG 554
         |||||||||||||||
Db    45 CAAGTAAATATTTTGAAGTTCTCATTCATCTACTTCTTTTTCTTTTCTGCATGCCAAGGACAGTG 104
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RESULT 15
US-10-986-501-27/c
; Sequence 27, Application US/10986501
; Publication No. US20050244845A1
; GENERAL INFORMATION:

; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: PZ013P2C1
; CURRENT APPLICATION NUMBER: US/10/986,501
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US/10/621,363
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/969,730
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 09/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: Patentin Ver. 2.0
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; SEQ ID NO 27
;   LENGTH: 1307
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-986-501-27

Query Match   3.2%;   Score 32.4; DB 6;   Length 1307;
Best Local Similarity   50.5%;   Pred. No. 8.7;
Matches 111; Conservative 0; Mismatches 101; Indels   8; Gaps   1;

Qy   590 ATCAACAGGTCCAACAAAATAAAGAAGAATGCCTGGATTGAGCATGAATGTTTGGAGAATGG 649
               || ||||||| |||||| || ||| |||||||
Db   573 ATCCACAGGTGTGGCAAAATGGAGAAGACCTCCTGATTGAACTGATTGATTTATTAAACCA 514

Qy   650 AGATTTATGTGTCTCTGGGGAATTGTGGGATTGGCAATACTGGCCTCTGTTGGCTGTGACAT 709
               ||| | || ||||||||| | ||| ||| ||| ||| |||| || | |||
Db   573 AGAATGGTGTTTTTTCCTTGAAAAACTTTTACTTCAAACACAGCTGCTTGTA------GACAC 462

Qy   710 CTATTCCATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGC 769
               ||||| ||| |||||| ||| || || || | |||
Db   461 ATATTGACAAGTAAAATGGCTCCTTCTCCTGACAGGGGTTACCAGTTTTACAAACATT 402

Qy   770 TAGGAATTGTTTCCCTTCTACTGGGCACAAATACACGCATT 809
               ||||| ||| || | || |||
Db   401 AGCCCATTTTTCATCTTCTTTGAAGCATCTTTTAAATATT 362

Search completed: December 5, 2005, 08:05:52
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OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on:　　December 5, 2005, 00:23:57 ; Search time 949.415 Seconds
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Scoring table: IDENTITY_NUC
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Searched:　　9793542 seqs, 413469005 residues
Total number of hits satisfying chosen parameters:　19587084

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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　　　　　　　　　　Listing first 45 summaries

Database : Published Applications NA Main:*
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　　/cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	1017	100.0	1177	8	US-10-696-639-15	Sequence 15, Appl
2	1017	100.0	1193	6	US-10-165-044-1	Sequence 1, Appli
3	1017	100.0	1193	6	US-10-408-009-1	Sequence 1, Appli
4	1017	100.0	1193	7	US-10-857-785-1	Sequence 1, Appli
5	1017	100.0	1193	8	US-10-856-109-1	Sequence 1, Appli
6	1017	100.0	1193	8	US-10-930-899-2	Sequence 2, Appli
7	1017	100.0	1193	8	US-10-753-195-1	Sequence 1, Appli
8	1017	100.0	1193	9	US-10-752-421-1	Sequence 1, Appli
9	1017	100.0	1193	9	US-10-861-662-2	Sequence 2, Appli
10	1017	100.0	1195	3	US-09-759-143-878	Sequence 878, App
11	1017	100.0	1195	3	US-09-780-669-878	Sequence 878, App
12	1017	100.0	1195	3	US-09-822-827-878	Sequence 878, App
13	1017	100.0	1195	3	US-09-895-793-878	Sequence 878, App
14	1017	100.0	1195	5	US-09-895-814-878	Sequence 878, App
15	1017	100.0	1195	5	US-10-012-996-878	Sequence 878, App
16	1017	100.0	1195	5	US-10-011-095-1	Sequence 1, Appli
17	1017	100.0	1195	5	US-10-010-667A-1	Sequence 1, Appli
18	1017	100.0	1195	5	US-10-205-823-396	Sequence 396, App
19	1017	100.0	1195	6	US-10-144-678A-878	Sequence 878, App
20	1017	100.0	1195	6	US-10-294-025-878	Sequence 878, App
21	1017	100.0	1195	6	US-10-393-590-35	Sequence 35, Appl
22	1017	100.0	1195	6	US-10-393-567-35	Sequence 35, Appl
23	1017	100.0	1195	6	US-10-394-087-35	Sequence 35, Appl
24	1017	100.0	1195	6	US-10-295-027-713	Sequence 713, App
25	1017	100.0	1195	6	US-10-295-027-1130	Sequence 1130, Ap
26	1017	100.0	1195	8	US-10-643-795A-16	Sequence 16, Appl
27	1017	100.0	1195	8	US-10-643-795A-42	Sequence 42, Appl
28	1017	100.0	1195	6	US-10-750-262-1	Sequence 1, Appli
29	1017	100.0	1195	9	US-10-948-518-16	Sequence 16, Appl
30	1017	100.0	1195	9	US-10-948-518-42	Sequence 42, Appl
31	1017	100.0	1195	9	US-10-956-157-1811	Sequence 1811, Ap
32	1017	100.0	1195	9	US-10-956-157-7046	Sequence 7046, Ap
33	1017	100.0	1195	8	US-10-858-887-1	Sequence 1, Appli
34	1017	100.0	1195	9	US-10-631-467-428	Sequence 428, App
35	1017	100.0	1177	7	US-11-051-454-396	Sequence 396, App
36	1017	100.0	1201	7	US-10-425-114-16645	Sequence 16645, A
37	1017	100.0	1277	3	US-09-814-353-19910	Sequence 19910, A
38	1017	100.0	1330	7	US-10-755-889-191	Sequence 191, App
39	988	97.1	1354	8	US-10-723-860-5120	Sequence 5120, Ap
40	870	85.5	1365	8	US-10-830-899-6	Sequence 6, Appli
41	870	85.5	1365	9	US-10-948-518-42	Sequence 42, Appli
42	762.2	74.9	1365	8	US-10-861-662-6	Sequence 6, Appli
43	762.2	74.9	3627	8	US-10-861-662-10	Sequence 10, Appl
44	760.6	74.8	3627	6	US-10-011-095-6	Sequence 6, Appli
45	760.6	74.8	3627	5	US-10-010-667A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-10-696-639-15
; Sequence 15, Application US/10696639
; Publication No. US2005003743941
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corporation
; APPLICANT: Bourner, Maureen J.
; TITLE OF INVENTION: DIFFERENTIALLY EXPRESSED GENES INVOLVED IN CANCER, THE
; TITLE OF INVENTION: POLYPEPTIDES ENCODED THEREBY, AND METHODS OF USING THE SAME
; FILE REFERENCE: 01040/1
; CURRENT APPLICATION NUMBER: US/10/696,639
; CURRENT FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/422,176
; PRIOR FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 3114
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 15
; LENGTH: 1177
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-696-639-15

Query Match　　100.0%;　Score 1017;　DB 8;　Length 1177;
Best Local Similarity 100.0%;　Pred. No. 6.9e-277;
Matches 1017;　Conservative 0;　Mismatches 0;　Indels 0;　Gaps 0;

Qy　　　1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
　　　　　 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　　66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy　　　61 AATTTAGAAGAAGAACGAТTАTTTGCATAAGGACACCGGGAGAGAGACCAGCATGCTAAAAGA 120
　　　　　 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　　126 AATTTAGAAGAAGACGAТTАTTTGCATAAGGACACCGGGAGAGAGACCAGCATGCTAAAAGA 185

Qy　　　121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTCAGAA 180
　　　　　 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　　186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTCAGAA 245

Qy　　　181 CTTCAGCACACACAGGAGAACTCTTTCCACAGTGGCACTTGCCAAATTAAAATAGCTGCTATT 240
　　　　　 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　　246 CTTCAGCACACACAGGAGAACTCTTTCCACAGTGGCACTTGCCAAATTAAAATAGCTGCTATT 305

Qy　　　241 ATAGCACATCTCTGACTTTCTTCTTTACACTCTTCTGAGGGAAGTAAATTCACCCTTTAGCAACT 300
　　　　　 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　　306 ATAGCATCTCTGACTTTCTTCTTTACACTCTTCTGAGGGAAGTAAATTCACCCTTTAGCAACT 365

```
Qy    301  TCCCATCAACACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG  360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    366  TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG  425

Qy    361  GTTTCCATCACTCTCTTGGCATTGGTTACCTGCTGCAGGTGTGATAGCAGCAAATTGTCCAA  420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    426  GTTTCCATCACTCTCTTGGCATTGGTTACCTGCTGCCAGGTGTGATAGCAGCAAATTGTCCAA  485

Qy    421  CTTCATAATGGAACCAAAGTAATAAGAAAGTTTCCCACAATTGGTTTGGGATAAAGTGGATGTTAACA  480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    486  CTTCATAATGGAACCAAAGTAATAAGAAAGTTTCCCACAATTGGTTTGGGATAAAGTGGATGTTAACA  545

Qy    481  AGAAAGCAGTTTGGGCCTTCTCCAGTTTCTTTTTTTGCTGTAGTGGATAGCAGCAAATTTATAGTCTG  540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    546  AGAAAGCAGTTTGGGCCTTCTCCAGTTTCTTTTTTTGCTGTAGTGGATAGCAGCAAATTTATAGTCTG  605

Qy    541  TCTTACCCAATGAGGCGGATCCTACAGATACAAAGTTGCTAAAACTGGGCATATCAACACAGGTC  600
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Db    606  TCTTACCCAATGAGGCGGATCCTACAGATACAAAGTTGCTAAAACTGGGCATATCAACACAGGTC  665

Qy    601  CAACAAAATAAAGAGAAGATGCCTGGATTGAGCGATTGAGAGAATGGAGAATTCACTATATTTATGTG  660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    666  CAACAAAATAAAGAGAAGATGCCTGGATTGAGCGATTGAGAGAATGGAGAATTCACTATATTTATGTG  725

Qy    661  TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTCGTTGGCCTGTTGACATCTTATTCCATCT  720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    726  TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTCGTTGGCCTGTTGACATCTTATTCCATCT  785

Qy    721  GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGAGCAAGCTAGGAATTGTT  780
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    786  GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGAGCAAGCTAGGAATTGTT  845

Qy    781  TCCCTTCTACTGGGCCACAATACACGCCATTGGTGATGAATTTGACTGCCCTTCAGAA  840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    846  TCCCTTCTACTGGGCCACAATACACGCCATTGGTGATGAATTTGACTGCCCTTCAGAA  905

Qy    841  AAACAAATTTGTATGGGTATACACCTTCCAACTCTTTATGAGCTGTTTTCCTTCCCAATTGTT  900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    906  AAACAAATTTGTATGGGTATACACCTTCCAACTCTTTATGAGCTGTTTTCCTTCCCAATTGTT  965

Qy    901  GTCCTGATATTTAAAAGCATAACTACTGAAGATT  1025
           ||||||||||||||||||||||||||||||||||
Db    966  GTCCTGATATTTAAAAGCATAACTACTGAAGATT  1025

Qy    961  AGACATGGTTGGGAAGAGACGTCACCAAAAAATTAACAAAAACTGAGAGATAATGTTCCCAGTTG  1017
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1026 AGACATGGTTGGGAAGAGACGTCACCAAAAAATTAACAAAAACTGAGAGATAATGTTCCCAGTTG  1082
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Query Match            100.0%;   Score 1017;  DB 6;  Length 1193;
Best Local Similarity  100.0%;   Pred. No. 7e-277;
Matches 1017;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Qy    1    ATGGAAAGCAGAAAAAGACCATCACAAACCAAGAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA  60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    64   ATGGAAAGCAGAAAAAGACCATCACAAACCAAGAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA  123

Qy    61   AAATTTAGAAGAGACCAATTATTTTGCATAAGACACCAGGAGGAGAGACCAGCATGCTAAAAAGA  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    124  AAATTTAGAAGAGACCAATTATTTTGCATAAGACACCAGGAGGAGAGACCAGCATGCTAAAAAGA  183

Qy    121  CCTGTGTCTTTTGCATTTGACAAACAGCCCATGTCATGAATTTGGACTGCCCTTCAGAA  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    184  CCTGTGTCTTTTGCATTTGACAAACAGCCCATGTCATGAATTTGGACTGCCCTTCAGAA  243

Qy    181  CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    244  CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT  303

Qy    241  ATAGCATCTCGACTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAACTAACT  300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    304  ATAGCATCTCGACTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAACTAACT  363

Qy    301  TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG  360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    364  TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG  423

Qy    361  GTTTCCATCACTCTCTTGGCATTGGTTACCTGCTGCCAGGTGTGATAGCAGCAAATTGTCCAA  420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    424  GTTTCCATCACTCTCTTGGCATTGGTTACCTGCTGCCAGGTGTGATAGCAGCAAATTGTCCAA  483

Qy    421  CTTCATAATGGAACCAAAGTAATAAGAAAGTTTCCCACAATTGGTTTGGGATAAAGTGGATGTTAACA  480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    484  CTTCATAATGGAACCAAAGTAATAAGAAAGTTTCCCACAATTGGTTTGGGATAAAGTGGATGTTAACA  543

Qy    481  AGAAAGCAGTTTGGGCCTTCTCCAGTTTCTTTTTTTGCTGTAGTGGATAGCAGCAAATTTATAGTCTG  540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    544  AGAAAGCAGTTTGGGCCTTCTCCAGTTTCTTTTTTTGCTGTAGTGGATAGCAGCAAATTTATAGTCTG  603

Qy    541  TCTTACCCAATGAGGCGGATCCTACAGATACAAAGTTGCTAAAACTGGGCATATCAACACAGGTC  600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    604  TCTTACCCAATGAGGCGGATCCTACAGATACAAAGTTGCTAAAACTGGGCATATCAACACAGGTC  663

Qy    601  CAACAAAATAAAGAGAAGATGCCTGGATTGAGCGATTGAGAGAATGGAGAATTCACTATATTTATGTG  660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    664  CAACAAAATAAAGAGAAGATGCCTGGATTGAGCGATTGAGAGAATGGAGAATTCACTATATTTATGTG  723

Qy    661  TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTCGTTGGCCTGTTGACATCTTATTCCATCT  720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    724  TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTCGTTGGCCTGTTGACATCTTATTCCATCT  783

Qy    721  GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGAGCAAGCTAGGAATTGTT  780
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    784  GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGAGCAAGCTAGGAATTGTT  843
```

RESULT 3
US-10-408-009-1
Sequence 1, Application US/10408009
Publication No. US20040072196A1
GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; APPLICANT: Stephen C. Mitchell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 51158201603
; CURRENT APPLICATION NUMBER: US/10/408,009
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 09/455,486
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/323,873
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)...(1083)

Query Match   100.0%;   Score 1017;   DB 7;   Length 1193;
Best Local Similarity   100.0%;   Pred. No. 7e-277;
Matches 1017;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

```
Qy      1 ATGGAAAGCAGAAAAAGACATCACAAACCAGAGAAGAGAACTTTGGAAAATGAAGCCTAGGAGA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     64 ATGGAAAGCAGAAAAAGACATCACAAACCAGAGAAGAGAACTTTGGAAAATGAAGCCTAGGAGA 123

Qy     61 AATTTAGAAGAAGAGACGATTATTTGCATAAGGACACCGGGAGGAGAGAGACCAGCATGCTAAAGCCTAGGAGA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    124 AATTTAGAAGAAGAGACGATTATTTGCATAAGGACACCGGGAGGAGAGAGACCAGCATGCTAAAAAGA 183

Qy    121 CCTGTGCTTTTGCATTTGCACCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    184 CCTGTGCTTTTGCATTTGCACCCATGCTGATGAATTTGACTGCCCTTCAGAA 243

Qy    181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    244 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 303

Qy    241 ATAGCATCTCTGACTTTTCTTCTTACACTCCCTTTAGCAACT 300
          ||||||||||||||||||||||||||||||||||||||||
Db    304 ATAGCATCTCTGACTTTTCTTCTTACACTCCCTTTAGCAACT 363

Qy    301 TCCCATCAACAATATTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    364 TCCCATCAACAATATTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 423
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RESULT 4
US-10-857-785-1
Sequence 1, Application US/10857785
Publication No. US20040219162A1
GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; APPLICANT: Stephen C. Mitchell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 51158201607
; CURRENT APPLICATION NUMBER: US/10/857,785
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: US 09/455,486
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 09/323,873
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: US 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: US 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1

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Db    364 TCCCATCAACAATATTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 423
          
Qy    361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCGCCAGGTGTGATAGAGCAATTGTCCAA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    424 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCGCCAGGTGTGATAGAGCAATTGTCCAA 483

Qy    421 CTTCATAATGGAAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTAACA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    484 CTTCATAATGGAAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTAACA 543

Qy    481 AGAAAGCAGTTTGGGCTTCCACGTTTCTTTGCTGTACTGCATGCAAATTTATAGTCTG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    544 AGAAAGCAGTTTGGGCTTCCACGTTTCTTTGCTGTACTGCATGCAAATTTATAGTCTG 603

Qy    541 TCTTACCCAATGAGGCCGATCCTTACAGATACAAGTTGCTAAACTGGGCCATATCAACAGGTC 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    604 TCTTACCCAATGAGGCCGATCCTTACAGATACAAGTTGCTAAACTGGGCCATATCAACAGGTC 663

Qy    601 CAACAAAATAAAAGAAGATGCCTGGATTGAGCAATGACATGATGTTTGAGAATGGAGAGATTTAGTG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    664 CAACAAAATAAAAGAAGATGCCTGGATTGAGCAATGACATGATGTTTGAGAATGGAGAGATTTAGTG 723

Qy    661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCCTCTGTTGGCTGTGACATCTATTCCATCT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    724 TCTCTGGGAATTGTGGGATTGGCAATACTGGCCTCTGTTGGCTGTGACATCTATTCCATCT 783

Qy    721 GTGAGTGACTCTTTGACATGGAGAGAATTCACTATATATCAGAGCAAGCACTAGGAATTGTT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    784 GTGAGTGACTCTTTGACATGGAGAGAATTCACTATATATCAGAGCAAGCACTAGGAATTGTT 843

Qy    781 TCCCTTCTACTCGGGGCACAATACACACGCCATTGATTTGATTTTTGCCTGGAATAATGGAATAAGTAGTAGAGATATA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    844 TCCCTTCTACTCGGGGCACAATACACACGCCATTGATTTGATTTTTGCCTGGAATAATGGAATAAGTAGTAGAGATATA 903

Qy    841 AAACAATTTGTATGGTATACACCTCCAACTTTATGATAGCTGTGTTTTTTCCTTCCAATTGTT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    904 AAACAATTTGTATGGTATACACCTCCAACTTTATGATAGCTGTGTTTTTTCCTTCCAATTGTT 963

Qy    901 GTCCTGATATTTAAAGCATACTATTCCTGCCCATGCTTGAGGAGAGAGAGATACTGAAGATT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    964 GTCCTGATATTTAAAGCATACTATTCCTGCCCATGCTTGAGGAGAGAGAGATACTGAAGATT 1023

Qy    961 AGACATGGTTGGGAAGCAGACGTCACCCAAAAATTAACAAAAACTGAGATATGTTCCCAGTTG 1017
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1024 AGACATGGTTGGGAAGACGTCACCCAAAAATTAACAAAAACTGAGATATGTTCCCAGTTG 1080
```

; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)...(1083)
US-10-857-785-1

Query Match   100.0%;   Score 1017; DB 8; Length 1193;
Best Local Similarity   100.0%;   Pred. No.7e-277;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1  ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTGGAAAATGAAGCCTAGGAGA   60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     64  ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTGGAAAATGAAGCCTAGGAGA  123

Qy     61  AATTTAGAGAAGACGATTATTTGCATAAGGACACGGGAGACCAGCATGCTAAAAAGA   120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    124  AATTTAGAGAAGACGATTATTTGCATAAGGACACGGGAGACCAGCATGCTAAAAAGA  183

Qy    121  CCTGTGCTTTTGCATTGCACCAAACAGCCCATGCTGATGAAATTTGACTGCCCTTCAGAA  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    184  CCTGTGCTTTTGCATTGCACCAAACAGCCCATGCTGATGAAATTTGACTGCCCTTCAGAA  243

Qy    181  CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    244  CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT  303

Qy    241  ATAGCATCTCTGACTTTCTTTACACTCTTCTGAGGGAAGTAAATTCACCCTTTAGCAACT  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    304  ATAGCATCTCTGACTTTCTTTACACTCTTCTGAGGGAAGTAAATTCACCCTTTAGCAACT  363

Qy    301  TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG  360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    364  TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG  423

Qy    361  GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA  420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    424  GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA  483

Qy    421  CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA  480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    484  CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA  543

Qy    481  AGAAAGCAGTTTGGGCTTCCAGTTTCTTTTTGCTGTACTGCATGCAATTTATAGTCTG   540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    544  AGAAAGCAGTTTGGGCTTCCAGTTTCTTTTTGCTGTACTGCATGCAATTTATAGTCTG  603

Qy    541  TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC  600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    604  TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC  663

Qy    601  CAACAAAATAAAGAAGATGAGCATGATGAGTTGGGAGAAATGAGAGATTTTATGTG   660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    664  CAACAAAATAAAGAAGATGAGCATGATGAGTTGGGAGAAATGAGAGATTTTATGTG  723

Qy    661  TCTCTGGGAATTGTGGGATTGGCAATACTCGGCTCTCGTTGCCTCGTTGCCTCTATTCCATCT  720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    724  TCTCTGGGAATTGTGGGATTGGCAATACTCGGCTCTCGTTGCCTCGTTGCCTCTATTCCATCT  783

Qy    721  GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGGAAGCAAGCTAGGAATT  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    784  GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGGAAGCAAGCTAGGAATT  843

Qy    781  TCCCTTCTACTGGGGCACAATACACCGCCATTGATTTTTTGCCTTGGAATAAGTGGATAGAATATA  840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    844  TCCCTTCTACTGGGGCACAATACACCGCCATTGATTTTTTGCCTTGGAATAAGTGGATAGAATATA  903

Qy    841  AAACAAATTTGTATGGTATACACCTCCACACTTTATGATGAGCTGTTTCCTTCCTGAAGATT  900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    904  AAACAAATTTGTATGGTATACACCTCCACACTTTATGATGAGCTGTTTCCTTCCTGAAGATT  963

Qy    901  GTCCTGATATTTAAAAGCATACTATTCCTGCCATCCTTGAGGAAGAAGATACTGAAAGATT  960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    960
```

RESULT 5
US-10-856-109-1
Sequence 1, Application US/10856109
Publication No. US20040219591A1
GENERAL INFORMATION:
; APPLICANT: Daniel B. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; APPLICANT: Stephen C. Mitchell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 511582001606
; CURRENT APPLICATION NUMBER: US/10/856,109
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: US 09/455,486
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 09/323,873
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: US 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: US 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)...(1083)
US-10-856-109-1

Query Match   100.0%;   Score 1017; DB 8; Length 1193;
Best Local Similarity   100.0%;   Pred. No.7e-277;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1  ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTGGAAAATGAAGCCTAGGAGA   60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     64  ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTGGAAAATGAAGCCTAGGAGA  123

Qy     61  AATTTAGAGAAGACGATTATTTGCATAAGGACACGGGAGACCAGCATGCTAAAAAGA   120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    124  AATTTAGAGAAGACGATTATTTGCATAAGGACACGGGAGACCAGCATGCTAAAAAGA  183

Qy    121  CCTGTGCTTTTGCATTGCACCAAACAGCCCATGCTGATGAAATTTGACTGCCCTTCAGAA  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    184  CCTGTGCTTTTGCATTGCACCAAACAGCCCATGCTGATGAAATTTGACTGCCCTTCAGAA  243

Qy    181  CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    244  CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT  303

Qy    241  ATAGCATCTCTGACTTTCTTTACACTCTTCTGAGGGAAGTAAATTCACCCTTTAGCAACT  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    304  ATAGCATCTCTGACTTTCTTTACACTCTTCTGAGGGAAGTAAATTCACCCTTTAGCAACT  363

Qy    301  TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG  360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    364  TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG  423

Qy    361  GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA  420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    424  GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA  483
```

; RESULT 6
; US-10-830-899-2
; Sequence 2, Application US/10830899
; Publication No. US20040252232A1
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Etessami, Soudabeh
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Perez-Villar, Juan
; APPLICANT: Meyrick Morrison, Karen Jane
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Faris, Mary
; APPLICANT: Gudas, Jean
; APPLICANT: Raitano, Arthur B.
; TITLE OF INVENTION: Antibodies and Molecules Derived
; TITLE OF INVENTION: therefrom that Bind to STEAP-1 Proteins
; FILE REFERENCE: 51158-20016.26
; CURRENT APPLICATION NUMBER: US/10,830,899
; CURRENT FILING DATE: 2004-04-23
; CURRENT APPLICATION NUMBER: 09/323,873
; CURRENT FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 10/010,667
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 10/011,095
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 10/236,878
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 09/455,486
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 60/091,183
; PRIOR FILING DATE: 1998-06-30

; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO, 2
; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)...(1085)
; US-10-830-899-2

Query Match 100.0%; Score 1017; DB 8; Length 1193;
Best Local Similarity 100.0%; Pred. No. 7e-277;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[DNA sequence alignment — Query (Qy) vs Database (Db) pairs from positions 1/66 through 900/905 and 421/480 through 1024/1080, all positions matching 100%]

RESULT 7
US-10-753-195-1
; Sequence 1, Application US/10753195
; Publication No. US20050004349A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Rene S. Hubert
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas Saffran
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Steven Chappell Mitchell
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 51158-20016.02
; CURRENT APPLICATION NUMBER: US/10/753,195
; CURRENT FILING DATE: 2004-01-06
; PRIOR APPLICATION NUMBER: US/10/165,044
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: US 60/091,183
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 09/323,873
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: US 09/455,486
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: WO 99/62941
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: PCT/US00/33040
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 1
; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)...(1191)
US-10-753-195-1

Query Match   100.0%; Score 1017; DB 8; Length 1193;
Best Local Similarity   100.0%; Pred. No. 7e-277;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ATGGAAAAGCAGAAAGAACATCAAACCAAGAAGAGAACTTTGGAAAATGNAGGCCTAGGAGA 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ATGGAAAAGCAGAAAGAACATCAAACCAAGAAGAGAACTTTGGAAAATGNAGGCCTAGGAGA 120

Qy   61 AATTTAGAAGAAGAACGATTATTTCGCATAAGGACGACGGGAGAGCAAGCTACGGGAGAGA 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AATTTAGAAGAAGAACGATTATTTCGCATAAGGACGACGGGAGAGCAAGCTACGGGAGAGA 180

Qy   121 CCTGTGCTTTTGCATTTGCACCAAAACAGCCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CCTGTGCTTTTGCATTTGCACCAAAACAGCCCCATGCTGATGAATTTGACTGCCCTTCAGAA 240

Qy   181 CTTCAGCACACACAGGAACTCTTTCCACACAGTGGGCACTTGCCAATTAAAATAGCTGCTATT 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CTTCAGCACACACAGGAACTCTTTCCACACAGTGGGCACTTGCCAATTAAAATAGCTGCTATT 303

RESULT 8
US-10-752-421-1
; Sequence 1, Application US/10752421
; Publication No. US20050063975A1
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; APPLICANT: Stephen C. Mitchell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 51158200612
; CURRENT APPLICATION NUMBER: US/10/752,421
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US 09/455,486
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 09/323,873
; PRIOR FILING DATE: 1999-06-01

;   PRIOR APPLICATION NUMBER: US 60/087,520
;   PRIOR FILING DATE: 1998-06-01
;   PRIOR APPLICATION NUMBER: US 60/091,183
;   PRIOR FILING DATE: 1998-06-30
;   NUMBER OF SEQ ID NOS: 47
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1193
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (64)...(1083)
US-10-752-421-1

Query Match   100.0%;   Score 1017;   DB 9;   Length 1193;
Best Local Similarity   100.0%;
Matches 1017;   Conservative   0;   Mismatches   0;   Pred No. 7e-277;   Indels   0;   Gaps   0;

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Qy      1 ATGGAAAAGCAGAAAAAGACAATCACAAAACCAAGAAGAGAACTTTGGAAAATGAAGCCTAGGAGA   60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     64 ATGGAAAAGCAGAAAAAGACAATCACAAAACCAAGAAGAGAACTTTGGAAAATGAAGCCTAGGAGA  123

Qy     61 AATTTAGAAGAAGAACGAGATTATTTGCATAAGGACACGGGAGAGAGACCAGCATGCTAAAAAGA  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    124 AATTTAGAAGAAGAACGAGATTATTTGCATAAGGACACGGGAGAGAGACCAGCATGCTAAAAAGA  183

Qy    121 CCTGTGCTTTTGCATTGACCAAAACAGCCCATGCTGATGAATTTGACTGCCCCTTCAGAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    184 CCTGTGCTTTTGCATTGACCAAAACAGCCCATGCTGATGAATTTGACTGCCCCTTCAGAA  243

Qy    181 CTTCAGCACACACAGGAACTCTTCCACACTGCCCAATTAAAATAGCTGCTATT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    244 CTTCAGCACACACAGGAACTCTTCCACACTGCCCAATTAAAATAGCTGCTATT  303

Qy    241 ATAGCATCTCTGACTTTTCTTCTTACACTCTTCTGAGGGAGGTAATTCACCCCTTTAGACAACT  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    304 ATAGCATCTCTGACTTTTCTTCTTACACTCTTCTGAGGGAGGTAATTCACCCCTTTAGACAACT  363

Qy    301 TCCCATCAACAATATTTTTATAAAAAATTCCAATCCTGGTCATCAACAAAGTCTTCCCAATG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    364 TCCCATCAACAATATTTTTATAAAAAATTCCAATCCTGGTCATCAACAAAGTCTTCCCAATG  423

Qy    361 GTTTCCATCATCATCTTGCATTGGTTTTACCTGCCAGGTGTGATAGCGCACGCAAATTGTCCAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    424 GTTTCCATCATCATCTTGCATTGGTTTTACCTGCCAGGTGTGATAGCGCACGCAAATTGTCCAA  483

Qy    421 CTTCATATAATGGAACCAAGTATAGAGTTCCACATTGGTTGGATAAGTGGATGGTTAACA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    484 CTTCATATAATGGAACCAAGTATAGAGTTCCACATTGGTTGGATAAGTGGATGGTTAACA  543

Qy    481 AGAAAGACAGTTTGGGGCCTTCTCAGTTTCTTCTTTTTGCTGTACTGCAAATTTATAGTCTG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    544 AGAAAGACAGTTTGGGGCCTTCTCAGTTTCTTCTTTTTGCTGTACTGCAAATTTATAGTCTG  603

Qy    541 TCTTACCCAATGAGGCGGATCCTACAGATACAAGTTGCTAAAACTGGGCCATATACAACAGGTC  600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    604 TCTTACCCAATGAGGCGGATCCTACAGATACAAGTTGCTAAAACTGGGCCATATACAACAGGTC  663

Qy    601 CAACAAAATAAAGGAGAGATGCCTGGAATTGAGCATGAGTGTTGGAGAAATGGAGAATTATGTG  660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    664 CAACAAAATAAAGGAGAGATGCCTGGAATTGAGCATGAGTGTTGGAGAAATGGAGAATTATGTG  723

Qy    661 TCTCTGGGAAATTGTGGGGATTGGGCAATACTCGGCTCTGTTGGCTGTGACATCTATTCCATCT  720
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    724 TCTCTGGGAAATTGTGGGGATTGGGCAATACTCGGCTCTGTTGGCTGTGACATCTATTCCATCT  783

Qy    721 GTGAGTGACTCTTTGACATGGAGAATTCACTATATATTCAGAGAGCAAGCTAGGAATTCGTT  780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    784 GTGAGTGACTCTTTGACATGGAGAATTCACTATATATTCAGAGAGCAAGCTAGGAATTCGTT  843

Qy    781 TCCCTTCTTACTGGGGCACAATACACGCATTGATTTTGCCTGGAATAAGTGGATAGAGATA  840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    844 TCCCTTCTTACTGGGGCACAATACACGCATTGATTTTGCCTGGAATAAGTGGATAGAGATA  903

Qy    841 AAACAAATTGTATGGTATACACCTCCAAACTTTTATGATTAGCTGTGTTTTCCTTCCAAATTGTT  900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    904 AAACAAATTGTATGGTATACACCTCCAAACTTTTATGATTAGCTGTGTTTTCCTTCCAAATTGTT  963

Qy    901 GTCCTGATATTTTAAAAGCATACTATTCTCCTGCCATGCTTGAGGAAGGAGAAGGAGATTGAAGATT  960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    964 GTCCTGATATTTTAAAAGCATACTATTCTCCTGCCATGCTTGAGGAAGGAGAAGGAGATTGAAGATT 1023

Qy    961 AGACAATGGTTGGGAAGACGGTCACCAAAAATTAACAAAAACTGAGATATGGTTCCCAGTTG 1017
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1024 AGACAATGGTTGGGAAGACGGTCACCAAAAATTAACAAAAACTGAGATATGGTTCCCAGTTG 1080
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RESULT 9
US-10-861-662-2
; Sequence 2, Application US/10861662
; Publication No. US20050086707A1
; GENERAL INFORMATION:
;   APPLICANT: Jakobovits, Aya
;   APPLICANT: Etessami, Soudabeh
;   APPLICANT: Challita-Eid, Pia M.
;   APPLICANT: Perez-Villar, Juan
;   APPLICANT: Meyrick Morrison, Karen Jane
;   APPLICANT: Jia, Xiao-Chi
;   APPLICANT: Faris, Mary
;   APPLICANT: Gudas, Jean
;   APPLICANT: Raitano, Arthur B.
;   TITLE OF INVENTION: Antibodies and Molecules Derived
;   TITLE OF INVENTION: therefrom that Bind to STEAP-1 Proteins
;   FILE REFERENCE: 51158-20016.26
;   CURRENT APPLICATION NUMBER: US/10/861,662
;   CURRENT FILING DATE: 2004-06-04
;   PRIOR APPLICATION NUMBER: 09/323,873
;   PRIOR FILING DATE: 1999-06-01
;   PRIOR APPLICATION NUMBER: 10/010,667
;   PRIOR FILING DATE: 2001-12-06
;   PRIOR APPLICATION NUMBER: 10/011,095
;   PRIOR FILING DATE: 2001-12-06
;   PRIOR APPLICATION NUMBER: 10/236,878
;   PRIOR FILING DATE: 2002-09-06
;   PRIOR APPLICATION NUMBER: 09/455,486
;   PRIOR FILING DATE: 1999-12-06
;   PRIOR APPLICATION NUMBER: 60/091,183
;   PRIOR FILING DATE: 1998-06-30
;   NUMBER OF SEQ ID NOS: 103
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 1193
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (66)...(1085)
US-10-861-662-2

Query Match   100.0%;   Score 1017;   DB 9;   Length 1193;
Best Local Similarity   100.0%;
Matches 1017;   Conservative   0;   Mismatches   0;   Pred No. 7e-277;   Indels   0;   Gaps   0;

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Qy      1 ATGGAAAAGCAGAAAAAGACAATCACAAAACCAAGAAGAGAACTTTGGAAAATGAAGCCTAGGAGA   60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     66 ATGGAAAAGCAGAAAAAGACAATCACAAAACCAAGAAGAGAACTTTGGAAAATGAAGCCTAGGAGA  125

Qy     61 AATTTAGAAGAAGAACGAGATTATTTGCATAAGGACACGGGAGAGAGACCAGCATGCTAAAAAGA  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    126 AATTTAGAAGAAGAACGAGATTATTTGCATAAGGACACGGGAGAGAGACCAGCATGCTAAAAAGA  185

Qy    121 CCTGTGCTTTTGCATTGACCAAAACAGCCCATGCTGATGAATTTGACTGCCCCTTCAGAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    186 CCTGTGCTTTTGCATTGACCAAAACAGCCCATGCTGATGAATTTGACTGCCCCTTCAGAA  245
```

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 878
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo sapiens
US-09-759-143-878

RESULT 10
US-09-759-143-878
Sequence 878, Application US/09759143
Patent No. US20020224248A1

Query Match   100.0%; Score 1017; DB 3; Length 1195;
Best Local Similarity   100.0%; Pred. No. 7e-277;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ATGGAAAGCAGAGAAAAGAGACATCACAAAACCAAGAAGAAGAACTTTGAAAAATGAAGCCTAGGAGA 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   66 ATGGAAAGCAGAGAAAAGAGACATCACAAAACCAAGAAGAAGAACTTTGAAAAATGAAGCCTAGGAGA 125

Qy   61 AATTTAGAAGAAGACGAGATTATTTGCATAAGGACACGGGAGAAGACCAGCATGTCTAAAAAGA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 126 AATTTAGAAGAAGACGAGATTATTTGCATAAGGACACGGGAGAAGACCAGCATGTCTAAAAAGA 185

Qy 121 CCTGTGCTTTTGCATTTGCCACCAAAACAGCCCATGCTGATGAATTGACTGGCCCTTCAGAA 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 186 CCTGTGCTTTTGCATTTGCCACCAAAACAGCCCATGCTGATGAATTGACTGGCCCTTCAGAA 245

Qy 181 CTTCAGCACACACAGGAACTCTTTCCACAGTCTTGCCACTATTA... 240
Db 246 CTTCAGCACACACAGGAACTCTTTCCACAGTCTTGCCACTATTA... 305

Qy 241 ATAGCATCTCGACTTTCTTTACACTCTTCTCTGAGGGGAAGTAATTCACCCTTTAGCAACT 300
Db 306 ATAGCATCTCGACTTTCTTTACACTCTTCTCTGAGGGGAAGTAATTCACCCTTTAGCAACT 365

Qy 301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
Db 366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy 361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCCAGGTGTGATAGCAGCAAATTGTCCAA 420
Db 426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCCAGGTGTGATAGCAGCAAATTGTCCAA 485

Qy 421 CTTCATAATGGAACCAAGTAATATAAGAAGTTTCCACATTGGTTGGAT... 480
Db 486 CTTCATAATGGAACCAAGTAATATAAGAAGTTTCCACATTGGTTGGAT... 545

Qy 481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCAATTTATAGTCTG 540
Db 546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCAATTTATAGTCTG 605

Qy 541 TCTTACCCAATGAGGGCGATCCTACAGATACAAGTTGCTAAAACTGGGCATATCAACAGGTC 600
Db 606 TCTTACCCAATGAGGGCGATCCTACAGATACAAGTTGCTAAAACTGGGCATATCAACAGGTC 665

Qy 601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGAGCATGAGAGAATTTATGTG 660
Db 666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGAGCATGAGAGAATTTATGTG 725

Qy 661 TCTCTGGGAATTGTGGGATTGGGCAATACTACTGGCTCTCGTTTGGCTGTTGACATCTATTCCATCT 720
Db 726 TCTCTGGGAATTGTGGGATTGGGCAATACTACTGGCTCTCGTTTGGCTGTTGACATCTATTCCATCT 785

Qy 721 GTGAGTGACTCTTTGACATGGAGAGAGAATTTCACTATAATTCAGAGAGCAAGCTAGGAATTGTT 780
Db 786 GTGAGTGACTCTTTGACATGGAGAGAGAATTTCACTATAATTCAGAGAGCAAGCTAGGAATTGTT 845

Qy 781 TCCCTTCTACTGGGGCACAATACACGGCATTGATTTTTGCCTGGAATAAGTGGATAGAGTATA 840
Db 846 TCCCTTCTACTGGGGCACAATACACGGCATTGATTTTTGCCTGGAATAAGTGGATAGAGTATA 905

Qy 841 AAACAATTTGTATGGTATACACCTCCAACTTTTTATGATAGCTGTTTCCTTCCAATTGTT 900
Db 906 AAACAATTTGTATGGTATACACCTCCAACTTTTTATGATAGCTGTTTCCTTCCAATTGTT 965

Qy 901 GTCCTGATATTTTAAAAGCATACTATTCCTGCCAATGCTTGAGGAGGAAGADATACTGAAGATT 960
Db 966 GTCCTGATATTTTAAAAGCATACTATTCCTGCCAATGCTTGAGGAGGAAGADATACTGAAGATT 1025

Qy 961 AGACATGGTTGGGGAGAAGCGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
Db 1026 AGACATGGTTGGGGAGAAGCGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082

RESULT 11
US-09-780-669-878
; Sequence 878, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens

Query Match   100.0%; Score 1017; DB 3; Length 1195;
Best Local Similarity 100.0%; Pred. No. 7e-277;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAGAACTTTGGAAAATGAAGCCTAGGAGAGA     60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAGAACTTTGGAAAATGAAGCCTAGGAGA    125

Qy     61 AATTTAGAAGAAGAGACGATTATTTGCATAAGGACACGGGAGGAGGACCAGCATGCTAAAAGA    120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    126 AATTTAGAAGAAGAGACGATTATTTGCATAAGGACACGGGAGGAGGACCAGCATGCTAAAAGA    185

Qy    121 CCTGTGCTTTTGCATTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA    180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    186 CCTGTGCTTTTGCATTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA    245
```

RESULT 12
US-09-822-827-878
; Sequence 878, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA

; ORGANISM: Homo sapiens
US-09-822-827-878

Query Match   100.0%; Score 1017; DB 3; Length 1195;
Best Local Similarity   100.0%; Pred. No. 7e-277;
Matches 1017; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy      1 ATGGAAAAGCAGAAAAAGACATCACAAACCAAGAAGAAGAACTTTGGAAAATGAAAGCCTAGGAGA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     66 ATGGAAAAGCAGAAAAAGACATCACAAACCAAGAAGAAGAACTTTGGAAAATGAAAGCCTAGGAGA 125

Qy     61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGAGACCAGCATGCTAAAAAGA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGAGACCAGCATGCTAAAAAGA 185

Qy    121 CCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    186 CCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy    181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCCACTTGCCAATTAAAATAGCTGCTATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCCACTTGCCAATTAAAATAGCTGCTATT 305

Qy    241 ATAGCATCTCTGACTTTCTTTACACTCTTCCACAGTGAATTCACCCTTTAGCAACT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    306 ATAGCATCTCTGACTTTCTTTACACTCTTCCACAGTGAATTCACCCTTTAGCAACT 365

Qy    301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy    361 GTTTCCATCACTCTCTTGGCATGGTTTACCTGCCAGTGTGATAGCAGCAATTGTCCAA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    426 GTTTCCATCACTCTCTTGGCATGGTTTACCTGCCAGTGTGATAGCAGCAATTGTCCAA 485

Qy    421 CTTCATAATGGAACCAAGTATATAAGAAGTTTCCACATTGGTGGATAAGTGGATGTTAACA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    486 CTTCATAATGGAACCAAGTATATAAGAAGTTTCCACATTGGTGGATAAGTGGATGTTAACA 545

Qy    481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTGCTGTTACTGCATGCAAATTTATAGTCTG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTGCTGTTACTGCATGCAAATTTATAGTCTG 605

Qy    541 TCTTACCCAAATGAGGCGATCCTACAGATACAAGGTTGCTAAACTGGGCATATCAACAGGTC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    606 TCTTACCCAAATGAGGCGATCCTACAGATACAAGGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy    601 CAACAAAATAAAGAGAGATGCCTGGATTGAGCATGAATGGAAGATTTATGTG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    666 CAACAAAATAAAGAGAGATGCCTGGATTGAGCATGAATGGAAGATTTATGTG 725

Qy    661 TCTCTGGGAATTGTGGGATTGGGCAAATACTGGCTCTGTTGGGCTGTGACTACTATTCCATCT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    726 TCTCTGGGAATTGTGGGATTGGGCAAATACTGGCTCTGTTGGGCTGTGACTACTATTCCATCT 785

Qy    721 GTGAGTGACTCTTTGACATGGAGAATTTCACTATATTATTCAGAGCCAAGCTAGGAATTGTT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    786 GTGAGTGACTCTTTGACATGGAGAATTTCACTATATTATTCAGAGCCAAGCTAGGAATTGTT 845

Qy    781 TCCCTTCTACTGGGGCACAATACACGCATTGAATTGGGATAAGTAGAGAATATA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    846 TCCCTTCTACTGGGGCACAATACACGCATTGAATTGGGATAAGTAGAGAATATA 905

Qy    841 AAACAATTTGTATGGTATACACCTCCAACTTTATGATAGCTGTTTTTCCTTCCAATTGTT 900
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Db    906 AAACAATTTGTATGGTATACACCTCCAACTTTATGATAGCTGTTTTTCCTTCCAATTGTT 965

Qy    901 GTCCTGATATTTAAAAGCATACTATTCCTGCCAATGCCTTGAGGAAGAAGAATACTGAAAGATT 960
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Db    966 GTCCTGATATTTAAAAGCATACTATTCCTGCCAATGCCTTGAGGAAGAAGAATACTGAAAGATT 1025

Qy    961 AGACATGGTTGGGAAGAGAGGTCACCAAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
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Db   1026 AGACATGGTTGGGAAGAGAGGTCACCAAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082
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RESULT 13
US-09-895-793-878
; Sequence 878, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hiral, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-793-878

Query Match   100.0%; Score 1017; DB 3; Length 1195;
Best Local Similarity   100.0%; Pred. No. 7e-277;
Matches 1017; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy      1 ATGGAAAAGCAGAAAAAGACATCACAAACCAAGAAGAAGAACTTTGGAAAATGAAAGCCTAGGAGA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     66 ATGGAAAAGCAGAAAAAGACATCACAAACCAAGAAGAAGAACTTTGGAAAATGAAAGCCTAGGAGA 125

Qy     61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGAGACCAGCATGCTAAAAAGA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGAGACCAGCATGCTAAAAAGA 185

Qy    121 CCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    186 CCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy    181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCCACTTGCCAATTAAAATAGCTGCTATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCCACTTGCCAATTAAAATAGCTGCTATT 305

Qy    241 ATAGCATCTCTGACTTTCTTTACACTCTTCCACAGTGAATTCACCCTTTAGCAACT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    306 ATAGCATCTCTGACTTTCTTTACACTCTTCCACAGTGAATTCACCCTTTAGCAACT 365

Qy    301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy    361 GTTTCCATCACTCTCTTGGCATGGTTTACCTGCCAGTGTGATAGCAGCAATTGTCCAA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Query Match   100.0%;   Score 1017; DB 3; Length 1195;
Best Local Similarity   100.0%;   Pred. No. 7e-277;
Matches 1017; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy         1 ATGGAAAGCAGAAAAGAGACATCACAAACCAAGAGAGAGAACTTTGGAAAATGAAGCCTAGGAGA 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        66 ATGGAAAGCAGAAAAGAGACATCACAAACCAAGAGAGAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy        61 AATTTAGAAGAAGAGGATTATTGCATAAGACCAAGAGAAGAAGCTTTGCATAAGAC 120
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       126 AATTTAGAAGAAGAGGATTATTGCATAAGACCAAGAGAAGAAGCTTTGCATAAGAC 185

Qy       121 CCTGTGCTTTTGCATTTGCACCAAAACAGCCCAATGCTGATGAATTTGACTGCCTGTATT 180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       186 CCTGTGCTTTTGCATTTGCACCAAAACAGCCCAATGCTGATGAATTTGACTGCCTGTATT 245

Qy       181 CTTCAGCACACACAGGAACTCTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       246 CTTCAGCACACACAGGAACTCTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy       241 ATAGCATCTCGACTTTTCTTTACACTCTTCTGAGGGAGTAATTCACCCTTTAGCAACT 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       306 ATAGCATCTCGACTTTTCTTTACACTCTTCTGAGGGAGTAATTCACCCTTTAGCAACT 365

Qy       301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy       361 GTTTCCATCACTCTCTTGGGCATTGGTTTACCTGCCAGGTGTGATAAGTGCAGCAATTGTTCCAA 420
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Db       426 GTTTCCATCACTCTCTTGGGCATTGGTTTACCTGCCAGGTGTGATAAGTGCAGCAATTGTTCCAA 485

Qy       421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy       481 AGAAAGCAGTTTGGGGCTTCTCAGTTTCTTTTTGCTGTACTGGGCATATCACACAGGTCTG 540
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Db       546 AGAAAGCAGTTTGGGGCTTCTCAGTTTCTTTTTGCTGTACTGGGCATATCACACAGGTCTG 605

Qy       541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCATATCACACAGGTC 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCATATCACACAGGTC 665

Qy       601 CAACAAAATAAAGAGAATGCCTGGATTGAGCATGAATGGAGAATTTATGTG 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       666 CAACAAAATAAAGAGAATGCCTGGATTGAGCATGAATGGAGAATTTATGTG 725

Qy       661 TCTCTGGGAATTGTGGGATTGGGCAAATACTGGCCTCGTGTTGGCCTGTGTG 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       726 TCTCTGGGAATTGTGGGATTGGGCAAATACTGGCCTCGTGTTGGCCTGTGTG 785

Qy       721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATATTCAGAGCAAGCTTAGGAATTGTTGTT 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATATTCAGAGCAAGCTTAGGAATTGTTGTT 845

Qy       781 TCCCTTCTACTGGGCCACAATACACGGCATTGATTTTGCCTGGAATAAGTGGATTAGAATATA 840
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       846 TCCCTTCTACTGGGCCACAATACACGGCATTGATTTTGCCTGGAATAAGTGGATTAGAATATA 905

Qy       841 AAACAAATTGTATGGGTATACACCTCCAACTTTTATGATAGCTGTGTTTCCTTCCAATTGTT 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       906 AAACAAATTGTATGGGTATACACCTCCAACTTTTATGATAGCTGTGTTTCCTTCCAATTGTT 965

Qy       901 GTCCTGATATTTTAAAAGCATAACTATTCCTGCCATGCCATGCATTGAAGATT 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       966 GTCCTGATATTTTAAAAGCATAACTATTCCTGCCATGCCATGCATTGAAGATT 1025

Qy       961 AGACATGGTTGGGGAAGACGTCACCAAAAATTAACAAAAACTGAGATATAGTGTTCCCAGTTG 1017
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1026 AGACATGGTTGGGGAAGACGTCACCAAAAATTAACAAAAACTGAGATATAGTGTTCCCAGTTG 1082
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Qy    901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGAAGAGATACTTGAAGATT 960
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Db    966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGAAGAGATACTTGAAGATT 1025

Qy    961 AGACAATGGTTGGGAAGAGACGTCACCAAAAATTAACAAAAACTGAGATATGTTCCCAGTTG 1017
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1026 AGACAATGGTTGGGAAGAGACGTCACCAAAAATTAACAAAAACTGAGATATGTTCCCAGTTG 1082
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RESULT 15

US-10-012-896-878

Sequence 878, Application US/10012896

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Wantanabe, Yoshihiro

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

US-10-012-896-878

Query Match   100.0%;   Score 1017;   DB 5;   Length 1195;
Best Local Similarity   100.0%;   Pred. No. 7e-277;
Matches 1017;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     66 ATGGAAAAGCAGAAAAGACATCACAAACCAAGAAGAACATTTGGAAAATGAAGCCTAGGAGA 125

Qy     61 AATTTAGAAGAAGACGATTATTCCATAAGGACACCGGAGAGACCAGCATGCTTAAAAAGA 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    126 AATTTAGAAGAAGACGATTATTCCATAAGGACACCGGAGAGACCAGCATGCTTAAAAAGA 185

Qy    121 CCTGTGCTTTTGCAATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    186 CCTGTGCTTTTGCAATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy    181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCCAATTAAAATAGCTGCTATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCCAATTAAAATAGCTGCTATT 305

Qy    241 ATAGCATCTCGACTTTTCTTTACACTCTTCTGAGGGAGTAATTCACCCTTTAGCAACT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ... (continued)

Db    306 ATAGCATCTCGACTTTTCTTTACACTCTTCTGAGGGAGTAATTCACCCTTTAGCAACT 365

Qy    301 TCCCATCAACAATATATTTTATAAAAATTCCAATCCTGCTTCATCAACAAAGTCTTGCCAATG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    366 TCCCATCAACAATATATTTTATAAAAATTCCAATCCTGCTTCATCAACAAAGTCTTGCCAATG 425

Qy    361 GTTTCCATCACTCTTCTTGGCATTGGTTTACCTGCCCAGGTGTGATAGCAGCAATTGTCCAA 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    426 GTTTCCATCACTCTTCTTGGCATTGGTTTACCTGCCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy    421 CTTCATAATGGAACCAAGTATAAGAAGTTCCACAATTGGTTGGATAAGTGGATGTGTTAACA 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    486 CTTCATAATGGAACCAAGTATAAGAAGTTCCACAATTGGTTGGATAAGTGGATGTGTTAACA 545

Qy    481 AGAAAAGCAGTTTGGGGCTTCCTCAGTTTCTTTTTTTTTGCTGTACTGCATGCAATTTTATAGTCTG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    546 AGAAAAGCAGTTTGGGGCTTCCTCAGTTTCTTTTTTTTTGCTGTACTGCATGCAATTTTATAGTCTG 605

Qy    541 TCTTACCCAATGAGGCCATCCTACACGATACAACAAGTTGCTAAAACTGGGCATATCAAACAGTC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    606 TCTTACCCAATGAGGCCATCCTACACGATACAACAAGTTGCTAAAACTGGGCATATCAAACAGTC 665

Qy    601 CAACAAAATAAAGAAAGATGCCTGGATTGCAATGATGAGTTTGGAGAATGGAGAATTTAGTG 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    666 CAACAAAATAAAGAAAGATGCCTGGATTGCAATGATGAGTTTGGAGAATGGAGAATTTAGTG 725

Qy    661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGGCTGTGACATCTATTCCATCT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGGCTGTGACATCTATTCCATCT 785

Qy    721 GTGAGTGGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    786 GTGAGTGGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy    781 TCCCTTCTACTGGGCACAAATACACGCATGCATTGAATTTTTGCCTGGAATAAGTGGATAGATATA 840
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Db    846 TCCCTTCTACTGGGCACAAATACACGCATGCATTGAATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy    841 AAACAAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    906 AAACAAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy    901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGAAGAGATACTTGAAGATT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGAAGAGATACTTGAAGATT 1025

Qy    961 AGACAATGGTTGGGAAGAGACGTCACCAAAAATTAACAAAAACTGAGATATGTTCCCAGTTG 1017
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1026 AGACAATGGTTGGGAAGAGACGTCACCAAAAATTAACAAAAACTGAGATATGTTCCCAGTTG 1082
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Search completed: December 5, 2005, 07:54:11
Job time : 952.415 secs

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OM nucleic - nucleic search, using sw model

                        Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                            GenCore version 5.1.6

Run on:        December  4, 2005, 20:43:36 ; Search time 202.756 Seconds
                                                            (without alignments)
                                                        8916.024 Million cell updates/sec

Title:         US-10-750-262-1_COPY_66_1082
Perfect score: 1017
Sequence:      1 atggaaagcagaaaagacat...........ctgagatatgtccagctg 1017

Scoring table: IDENTITY NUC
               Gapop 10.0 , Gapext 1.0

Searched:      1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters:      2606114

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     Issued_Patents NA:*
               1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
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               4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
               5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
               6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
               7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
               8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
               9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES
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Result No.	Score	% Query Match	Length	DB	Match ID	Description
1	1017	100.0	1193	3	US-09-455-486-1	Sequence 1, Appli
2	1017	100.0	1195	3	US-09-323-873A-1	Sequence 1, Appli
3	1017	100.0	1195	3	US-09-685-166A-878	Sequence 878, App
4	1017	100.0	1195	3	US-09-679-426-878	Sequence 878, App
5	1017	100.0	1195	3	US-09-759-143-878	Sequence 878, App
6	1017	100.0	1195	3	US-10-010-667A-1	Sequence 1, Appli
7	1017	100.0	1195	3	US-09-012-896-878	Sequence 878, App
8	1015.4	99.8	1147	3	US-09-949-016-2686	Sequence 2686, Ap
9	760.6	74.8	1147	3	US-09-323-873A-6	Sequence 6, Appli
10	760.6	74.8	3627	3	US-09-455-486-4	Sequence 4, Appli
11	760.6	74.8	3627	3	US-10-010-667A-6	Sequence 6, Appli
12	760.6	74.8	3627	3	US-09-439-313-342	Sequence 342, Appli
13	516	50.7	592	3	US-09-352-616A-342	Sequence 342, App
14	516	50.7	592	3	US-09-636-215-342	Sequence 342, App
15	516	50.7	592	3	US-09-685-166A-342	Sequence 342, App
16	516	50.7	592	3	US-09-679-426-342	Sequence 342, App
17	516	50.7	592	3	US-09-759-143-342	Sequence 342, App
18	516	50.7	592	3	US-09-651-236-342	Sequence 342, App
19	516	50.7	592	3	US-09-657-279-342	Sequence 342, App
20	516	50.7	592	3	US-10-012-896-342	Sequence 342, App
21	515.6	50.7	9073	3	US-09-949-016-14428	Sequence 14428, A
22	266.6	26.2	2453	3	US-10-455-486-5	Sequence 5, Appli
23	266.6	26.2	2469	3	US-10-104-047-1185	Sequence 1185, Ap
24	265	26.1	1403	3	US-10-012-896-995	Sequence 995, App
c 25	256.8	25.3	455	3	US-09-621-976-9264	Sequence 9264, Ap
c 26	229.6	22.6	848	3	US-10-012-896-993	Sequence 993, App
c 27	221.4	21.8	519	3	US-09-455-486-7	Sequence 7, Appli
c 28	221.4	21.8	521	3	US-09-323-873A-7	Sequence 7, Appli
c 29	212.8	20.9	2714	3	US-09-562-930-5	Sequence 5, Appli
c 30	212.8	20.9	3884	3	US-09-562-930-10	Sequence 10, Appl
c 31	187.4	18.4	4429	3	US-09-455-486-7	Sequence 7, Appli
c 32	184.8	18.2	1213	3	US-09-083-521-3	Sequence 3, Appli
c 33	171	16.8	1886	3	US-09-562-930-1	Sequence 1, Appli
c 34	166.6	16.4	1203	3	US-09-544-618-6	Sequence 6, Appli
c 35	162.4	16.0	366	3	US-09-030-607-215	Sequence 215, App
c 36	162.4	16.0	366	3	US-09-439-313-215	Sequence 215, App
c 37	162.4	16.0	366	3	US-09-352-616A-215	Sequence 215, App
c 38	162.4	16.0	366	3	US-09-232-149A-215	Sequence 215, App
c 39	162.4	16.0	366	3	US-09-159-812-215	Sequence 215, App
c 40	162.4	16.0	366	3	US-09-685-166A-215	Sequence 215, App
c 41	162.4	16.0	366	3	US-09-115-453-215	Sequence 215, App
c 42	162.4	16.0	366	3	US-09-688-489-215	Sequence 215, App
c 43	162.4	16.0	366	3	US-09-679-426-215	Sequence 215, App
c 44	162.4	16.0	366	3	US-09-759-143-215	Sequence 215, App
c 45	162.4	16.0	366	3	US-09-759-143-215	Sequence 215, App

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                              ALIGNMENTS

RESULT 1
US-09-455-486-1

; Sequence 1, Application US/09455486
; Patent No. 6833438
; GENERAL INFORMATION:
;  APPLICANT: Daniel E. Afar
;  APPLICANT: Rene S. Hubert
;  APPLICANT: Arthur B. Raitano
;  APPLICANT: Douglas C. Saffran
;  APPLICANT: Stephen C. Mitchell
;  TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
;  TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
;  FILE REFERENCE: 129.17-US-I1
;  CURRENT APPLICATION NUMBER: US/09/455,486
;  CURRENT FILING DATE: 1999-12-06
;  PRIOR APPLICATION NUMBER: 09/323,873
;  PRIOR FILING DATE: 1999-06-01
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;  LENGTH: 1193
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (64)...(1083)
US-09-455-486-1

Query Match         100.0%;  Score 1017;  DB 3;  Length 1193;
Best Local Similarity   100.0%;  Pred. No. 2.5e-304;
Matches 1017;  Conservative   0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAGAACTTTGGAAAATGAAAGCCTAGAGA 60
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Db         64 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAGAACTTTGGAAAATGAAAGCCTAGAGA 123

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGAGACCAGCATGCTAAAAAGA 183

Qy        121 CCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 CCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTGACTGCCCTTCAGAA 243

Qy        181 CTTCAGCACACACAGGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 CTTCAGCACACACAGGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 303
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RESULT 2
US-09-323-873A-1

; Sequence 1, Application US/0932873A
; Patent No. 6329503
; GENERAL INFORMATION:
;   APPLICANT: Daniel E. Afar
;   APPLICANT: Rene S. Hubert
;   APPLICANT: Kahan Leong
;   APPLICANT: Arthur B. Raitano
;   APPLICANT: Douglas C. Saffran
;   APPLICANT: Steve Chappell Mitchell
;   TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
;   TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
;   FILE REFERENCE: 129.16USU2
;   CURRENT APPLICATION NUMBER: US/09/323,873A
;   CURRENT FILING DATE: 1999-06-01
;   PRIOR APPLICATION NUMBER: 60/087,520
;   PRIOR FILING DATE: 1998-06-01
;   PRIOR APPLICATION NUMBER: 60/091,183

; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-09-323-873A-1

Query Match 100.0%; Score 1017; DB 3; Length 1195;
Best Local Similarity 100.0%;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGGAAAAGCACGAAAAAGAACATCACAAAACCAAGAAGAACACTTTGGAAAAATGAGACCTAGGAGA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     66 ATGGAAAAGCACGAAAAAGAACATCACAAAACCAAGAAGAACACTTTGGAAAAATGAGACCTAGGAGA 125

Qy     61 AATTTAGAAGAAGAAGACGAATTATTGCATAAGGATACAGAGCCCATGGCATCAAAAAGA 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    126 AATTTAGAAGAAGAAGACGAATTATTGCATAAGGATACAGAGCCCATGGCATCAAAAAGA 185

Qy    121 CCTGTGCTTTTGCATTTGACCCAAAACAGAGCCCATGGGATGAAATTTGACTGCCTTCAGAA 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    186 CCTGTGCTTTTGCATTTGACCCAAAACAGAGCCCATGGGATGAAATTTGACTGCCTTCAGAA 245

Qy    181 CTTCAGCACACAGGAACTCTTTCCACACGGCACTTGCCAATTAAAAATAGCTGCTATT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    246 CTTCAGCACACAGGAACTCTTTCCACACGGCACTTGCCAATTAAAAATAGCTGCTATT 305

Qy    241 ATAGCATCTCTGACTTTTCTTCTTTCACTCTTCTGCGAGGGAAGTAATTCACCCTTTAGCAACT 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    306 ATAGCATCTCTGACTTTTCTTCTTTCACTCTTCTGCGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy    301 TCCCATCAACAATATTTTATAAAATTCCAATCCTGGGTCATCAACAAAGTCTTGCCAATG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    366 TCCCATCAACAATATTTTATAAAATTCCAATCCTGGGTCATCAACAAAGTCTTGCCAATG 425

Qy    361 GTTTCCATCACACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    426 GTTTCCATCACACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy    421 CTTCATAATGGAACCAAAGTATAAAGAAGTTCCACATTGGTTGGAATAAGTGGAATGTTAACA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    486 CTTCATAATGGAACCAAAGTATAAAGAAGTTCCACATTGGTTGGAATAAGTGGAATGTTAACA 545

Qy    481 AGAAAGCACGTTTGGGCCTTCTCAGTTTCTTTTTGCTGTACTGCAATTTATAGTCTG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    546 AGAAAGCACGTTTGGGCCTTCTCAGTTTCTTTTTGCTGTACTGCAATTTATAGTCTG 605

Qy    541 TCTTACCCAATGAGGCGGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACACAGGTC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    606 TCTTACCCAATGAGGCGGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACACAGGTC 665

Qy    601 CAACAAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTGCTAAACTGGGCATATCAACAAGGTC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    666 CAACAAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTGCTAAACTGGGCATATCAACAAGGTC 725

Qy    661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCCTCGTTGGCTGCTGTCAGTAGGAATTGTT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCCTCGTTGGCTGCTGTCAGTAGGAATTGTT 785

Qy    721 GTGAGTGACTCCTTTGACATGGAGACAAATTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    786 GTGAGTGACTCCTTTGACATGGAGACAAATTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy    781 TCCCTTCTACTGGGCCACAATACTACCTCCAACTTTTATGATAGCTGTTTTCCTTCCA 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    846 TCCCTTCTACTGGGCCACAATACTACCTCCAACTTTTATGATAGCTGTTTTCCTTCCA 905

Qy    841 AAACAAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAAATTGTT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    906 AAACAAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAAATTGTT 965

Qy    901 GTCCTGATATTTAAAAGCATAATACTATTCCTGCCAATACAGTTCGGGCTTCTCAGTTTCTTTTTG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    966 GTCCTGATATTTAAAAGCATAATACTATTCCTGCCAATACAGTTCGGGCTTCTCAGTTTCTTTTTG 1023

Qy    961 AGCATGGTTGGGGAGAGACGTCACCAAAATTAACAAAAACTGAGATATGTTCCCAGTTG 1017
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1024 AGACATGGTTGGGGAGAGACGTCACCAAAATTAACAAAAACTGAGATATGTTCCCAGTTG 1080
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Qy 901 GTCCTGATATTTAAAAGCATACTATTCCTCCCATGCTCTTGAGGAAGAGAAGATACTGAAGATT 960
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Db 966 GTCCTGATATTTAAAAGCATACTATTCCTCCCATGCTCTTGAGGAAGAGAAGATACTGAAGATT 1025

Qy 961 AGACATGGTTGGGGAAGACGTCACCAAAAATTAACAAAAACTGAGATAGTGTTCCCAGTTG 1017
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1026 AGACATGGTTGGGGAAGACGTCACCAAAAATTAACAAAAACTGAGATATGTTCCCAGTTG 1082

RESULT 3
US-09-685-166A-878
; Sequence 878, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
;   APPLICANT: Xu, Jiangchun
;   APPLICANT: Dillon, Davin C.
;   APPLICANT: Mitcham, Jennifer L.
;   APPLICANT: Harlocker, Susan L.
;   APPLICANT: Jiang, Yuqui
;   APPLICANT: Henderson, Robert A.
;   APPLICANT: Kalos, Michael D.
;   APPLICANT: Fanger, Gary R.
;   APPLICANT: Retter, Marc W.
;   APPLICANT: Stolk, John A.
;   APPLICANT: Day, Craig H.
;   APPLICANT: Vedvick, Thomas S.
;   APPLICANT: Carter, Darrick
;   APPLICANT: Li, Samuel
;   APPLICANT: Wang, Aijun
;   APPLICANT: Skeiky, Yasir A.W.
;   APPLICANT: Hepler, William
;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;   TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
;   FILE REFERENCE: 210121.427C21
;   CURRENT APPLICATION NUMBER: US/09/685,166A
;   CURRENT FILING DATE: 2000-10-10
;   NUMBER OF SEQ ID NOS: 898
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-685-166A-878

Query Match   100.0%; Score 1017; DB 3; Length 1195;
Best Local Similarity   100.0%; Pred. No. 2.5e-304;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ATGGAAAAGCAGAAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
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Db   66 ATGGAAAAGCAGAAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy   61 AATTTAGAGAAGAAGACGATTATTGCATAAGGACACGGGAGAGAGACCAGCATGCTAAAAAGA 120
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Db 126 AATTTAGAGAAGAAGACGATTATTGCATAAGGACACGGGAGAGAGACCAGCATGCTAAAAAGA 185

Qy 121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
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Db 186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy 181 CTTCAGCACACACAGGAAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
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Db 246 CTTCAGCACACACAGGAAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy 241 ATAGAACATCTCTGACTTTTCTTTACACTCTTCTTCTGAGGGAAGTAATTCACCCTTTAGACAACT 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 306 ATAGAACATCTCTGACTTTTCTTTACACTCTTCTTCTGAGGGAAGTAATTCACCCTTTAGACAACT 365

Qy 301 TCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCATCAACAAAGTCTTGCCAATG 360
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Db 366 TCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy 361 GTTTCCATCACTCTCTTGGCATTGGTTTTACCTGCGCCAGGTGGTGTGATAGCAGCAAATTGTCCAA 420

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Db 426 GTTTCCATCACTCTCTTGGCATTGGTTTTACCTGCGCCAGGTGGTGTGATAGCAGCAAATTGTCCAA 485

Qy 421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGAGCAGTTAACA 480
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Db 486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGAGCAGTTAACA 545

Qy 481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTTGCTGTACTGCCATGCAATTTATGTCTG 540
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Db 546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCCATGCAATTTATGTCTG 605

Qy 541 TCTTACCCAATGAGGCGGGATCCTTCACGATACTACAAGTTGCTAAAACTGGCATATCAAACAGGTC 600
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Db 606 TCTTACCCAATGAGGCGGGATCCTTCACGATACTACAAGTTGCTAAAACTGGCATATCAAACAGGTC 665

Qy 601 CAACAAAATAAAGAAGAATGCCTGGATTGAGCAATGATGATGTTGGAGAATGAGATTTATGTG 660
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 666 CAACAAAATAAAGAAGAATGCCTGGATTGAGCAATGATGATGTTGGAGAATGAGATTTATGTG 725

Qy 661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCCTTGTTGGCTGTTGACATCTATTCCATCT 720
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Db 726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCCTTGTTGGCTGTTGACATCTATTCCATCT 785

Qy 721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGAGAAATGTT 780
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Db 786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGAGAAATGTT 845

Qy 781 TCCCTTCTACTGGGCACAAATACACGCAATGATTTGATTTTTGCCTGGAAATAAAGTGGATAGAATA 840
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Db 846 TCCCTTCTACTGGGCACAAATACACGCAATGATTTGATTTTTGCCTGGAAATAAAGTGGATAGAATA 905

Qy 841 AAACAATTTGTATGGTATACACCTCCAAACTTTTATGATAGTTGTTTTCCTTCCAAATTGTT 900
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Db 906 AAACAATTTGTATGGTATACACCTCCAAACTTTTATGATAGTTGTTTTCCTTCCAAATTGTT 965

Qy 901 GTCCTGATATTTAAAAGCATACTATTCCTCCCATGCTCTTGAGGAAGAGAAGATACTGAAGATT 960
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Db 966 GTCCTGATATTTAAAAGCATACTATTCCTCCCATGCTCTTGAGGAAGAGAAGATACTGAAGATT 1025

Qy 961 AGACATGGTTGGGGAAGACGTCACCAAAAATTAACAAAAACTGAGATAGTGTTCCCAGTTG 1017
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Db 1026 AGACATGGTTGGGGAAGACGTCACCAAAAATTAACAAAAACTGAGATATGTTCCCAGTTG 1082

RESULT 4
US-09-679-426-878
; Sequence 878, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
;   APPLICANT: Xu, Jiangchun
;   APPLICANT: Dillon, Davin C.
;   APPLICANT: Mitcham, Jennifer L.
;   APPLICANT: Harlocker, Susan L.
;   APPLICANT: Jiang, Yuqui
;   APPLICANT: Henderson, Robert A.
;   APPLICANT: Kalos, Michael D.
;   APPLICANT: Fanger, Gary R.
;   APPLICANT: Retter, Marc W.
;   APPLICANT: Stolk, John A.
;   APPLICANT: Day, Craig H.
;   APPLICANT: Vedvick, Thomas S.
;   APPLICANT: Carter, Darrick
;   APPLICANT: Li, Samuel
;   APPLICANT: Wang, Aijun
;   APPLICANT: Skeiky, Yasir A.W.
;   APPLICANT: Hepler, William
;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;   TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER.
;   FILE REFERENCE: 210121.427C20
;   CURRENT APPLICATION NUMBER: US/09/679,426
;   CURRENT FILING DATE: 2000-10-02
;   NUMBER OF SEQ ID NOS: 895
;   SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-426-878

Query Match   100.0%;   Score 1017;   DB 3;   Length 1195;
Best Local Similarity 100.0%;   Pred. No. 2.5e-304;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ATGGAAAAGCAGAAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   66 ATGGAAAAGCAGAAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy   61 AATTTAGAAGAAGAACGATTATTTGCATAAGGACACGGGAGAGAGACCAGCATGCTAAAAAGA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   126 AATTTAGAAGAAGAACGATTATTTGCATAAGGACACGGGAGAGAGACCAGCATGCTAAAAAGA 185

Qy   121 CCTGTGCTTTTGCATTTGCACAAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   186 CCTGTGCTTTTGCATTTGCACAAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy   181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy   241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAAATTCACCCTTTAGCAACT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAAATTCACCCTTTAGCAACT 365

Qy   301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy   361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy   421 CTTCATAATGGACCAAGTATAAGAAGTTTCCACATTGGTTGGGATAAGTGGGATGTTAACA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   486 CTTCATAATGGACCAAGTATAAGAAGTTTCCACATTGGTTGGGATAAGTGGGATGTTAACA 545

Qy   481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
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Db   546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy   541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGCATCATCAACAGGTC 600
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Db   606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGCATCATCAACAGGTC 665

Qy   601 CAACAAAATAAAGAAGATGCCCTGGATTCAGCATGATGATGTTTGGGAAATGGCAGATTTTATGTG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   666 CAACAAAATAAAGAAGATGCCCTGGATTCAGCATGATGATGTTTGGGAAATGGCAGATTTTATGTG 725

Qy   661 TCTCTGGGAATTGTTGGTTGGCAATAACTGGGCTCTCGTTGGCTCGTTGGCCAAGCTAGGATTT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   726 TCTCTGGGAATTGTTGGTTGGCAATAACTGGGCTCTCGTTGGCTCGTTGGCCAAGCTAGGATTT 785

Qy   721 GTGAGTGACTCTTTGACATGGAGAATTTCACTATATATTCAGAGCAAGCTAGGAATTGTT 780
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Db   786 GTGAGTGACTCTTTGACATGGAGAATTTCACTATATATTCAGAGCAAGCTAGGAATTGTT 845

Qy   781 TCCCTTCTACTGGGCACAATACACGCATTGATTGATTTTTTGCCTGGAATAAGTGGAATAGTTGTTATA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   846 TCCCTTCTACTGGGCACAATACACGCATTGATTGATTTTTTGCCTGGAATAAGTGGAATAGTTGTTATA 905

Qy   841 AAACAATTTGTATGGTATACACTTCCACCATTGATTTTTGCCTTCCTTCCAAATTGTT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   906 AAACAATTTGTATGGTATACACTTCCACCATTGATTTTTGCCTTCCTTCCAAATTGTT 965

Qy   901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGACATACTGAAAGATT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGACATACTGAAAGATT 1025

RESULT 5
US-09-759-143-878
; Sequence 878, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-878

Query Match   100.0%;   Score 1017;   DB 3;   Length 1195;
Best Local Similarity 100.0%;   Pred. No. 2.5e-304;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ATGGAAAAGCAGAAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
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Db   66 ATGGAAAAGCAGAAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy   61 AATTTAGAAGAAGAACGATTATTTGCATAAGGACACGGGAGAGAGACCAGCATGCTAAAAAGA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   126 AATTTAGAAGAAGAACGATTATTTGCATAAGGACACGGGAGAGAGACCAGCATGCTAAAAAGA 185

Qy   121 CCTGTGCTTTTGCATTTGCACAAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   186 CCTGTGCTTTTGCATTTGCACAAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy   181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy   241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAAATTCACCCTTTAGCAACT 300
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Db   306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAAATTCACCCTTTAGCAACT 365

Qy   301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy   361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy   961 AGACATGGTTGGGAGAGACGTCACCAAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1026 AGACATGGTTGGGAGAGACGTCACCAAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082

RESULT 6
US-10-010-667A-1
Sequence 1, Application US/10010667A
Patent No. 6887975
GENERAL INFORMATION:
  APPLICANT: Afar, Daniel
  APPLICANT: Hubert, Rene S.
  APPLICANT: Leong, Kahan
  APPLICANT: Raitano, Arthur B.
  APPLICANT: Saffran, Douglas C.
  APPLICANT: Mitchell, Steve Chappell
  TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
  TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
  FILE REFERENCE: 5115B2001601
  CURRENT APPLICATION NUMBER: US/10/010,667A
  CURRENT FILING DATE: 2001-12-06
  PRIOR APPLICATION NUMBER: 09/323,873
  PRIOR FILING DATE: 1999-06-01
  PRIOR FILING DATE: 1998-06-01
  PRIOR APPLICATION NUMBER: 60/087,520
  PRIOR APPLICATION NUMBER: 60/091,183
  PRIOR FILING DATE: 1998-06-30
  NUMBER OF SEQ ID NOS: 32
  SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1
  LENGTH: 1195
  TYPE: DNA
  ORGANISM: Homo Sapiens

US-10-010-667A-1
  Query Match   100.0%;   Score 1017;   DB 3;   Length 1195;
  Best Local Similarity 100.0%;   Pred. No. 2.5e-304;

Matches 1017;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

RESULT 7
US-10-012-896-878

; Sequence 878, Application US/10012896
; Patent No. 6943236
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSEQ for Windows Version 3.0
;
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-878

Query Match   100.0%;   Score 1017;   DB 3;   Length 1195;
Best Local Similarity   100.0%;   Pred. No. 2.5e-304;
Matches 1017;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy      1 ATGGAAAAGCAGAAAAAGAGCATCACAAAACCAAGAAGAGAACTTTGGAAAAATGAAGCCTAGGAGA  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     66 ATGGAAAAGCAGAAAAAGAGCATCACAAAACCAAGAAGAGAACTTTGGAAAAATGAAGCCTAGGAGA  125

Qy     61 AATTTAGAAGAAGAGACGATTATTTGCATAAGGACACGGGAGAGAGACCAGCATGCTAAAAAGA  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    126 AATTTAGAAGAAGAGACGATTATTTGCATAAGGACACGGGAGAGAGACCAGCATGCTAAAAAGA  185

Qy    121 CCTGTGCTTTTGCATTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    186 CCTGTGCTTTTGCATTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA  245

Qy    181 CTTCAGCACACACAGGGAACTCTTTCCACAGTGGCACTGCCCAATTAAAATAGCTGCTATT  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    246 CTTCAGCACACACAGGGAACTCTTTCCACAGTGGCACTGCCCAATTAAAATAGCTGCTATT  305

Qy    241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTCGAGGGAAGTAATTCACCCTTTAGCAACT  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTCGAGGGAAGTAATTCACCCTTTAGCAACT  365

Qy    301 TCCCATCAACAATATTTTATAAAATTCCAATCCTGGTCGTCATCAACAAAGTCTTGCCAATG  360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    366 TCCCATCAACAATATTTTATAAAATTCCAATCCTGGTCGTCATCAACAAAGTCTTGCCAATG  425

Qy    361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGTGATAGCACCAATTGTCCAA  420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGTGATAGCACCAATTGTCCAA  485

Qy    421 CTTCATATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTGTTAACA  480
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Db   486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTGTTAACA 545

Db   481 AGAAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTTTGTCTGTACTGCCATGGTGGATAAGTGGATGTCTG 540

Db   546 AGAAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTTTGTCTGTACTGCCATGGTGGATAAGTGGATGTCTG 605

Qy   541 TCTTACCCAATGAGGCGATCCTTACAGATATACAACAAGTTGCTAAAACTGGGCATATCAACAGGTC 600

Db   606 TCTTACCCAATGAGGCGATCCTTACAGATATACAACAAGTTGCTAAAACTGGGCATAATCAACAGGTC 665

Qy   601 CAACAAAATAAAGAAGATGCCTGGAATTGAGCATGAGTGTTTGGAGAATGGAGATTTATGTG 660

Db   666 CAACAAAATAAAGAAGATGCCTGGAATTGAGCATGAGTGTTTGGAGAATGGAGATTTATGTG 725

Qy   661 TCTCTGGGAAATGTGGGAATTGGGCAAATACTGGGCTTCTGTTGGGCGTGTGACATCTATTCCATCT 720

Db   726 TCTCTGGGAAATGTGGGAATTGGGCAAATACTGGGCTTCTGTTGGGCGTGTGACATCTATTCCATCT 785

Qy   721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATAATTCAGAGCAAGCTAGGAAATTGTT 780

Db   786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATAATTCAGAGCAAGCTAGGAAATTGTT 845

Qy   781 TCCCTTCTACTGGGGCACAAATACACGCATTGATTTTTGGCCTGGAAATAAGTGGATAAGTAGATATA 840

Db   846 TCCCTTCTACTGGGGCACAAATACACGCATTGATTTTTGGCCTGGAAATAAGTGGATAAGTAGATATA 905

Qy   841 AAACAAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTGTTTTCCTTCCAAATTGTT 900

Db   906 AAACAAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTGTTTTCCTTCCAAATTGTT 965

Qy   901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAGAAGATACTGAAGATT 960

Db   966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAGAAGATACTGAAGATT 1025

Qy   961 AGACATGGTTGGGAAGAGCGTCACCCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017

Db   1026 AGACATGGTTGGGAAGAGCGTCACCCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082

RESULT 8
US-09-949-016-2686
; Patent No. 6812339
; Sequence 2686, Application US/0994016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 2686
; LENGTH: 1147
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2686

Query Match   99.8%;   Score 1015.4;   DB 3;   Length 1147;
Best Local Similarity   99.9%;   Pred. No. 7.8e-304;
Matches 1016;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

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Qy      1 ATGGAAAAGCAGAAAAAGAGCATCACAAAACCAAGAAGAGAACTTTGGAAAAATGAAGCCTAGGAGA  60
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Db     33 ATGGAAAAGCAGAAAAAGAGCATCACAAAACCAAGAAGAGAACTTTGGAAAAATGAAGCCTAGGAGA  92
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Query Match   74.8%; Score 760.6; DB 3; Length 3627;
Best Local Similarity   99.5%; Pred. No. 1.2e-224;
Matches 763; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy    1 ATGGAAAGCAGAAAAAGACATCACAAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGAGA 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   96 ATGGAAAGCAGAAAAAGACATCACAAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGAGA 155

Qy   61 AATTTAGAAGAAGACGAATTATTTGCATAAGGACACACGGGAGAGACCAGCAGCATGCTAAAAAGA 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  156 AATTTAGAAGAAGACGAATTATTTGCATAAGGACACACGGGAGAGACCAGCAGCATGCTAAAAAGA 215

Qy  121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTGACTGCCCTTCAGAA 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  216 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTGACTGCCCTTCAGAA 275

Qy  181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  276 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 335

Qy  241 ATAGCATCCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCCTTTAGCAACT 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  336 ATAGCATCCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCCTTTAGCAACT 395

Qy  301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTCGGTCATCAACAAAAGTCTTGCCAATG 360
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Db  396 TCCCATCAACAATATTTTTATAAAATTCCAATCCTCGGTCATCAACAAAAGTCTTGCCAATG 455

Qy  361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCCAGGGTGTGATAGCAGCAATTGTCCAA 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  456 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCCAGGGTGTGATAGCAGCAATTGTCCAA 515

Qy  421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGTAGTAGATATA 480
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  516 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGTAGTAGATATA 575

Qy  481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTGCTTGTACTGCATGCAATTTATATGTCTG 540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  576 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTGCTTGTACTGCATGCAATTTATATGTCTG 635

Qy  541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAAACTGGGCTATATCAACAGGTC 600
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  636 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAAACTGGGCTATATCAACAGGTC 695

Qy  601 CAACAAAATAAAGAAGAAGAGTGCCTGGATTGAGCATGATGTTTGGAGAAATGAAGCCTAGTGTG 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  696 CAACAAAATAAAGAAGAAGAGTGCCTGGATTGAGCATGATGTTTGGAGAAATGAAGCCTAGTGTG 755

Qy  661 TCTCTGGGAATTGTGGGATTGGCAATACTGGGCTCTGTTGGCTCTGTTGACATCTATTCCATCT 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  756 TCTCTGGGAATTGTGGGATTGGCAATACTGGGCTCTGTTGGCTCTGTTGACATCTATTCCATCT 815

Qy  721 GTGAGTGACTCTTTGACATGGAGAGAATTCACTATATTCAGAGCAA 767
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Db  756 GTGAGTGACTCTTTGACATGGAGAGAATTCACTATATTCAGAGCAA 767
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Qy   61 AATTTAGAAGAAGACGAATTATTTGCATAAGGACACACGGGAGAGACCAGCAGCATGCTAAAAAGA 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   93 AATTTAGAAGAAGACGAATTATTTGCATAAGGACACACGGGAGAGACCAGCAGCATGCTAAAAAGA 152

Qy  121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTGACTGCCCTTCAGAA 180
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Db  153 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTGACTGCCCTTCAGAA 212

Qy  181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
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Db  213 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 272

Qy  241 ATAGCATCCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCCTTTAGCAACT 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  273 ATAGCATCCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCCTTTAGCAACT 332

Qy  301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTCGGTCATCAACAAAAGTCTTGCCAATG 360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  333 TCCCATCAACAATATTTTTATAAAATTCCAATCCTCGGTCATCAACAAAAGTCTTGCCAATG 392

Qy  361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCCAGGGTGTGATAGCAGCAATTGTCCAA 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  393 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCCAGGGTGTGATAGCAGCAATTGTCCAA 452

Qy  421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGTAGTAGATATA 480
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  453 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGTAGTAGATATA 512

Qy  481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTGCTTGTACTGCATGCAATTTATATGTCTG 540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  513 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTGCTTGTACTGCATGCAATTTATATGTCTG 572

Qy  541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAAACTGGGCTATATCAACAGGTC 600
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  573 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAAACTGGGCTATATCAACAGGTC 632

Qy  601 CAACAAAATAAAGAAGAAGAGTGCCTGGATTGAGCATGATGTTTGGAGAAATGAAGCCTAGTGTG 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  633 CAACAAAATAAAGAAGAAGAGTGCCTGGATTGAGCATGATGTTTGGAGAAATGAAGCCTAGTGTG 692

Qy  661 TCTCTGGGAATTGTGGGATTGGCAATACTGGGCTCTGTTGGCTCTGTTGACATCTATTCCATCT 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  693 TCTCTGGGAATTGTGGGATTGGCAATACTGGGCTCTGTTGGCTCTGTTGACATCTATTCCATCT 752

Qy  721 GTGAGTGACTCTTTGACATGGAGGAGAATTTCACTATATATTCAGAGCAAGCTAGGGAATTGTT 780
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  753 GTGAGTGACTCTTTGACATGGAGGAGAATTTCACTATATATTCAGAGCAAGCTAGGGAATTGTT 812

Qy  781 TCCCTTCTACTGGGCACAATACACAGCCATTGATTTTTTGCCTGGAATAAGTGGTAGAGATATA 840
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  813 TCCCTTCTACTGGGCACAATACACAGCCATTGATTTTTTGCCTGGAATAAGTGGTAGAGATATA 872

Qy  841 AAACAAATTTGTATGGGTATACACCTCCACAACAACTTTTATGATTAGCTGTTTCTTTCCTTCAATTGTT 900
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  873 AAACAAATTTGTATGGGTATACACCTCCACAACAACTTTTATGATTAGCTGTTTCTTTCCTTCAATTGTT 932

Qy  901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGAGATTACTGAAGATT 960
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  933 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGAGATTACTGAAGATT 992

Qy  961 AGACATGGTTGGGGAAGAGGTCACCCAAAAATTAACAAAAACTGAGATATAGTTCCCAGTTG 1017
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  993 AGACATGGTTGGGGAAGAGGTCACCCAAAAATTAACAAAAACTGAGATATAGTTCCCAGTTG 1049
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RESULT 10
US-09-455-486-4
; Sequence 4, Application US/09455486
; Patent No. 683438
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; APPLICANT: Stephen C. Mitchell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 129.17-US-11
; CURRENT APPLICATION NUMBER: US/09/455,486
; CURRENT FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/323,873
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 3627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-455-486-4

Query Match   74.8%;   Score 760.6; DB 3;   Length 3627;
Best Local Similarity   99.5%;   Pred. No. 1.2e-224;
Matches 763; Conservative   0; Mismatches   4; Indels   0; Gaps   0;

Qy   1 ATGGAAAGCAGAAAAGACATCACAAAACCAAGAAGAGAAACTTTGGAAAATGAAGCCTAGGAGA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   96 ATGGAAAGCAGAAAAGACATCACAAAACCAAGAAGAGAAACTTTGGAAAATGAAGCCTAGGAGA 155

Qy   61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   156 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 215

Qy   121 CCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   216 CCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 275

Qy   181 CTTCAGCACACACAGGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGTGTCTATT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   276 CTTCAGCACACACAGGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGTGTCTATT 335

Qy   241 ATAGCATCTCTGACTTTTCTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   336 ATAGCATCTCTGACTTTTCTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 395

Qy   301 TCCCATCAACAATATTTTATAAAATTCCAATCCTGGTCATCAACAAGTCTTGCCCAATG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   396 TCCCATCAACAATATTTTATAAAATTCCAATCCTGGTCATCAACAAGTCTTGCCCAATG 455

Qy   361 GTTTCCATCATCACTCTCTTGGCATTGGTTTACCTGCCACGCACAATTGTCCAA 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   456 GTTTCCATCATCACTCTCTTGGCATTGGTTTACCTGCCACGCACAATTGTCCAA 515

Qy   421 CTTCATAATGGAACCAAGTATAAGAGAGTTTCCACATTGGTTGGATAAGTGGACGTTAACA 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   516 CTTCATAATGGAACCAAGTATAAGAGAGTTTCCACATTGGTTGGATAAGTGGACGTTAACA 575

Qy   481 AGAAAGCAGTTTGGGCCTTCTCAGTTTCTTTTTGCTGTACTGCAATTTATAGTCTG 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   576 AGAAAGCAGTTTGGGCCTTCTCAGTTTCTTTTTGCTGTACTGCAATTTATAGTCTG 635

Qy   541 TCTTACCCAATGAGGCGATCCTACAGATACAAGATACAAGTTGCTAAAACTGGGCATATCAACAGGTC 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   636 TCTTACCCAATGAGGCGATCCTACAGATACAAGATACAAGTTGCTAAAACTGGGCATATCAACAGGTC 695

Qy   601 CAACAAAATAAAGAAGATGCCCGGATTGAGCATTGAGCATGAGCATTCATTCCACT 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   696 CAACAAAATAAAGAAGATGCCCGGATTGAGCATTGAGCATGAGCATTCATTCCACT 755

Qy   661 TCTCTGGGAATTGTGGGATTGCAATACTGGCTCTTGTTGGCTGTGACATCTATTATTCCATCT 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   756 TCTCTGGGAATTGTGGGATTGCAATACTGGCTCTTGTTGGCTGTGACATCTATTATTCCATCT 815

Qy   721 GTGAGTGACTCTTTGACATGGAGGAGAATTCACTATATATTCAGTGTG 767
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   816 GTGAGTGACTCTTTGACATGGAGGAGAATTCACTATATATTCAGTGTAA 862

RESULT 11
US-10-010-667A-6
; Sequence 6, Application US/10010667A
; Patent No. 6887975
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Hubert, Rene S.
; APPLICANT: Leong, Kahan
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Saffran, Douglas C.
; APPLICANT: Mitchell, Steve Chappell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 5115B2001601
; CURRENT APPLICATION NUMBER: US/10/010,667A
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 09/323,873
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 3627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-010-667A-6

Query Match   74.8%;   Score 760.6; DB 3;   Length 3627;
Best Local Similarity   99.5%;   Pred. No. 1.2e-224;
Matches 763; Conservative   0; Mismatches   4; Indels   0; Gaps   0;

Qy   1 ATGGAAAGCAGAAAAGACATCACAAAACCAAGAAGAGAAACTTTGGAAAATGAAGCCTAGGAGA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   96 ATGGAAAGCAGAAAAGACATCACAAAACCAAGAAGAGAAACTTTGGAAAATGAAGCCTAGGAGA 155

Qy   61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   156 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 215

Qy   121 CCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   216 CCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 275

Qy   181 CTTCAGCACACACAGGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGTGTCTATT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   276 CTTCAGCACACACAGGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGTGTCTATT 335

Qy   241 ATAGCATCTCTGACTTTTCTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   336 ATAGCATCTCTGACTTTTCTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 395

Qy   276 CTTCAGCACACACAGGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGTGTCCAA 335

Qy   301 TCCCATCAACAATATTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCCAATG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   180 TCCCATCAACAATATTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCCAATG 180

Qy   336 ATAGCATCTCTGACTTTTCTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 395

Qy   241 ATAGCATCTCTGACTTTTCTTACACTCTTCCACAGTGGCACTTGCCAATTAAAATAGTGTCTATT 240

Qy   361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCACGGTGTAGCAGCAATTGTCCAA 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Db  456 GTTTCCATCACTCCTCTGGCATTGGTTTACCTGCGCAGTGTGTGAATTGTCCAA          515
Qy  421 CTTCATATAATGGAACCAAGTATAAAGAAGTTCCACATTGGTTGGATAGTGGATTGTTAACA 480
Db  516 CTTCATATAATGGAACCAAGTATAAAGAAGTTCCACATTGGTTGGATAAGTGGATGTTAACA 575
Qy  481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTGCTATACTGCATCGCATCGAATTTGTCTG  540
Db  576 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTGCTGTACTGCATCGCATTTATAGTCTG    635
Qy  541 TCTTACCCAATGAGGGGATCCTACAGATAGTAAGTTGCTAAACTGGGCCATATCAACAGGTC 600
Db  636 TCTTACCCAATGAGGGGATCCTACAGATACAAAGTTGCTAAACTGGGCCATATCAACAGGTC 695
Qy  601 CAACAAAATAAAGAAGAGATGCCTGGATGTGTTGGAGAATGAGAGATTTATGTG         660
Db  696 CAACAAAATAAAGAAGAGATGCCTGGATGTGTTGGAGAATGAGAGATTTATGTG         755
Qy  661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTCGTTGGCTGTGTGACATCTATTCCATCT 720
Db  756 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTCGTTGGCTGTGTGACATCTATTCCATCT 815
Qy  721 GTGAGTGACTCTTTGACATGGAGAGAAATTCACTATATTCAGAGAGCAA              767
Db  816 GTGAGTGACTCTTTGACATGGAGAGAAATTCACTATATTCAGAGAGCAA              862
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RESULT 12
US-09-439-313-342/c
; Sequence 342, Application US/0949313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kaloe, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; SOFTWARE: FastSEQ for Windows Version 3.0
; NUMBER OF SEQ ID NOS: 575
; SEQ ID NO 342
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-342

Query Match   50.7%;   Score 516;   DB 3;   Length 592;
Best Local Similarity   99.6%;   Pred. No. 2.4e-149;
Matches 516;   Conservative 1;   Mismatches 1;   Indels 0;   Gaps 0;

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Qy    1 ATGGAAAAGCAGAAAAAGACATCACAAAACCAAGAAGAACATTTGGAAAATGAAGCCTAGGAGA  60
Db  518 ATGGAAAAGCAGAAAAAGACATCACAAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 459
Qy   61 AATTTAGAAGAAGCAGAAGACGATTATTTGCATAAGGACACAGGGAGGACCAGCATGCTAAAAAGA 120
Db  458 AATTTAGAAGAAGCAGAAGACGATTATTTGCATAAGGACACAGGGGAGGACCAGCATGCTAAAAAGA 399
Qy  121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTGACTGCCCTTCAGAA 180
Db  398 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTGACTGCCCTTCAGAA 339
Qy  181 CTTCAGCACACACAGGAACTCTTCCACAGTGGCACTTGCCAATTAAAAATAGCTGCTATT 240
Db  338 CTTCAGCACACACAGGAACTCTTCCACAGTGGCACTTGCCAATTAAAAATAGCTGCTATT 279
Qy  241 ATAGCATCTCTGACTTTTCTTACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
Db  278 ATAGCATCTCTGACTTTTCTTACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 219
Qy  301 TCCCATCAACAATATTTTATAAAATTCCAATCTGGTCATCAACAAAGTCTTGCCAATG 360
Db  218 TCCCATCAACAATATTTTATAAAATTCCAATCTGGTCATCAACAAAGTCTTGCCAATG 159
Qy  361 GTTTCCATCACTCCTCTGGCATTGGTTTACCTGCGCAGGTGTGTGAATTGTCCAA 420
Db  158 GTTTCCATCACTCCTCTGGCATTGGTTTACCTGCCAGGTGTGTGATAGGCAGCAATTGTCCAA 99
Qy  421 CTTCATATAATGGAACCAAGTATAAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
Db   98 CTTCATATAATGGAACCAAGTATAAGAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 39
Qy  481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTTGCTGT 518
Db   38 AGAAAGCAGAATTGGGCTTCTCAGTTTCTTTTTTTGCTGT 1
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RESULT 13
US-09-352-616A-342/c
; Sequence 342, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqui
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; SOFTWARE: FastSEQ for Windows Version 3.0
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 342
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-342

Query Match   50.7%;   Score 516;   DB 3;   Length 592;
Best Local Similarity   99.6%;   Pred. No. 2.4e-149;
Matches 516;   Conservative 1;   Mismatches 1;   Indels 0;   Gaps 0;

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Qy    1 ATGGAAAAGCAGAAAAAGACATCACAAAACCAAGAAGAACATTTGGAAAATGAAGCCTAGGAGA  60
Db  518 ATGGAAAAGCAGAAAAAGACATCACAAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 459
Qy   61 AATTTAGAAGAAGCAGAAGACGATTATTTGCATAAGGACACAGGGGAGGACCAGCATGCTAAAAAGA 120
Db  458 AATTTAGAAGAAGCAGAAGACGATTATTTGCATAAGGACACAGGGGAGGACCAGCATGCTAAAAAGA 399
Qy  121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTGACTGCCCTTCAGAA 180
Db  398 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTGACTGCCCTTCAGAA 339
Qy  181 CTTCAGCACACACAGGAACTCTTCCACAGTGGCACTTGCCAATTAAAAATAGCTGCTATT 240
Db  338 CTTCAGCACACACAGGAACTCTTCCACAGTGGCACTTGCCAATTAAAAATAGCTGCTATT 279
Qy  241 ATAGCATCTCTGACTTTTCTTACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
Db  278 ATAGCATCTCTGACTTTTCTTACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 219
Qy  301 TCCCATCAACAATATTTTATAAAATTCCAATCTGGTCATCAACAAAGTCTTGCCAATG 360
Db  219 TCCCATCAACAATATTTTATAAAATTCCAATCTGGTCATCAACAAAGTCTTGCCAATG 360
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Db 218 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 159
Qy 361 GTTTCCATCACTCTCTTGGGCATTGGTTTTACCTGCCCAGGTGTGATAGGCAGCAATTGTCCAA 420
Db 158 GTTTCCATCACTCTCTTGGGCATTGGTTTTACCTGCCCAGGTGTGATAGGCAGCAATTGTCCAA 99
Qy 421 CTTCATAAATGGAACCAAGTATAAGAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
Db   98 CTTCATAAATGGAACCAAGTATAAGAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 39
Qy 481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGT 518
Db   38 AGAAAGCAGAATTGGGCTTCTCAGTTTCTTTTTTGCTGT 1

RESULT 14
US-09-636-215-342/c
; Sequence 342, Application US/0963621S
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427I7C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-636-215-342

Query Match   50.7%; Score 516; DB 3; Length 592;
Best Local Similarity   99.6%; Pred. No. 2.4e-149;
Matches 516; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAGAACTTTGGAAAATGAAGCCTAGGAGA 60
Db 518 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAGAACTTTGGAAAATGAAGCCTAGGAGA 459
Qy   61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACAGGGAGAGAGACCAGCATGCTAAAAAGA 120
Db 458 AATTTAGAAGAAGACGATTATTTGCATAAGGACACAGGGAGAGAGACCAGCATGCTAAAAAGA 399
Qy 121 CCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCCTTCAGAA 180
Db 398 CCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCCTTCAGAA 339
Qy 181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
Db 338 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 279
Qy 241 ATAGCATCTCTGACTTTTCTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
Db 278 ATAGCATCTCTGACTTTTCTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 219

Db 301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
Qy 361 GTTTCCATCACTCTCTTGGGCATTGGTTTTACCTGCCCAGGTGTGATAGGCAGCAATTGTCCAA 420
Db 218 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 159
Qy 158 GTTTCCATCACTCTCTTGGGCATTGGTTTTACCTGCCCAGGTGTGATAGGCAGCAATTGTCCAA 99
Qy 421 CTTCATAAATGGAACCAAGTATAAGAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
Db   98 CTTCATAAATGGAACCAAGTATAAGAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 39
Qy 481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGT 518
Db   38 AGAAAGCAGAATTGGGCTTCTCAGTTTCTTTTTTGCTGT 1

RESULT 15
US-09-685-166A-342/c
; Sequence 342, Application US/0968516GA
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-685-166A-342

Query Match   50.7%; Score 516; DB 3; Length 592;
Best Local Similarity   99.6%; Pred. No. 2.4e-149;
Matches 516; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAGAACTTTGGAAAATGAAGCCTAGGAGA 60
Db 518 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAGAACTTTGGAAAATGAAGCCTAGGAGA 459
Qy   61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACAGGGAGAGAGACCAGCATGCTAAAAAGA 120
Db 458 AATTTAGAAGAAGACGATTATTTGCATAAGGACACAGGGAGAGAGACCAGCATGCTAAAAAGA 399
Qy 121 CCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCCTTCAGAA 180
Db 398 CCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCCTTCAGAA 339
Qy 181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAACTTGCCAATTAAAATAGCTGCTATT 240
Db 338 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 279
Db 301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
Db 218 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 159
Qy 361 GTTTCCATCACTCTCTTGGGCATTGGTTTTACCTGCCCAGGTGTGATAGGCAGCAATTGTCCAA 420
Db 158 GTTTCCATCACTCTCTTGGGCATTGGTTTTACCTGCCCAGGTGTGATAGGCAGCAATTGTCCAA 99
Qy 421 CTTCATAAATGGAACCAAGTATAAGAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
Db   98 CTTCATAAATGGAACCAAGTATAAGAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 39
Qy 481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGT 518
Db   38 AGAAAGCAGAATTGGGCTTCTCAGTTTCTTTTTTGCTGT 1

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Qy    241  ATAGCATCTCTGACTTTTCTTTACACTCTTCTCTGAGGGAAGTAATTCACCCTTTAGCAACT  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    278  ATAGCATCTCTGACTTTTCTTTACACTCTTCTCTGAGGGAAGTAATTCACCCTTTAGCAACT  219

Qy    301  TCCCATCAACAAATATTTTTATAAAAATTCCAAATCCTGGTCATCAACAAAGTCTTGCCAATG  360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    218  TCCCATCAACAAATATTTTTATAAAAATTCCAAATCCTGGTCATCAACAAAGTCTTGCCAATG  159

Qy    361  GTTTCCATCATCACTCTCTTGGCATTGGTTTACCTGCCAGGGTGTGATAGCAGCAATTGTCCAA  420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    158  GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGGTGTGATAGCAGCAATTGTCCAA  99

Qy    421  CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA  480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    98   CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA  39

Qy    481  AGAAAGCAGTTTGGGGCTTCTCAGTTTCTTTTTTTGCTGT  518
           |||||||||:.||||||||||||||||||||||||||||||
Db    38   AGAAAGCARATTGGGGCTTCTCAGTTTCTTTTTTTGCTGT  1
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OM nucleic - nucleic search, using sw model

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Searched: 4996997 seqs, 3332346308 residues
Total number of hits satisfying chosen parameters: 9993994

Maximum DB seq length: 2000000000
Minimum DB seq length: 0
Post-processing: Minimum Match 0%
                   Maximum Match 100%
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pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
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2	1017	100.0	1193	5	AAZ49395	Human STR
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4	1017	100.0	1193	8	ACD02597	cDNA enco
5	1017	100.0	1193	14	ADY92698	Human STE
6	1017	100.0	1195	4	AAH93924	P78P ful
7	1017	100.0	1195	4	AAS64160	Human pro
8	1017	100.0	1195	6	ACAS9968	Prostate
9	1017	100.0	1195	6	ABL95531	Human P78
10	1017	100.0	1195	8	ABK92128	Prostate
11	1017	100.0	1195	8	ACC95695	Prostate
12	1017	100.0	1195	10	ADB75572	Prostate
13	1017	100.0	1195	10	ADB14328	Human pro
14	1017	100.0	1195	10	AAD63162	Human STE
15	1017	100.0	1195	10	AAD62763	Human pro
16	1017	100.0	1195	10	ADG26744	Human pro
17	1017	100.0	1195	11	ADN39812	Cancer/an
18	1017	100.0	1195	11	ADN39395	Cancer/an
19	1017	100.0	1195	11	ADP88258	Prostate
20	1017	100.0	1195	12	AD106462	Human tum
21	1017	100.0	1195	12	AD106436	Human tum
22	1017	100.0	1195	12	ADJ75176	Marker ge
23	1017	100.0	1201	5	ADX33625	Plant ful
24	1017	100.0	1277	5	ADL46020	Human ova
25	1017	100.0	1294	4	AAK51978	Human pol
26	1017	100.0	1330	13	ADR14190	Human NF-
27	1017	100.0	1330	13	ADU06030	Novel bro
28	1017	100.0	1330	14	ADY15575	DNA encod
29	1017	100.0	1017	14	ADY19959	DNA encod
30	1004.4	98.8	1229	4	AAK52962	Human pol
31	1004	98.7	1198	8	ACD02628	STEAP-1 v
32	1002.4	98.6	1201	5	ACD02629	STEAP-1 v
33	988	97.1	1354	12	ADQ22300	Human sof
34	870	85.5	1365	8	ACD02599	STEAP-1 v
35	870	85.5	1365	8	ACD02630	STEAP-1 v
36	866	85.2	1369	8	ACD02632	STEAP-1 v
37	864.4	85.0	1369	8	ACD02631	cDNA enco
38	762.2	74.9	3627	6	ACD02601	STEAP-1 v
39	760.6	74.8	3627	3	AAZ49396	Human six
40	760.6	74.8	3627	5	AAD07071	Human STR
41	760.6	74.8	3627	8	ACD02613	cDNA enco
42	760.6	74.8	3627	8	ACD02605	cDNA enco
43	760.6	74.8	3627	8	ACD02606	cDNA enco
44	760.6	74.8	3627	8	ACD02598	cDNA enco
45	760.6	74.8	3627	8	ACD02612	cDNA enco

ALIGNMENTS

RESULT 1
ADV73174
ID   ADV73174 standard; DNA; 1177 BP.
XX
AC   ADV73174;
XX
DT   10-MAR-2005 (first entry)
XX
DE   Human colon tumor cell upregulated gene SEQ ID NO 15.
XX
KW   dsi; gene; cancer; neoplasm; cytostatic.
XX
OS   Homo sapiens.
XX
PN   WO200410345-A2.
XX
PD   23-DEC-2004.
XX
PF   28-OCT-2003; 2003WO-US034019.
XX
PR   29-OCT-2002; 2002US-0422176P.
XX
PA   (PHAA) PHARMACIA CORP.
XX
PI   Bourner MJ, Bu JJ, Head RD, Hippenmeyer PJ, Klein BK;
PI   Mazzarella RA, Staten NR;
XX
DR   WPI; 2005-039958/04.
DR   P-PSDB; ADV73212.
XX
PT   New antibody that immunospecifically binds to p-cadherin, useful in
PT   preparing a composition for treating or preventing a cancer-associated
PT   disorder.
XX
PS   Disclosure; SEQ ID NO 15; 257pp; English.
XX
CC   The invention relates to an antibody immunospecifically binds to p-
CC   cadherin or its fragment. The antibody is useful in preparing a p-
CC   composition for treating or preventing a cancer-associated disorder. The
CC   composition for treating or preventing a cancer-associated disorder. The
CC   present sequence represents a gene upregulated in human colon cancer
CC   cells.

```
SQ   Sequence 1177 BP; 364 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

     Query Match            100.0%;  Score 1017;  DB 14;  Length 1177;
     Best Local Similarity  100.0%;  Pred. 0;
     Matches 1017;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 ATGGAAAAGCAGAAAAAGCAATCACAAAACCAAGAGAGAACTTTGGAAAATGAAGCCTAGGAGA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     66 ATGGAAAAGCAGAAAAAGCAATCACAAAACCAAGAGAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy     61 AATTTAGAAGAAGAACGAGATTATTTGCATAAGGACACACGGGAGACAGGGAGGAGCCTAAAAGA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    126 AATTTAGAAGAAGAACGAGATTATTTGCATAAGGACACACGGGAGACAGGGAGGAGCCTAAAAGA 185

Qy    121 CCTGTTGCTTTTGCATTTGCACCAAACAGCCCATGCTGTGATGAAATTTGACTGCCCTTCAGAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGTGATGAAATTTGACTGCCCTTCAGAA 245

Qy    181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy    241 ATAGCATCTCTGACTTTTCTTACACTCTTCTGACGGGAGTAATTCACCCTTTAGCAACT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    306 ATAGCATCTCTGACTTTTCTTACACTCTTCTGACGGGAGTAATTCACCCTTTAGCAACT 365

Qy    301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy    361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGATAGCAGCAATTGTCCAA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGATAGCAGCAATTGTCCAA 485

Qy    421 CTTCATAATGGAACCAAGTATAGAAGAGTTTCCACATTGGTTGGATGTGTTAACA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    486 CTTCATAATGGAACCAAGTATAAGAAGAGTTTCCACATTGGTTGGATGTGTTAACA 545

Qy    481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTCTTTTTGCTGTACTGCAATTTATAGTCTG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTCTTTTTGCTGTACTGCAATTTATAGTCTG 605

Qy    541 TCTTACCCAAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCCATATCAACAGGTC 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    606 TCTTACCCAAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCCATATCAACAGGTC 665

Qy    601 CAACAAAATAAAAGAAGAATGCCTGGATTGAGCATGATGAGATTTATGTG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    666 CAACAAAATAAAAGAAGAATGCCTGGATTGAGCATGATGAGATTTATGTG 725

Qy    661 TCTCTGGGAATTGTGGGAATTGGCAATACTCGGCTCTGTTCGGCTGTGACATCTATTCCATCT 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    726 TCTCTGGGAATTGTGGGAATTGGCAATACTCGGCTCTGTTCGGCTGTGACATCTATTCCATCT 785

Qy    721 GTGCAGTGACTCTTTGACATGGAGAGAATTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    786 GTGAGTGACTCTTTGACATGGAGAGAATTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy    781 TCCCTTCTACTGGGCACAATACACGCCATGATGATTTTTGCCTGGAATAAGTGGATAGATATA 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    846 TCCCTTCTACTGGGCACAATACACGCCATGATGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy    841 AAACAAATTTGTATGGTATACACCTCCAACACTTTATGTAGTAGCTCGTTTTCCTTCCAAATTGTT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    906 AAACAAATTTGTATGGTATACACCTCCAACACTTTATGTAGTAGCTCGTTTTCCTTCCAAATTGTT 965

Qy    901 GTCCTGATTATTTAAAAGCATAACTATTCCTGGCCTTGAGGAAGAAGATACTGAAGATT 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    966 GTCCTGATTATTTAAAAGCATAACTATTCCTGGCCTTGAGGAAGAAGATACTGAAGATT 1025

Qy    961 AGACATGGTTGGGAAGAGGTCACCAAAAATTAACAAAAACTGAGATATGTTCCCAGTTG 1017
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1026 AGACATGGTTGGGAAGAGGTCACCAAAAATTAACAAAAACTGAGATATGTTCCCAGTTG 1082
```

CC   This sequence represents cDNA encoding a novel human protein, STRAP-1
CC   (serpentine transmembrane antigen of the prostate). STRAP-1 is the
CC   prototype member of the STRAP family of proteins (AAY58194-Y58197) which
CC   exhibit a high degree of structural conservation, but which show no
CC   significant structural homology to known human proteins. The STRAP-1 gene
CC   has been localised to chromosome 7p22. STRAP-1 is thought to be a type
CC   IIIa membrane protein and is expressed predominantly in prostate cells in
CC   normal human tissues. Structurally, STRAP-1 is a 339 amino acid protein
CC   characterised by six transmembrane domains and intracellular N- and C-
CC   termini, suggesting that it folds in a "serpentine" manner into three
CC   extracellular and two intracellular loops. STRAP-1 mRNA and protein
CC   expression is maintained at high levels and throughout all stages of
CC   prostate cancer. STRAP-1 mRNA and/or protein is also overexpressed in
CC   certain other cancers, including bladder, colon, pancreatic and ovarian
CC   cancer. The function of the STRAP proteins is not known. They may be ion
CC   channels (from the presence of six transmembrane domains, a feature which
CC   is shared by certain ion channels) or gap-junction proteins (from
CC   immunohistochemical staining). STRAP-1 and STRAP-2 are cell-surface
CC   tumour antigens. Immunisation with a STRAP protein induces cellular and

CC   humoral immune responses against STRAP-expressing cells. STRAP proteins
CC   may be used to identify specific-binding agents, to produce anticancer
CC   vaccines and to generate specific antibodies. The antibodies may be used
CC   for detection, prognosis, and monitoring of cancers (or susceptibility to
CC   cancer), as therapeutic inhibitors or to target therapeutic agents to
CC   their site of action. STRAP nucleic acids may be used for recombinant
CC   protein production, as diagnostic and prognostic reagents, for
CC   identifying STRAP-expressing cells for screening inhibitors of STRAP
CC   expression and for therapeutic modulation/inhibition of STRAP expression.
CC   Since high levels of STRAP proteins are exposed on the cell surface, they
CC   are easily targetted by systemically administered agents, and because
CC   they are expressed mainly on prostatic epithelial cells, agents targetted
CC   to them should have minimal side effects on other tissues
XX
SQ   Sequence 1193 BP; 382 A; 219 C; 233 G; 359 T; 0 U; 0 Other;

Query Match   100.0%; Score 1017; DB 3; Length 1193;
Best Local Similarity 100.0%; Pred. No. 2.6e-276;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGGAAAAGCAGAAAAGACATCACAAACCAAGAAGAGAAGAACTTTGGAAAATGAAGGCCTAGGAGA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     64 ATGGAAAAGCAGAAAAGACATCACAAACCAAGAAGAGAAGAACTTTGGAAAATGAAGGCCTAGGAGA 123

Qy     61 AATTTAGAAGAAGACGAGCATTATTTGCATTAAGGACACAACCGGGAGAGACCAGCCATGCTAAAAGA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    124 AATTTAGAAGAAGACGAGCATTATTTGCATTAAGGACACAACCGGGAGAGACCAGCCATGCTAAAAGA 183

Qy    121 CCTGTGCTTTTGCATTTGCACCAAACAGACCCATGCTGATGAATTTGACTGCCCTTCAGA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    184 CCTGTGCTTTTGCATTTGCACCAAACAGACCCATGCTGATGAATTTGACTGCCCTTCAGA 243

Qy    181 CTTCAGCACACACCAGGAACTCTTTCCCACAGTGGCACTTGCCCAATTAAATAGCTGCTATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    244 CTTCAGCACACACCAGGAACTCTTTCCCACAGTGGCACTTGCCCAATTAAATAGCTGCTATT 303

Qy    241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCCTTTAGCAACT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    304 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCCTTTAGCAACT 363

Qy    301 TCCCATCAACAACATATTTTTATAAAAAATTCCAATCCTGGTTCATCAACAACAAAGTCTTGCCAATG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    364 TCCCATCAACAACATATTTTTATAAAAAATTCCAATCCTGGTTCATCAACAACAAAGTCTTGCCAATG 423

Qy    361 GTTTCCATCACTCTCTTGGCAATGGTTTACCTGCCCAGGTGTCATAGCAGCAATTGTCCAA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    424 GTTTCCATCACTCTCTTGGCAATGGTTTACCTGCCCAGGTGTCATAGCAGCAATTGTCCAA 483

Qy    421 CTTCATAATGGAACCAAAGTTATAAGAAGTTTCCACATTGGTTGGATAAGTGAGTGTTAACA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    484 CTTCATAATGGAACCAAAGTTATAAGAAGTTTCCACATTGGTTGGATAAGTGAGTGTTAACA 543

Qy    481 AGAAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTGCTGTACTGCATGCAAATTTATAGTCTG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    544 AGAAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTGCTGTACTGCATGCAAATTTATAGTCTG 603

Qy    541 TCTTACCCAATGAGGCGGATCCTACAGATACAAGTTGCTAAACTGGGCCATATCAACAGGTC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    604 TCTTACCCAATGAGGCGGATCCTACAGATACAAGTTGCTAAACTGGGCCATATCAACAGGTC 663

Qy    601 CAACAAAATAAAGAAGATGCCTGGATGAGCATGAGGATGGGAGATTTATGTG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    664 CAACAAAATAAAGAAGATGCCTGGATGAGCATGAGGATGGGAGATTTATGTG 723

Qy    661 TCTCTGGGGAATTGTGGGATTGGCAATTACTGGCTCTCGTTGGCATCTATTCCATCT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    724 TCTCTGGGGAATTGTGGGATTGGCAATTACTGGCTCTCGTTGGCATCTATTCCATCT 783

Qy    721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATTATTCAGAGCAAGCTAGGAATTGTT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    784 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATTATTCAGAGCAAGCTAGGAATTGTT 843

Qy    781 TCCCTTCTACTGGGCACAAATACACGGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
```

Db 844 TCCCTTCTACTGGGCCACAAATACACGGCATTGATTTTTGCCTTGAGAATGATGGGATAGATATA 903
Qy 841 AAACAATTTGTATGGTATACACCTCCAAACTTTATGATAGCTGTTTTCCTTCCAAATTGTT 900
Db 904 AAACAATTTGTATGGTATACACCTCCAAACTTTATGATAGCTGTTTTCCTTCCAAATTGTT 963
Qy 901 GTCCTCGATATTTAAAAGCATATTATTCCTCGATGCTGTTGGGAGGAAGGAGATACTGAAGATT 960
Db 964 GTCCTGATATTTAAAAGCATATTATTCCTGCCATGCTTGAGGAAGGAAGATACTGAAGATT 1023
Qy 961 AGACATGGTTGGGAAGACGTCACCAAAAATTAACAAAACTGAATAATGTTCCCAGTTG 1017
Db 1024 AGACATGGTTGGGAAGACGTCACCAAAAATTAACAAAACTGAATAATGTTCCCAGTTG 1080

RESULT 3
AC   AAD07067
XX
ID   AAD07067 standard; cDNA; 1193 BP.
XX
DT   06-AUG-2001; (first entry)
XX
DE   Human six transmembrane epithelial antigen of prostate-1 clone 10 cDNA.
XX
KW   Human; cytostatic; antiproliferative; vaccine; gene therapy;
KW   six transmembrane epithelial antigen of the prostate-1; STEAP-1;
KW   chromosome 7p22.3; cancer; prostate; colon; bladder; lung; ovarian;
KW   pancreatic; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FH
FT   CDS   64..1191
FT   /tag= a
FT   /product= "Human six transmembrane epithelial antigen of
FT   the prostate (STEAP)-1"
FT   /note= "CDS does not include stop codon"
FT   /transl_except= (pos:1078..1086, aa:Leu-Asn)
FT   /note= "inframe stop codon alters the reading frame"
FT   /partial
XX
PN   WO20014O276-A2.
XX
PD   07-JUN-2001.
XX
PF   06-DEC-2000; 2000WO-US033040.
XX
PR   06-DEC-1999; 99US-00455486.
XX
PA   (UROG-) UROGENESYS INC.
XX
PI   Afar DEH, Hubert RS, Raitano AB, Saffran DC, Mitchell SC;
PI   Faris M, Jakobovits A;
XX
DR   WPI; 2001-367804/38.
DR   P-PSDB; AAE02780.
XX
PT   New STEAP (six transmembrane epithelial antigen of the prostate)
PT   proteins, expressed in human cancers, useful for detecting and treating
PT   cancer.
XX
PS   Example 2; Fig 1A-1B; 187pp; English.
XX
CC   The present sequence is human six transmembrane epithelial antigen of the
CC   prostate (STEAP)-1 clone 10 cDNA. STEAP-1 is a member of cell surface
CC   serpentine transmembrane antigens. STEAP-1 gene is located on chromosome
CC   7p22.3 and is used in gene therapy. Inhibiting the development or
CC   progression of a cancer (eg. prostate, colon, bladder, lung, ovarian and
CC   pancreatic) expressing STEAP or inhibiting growth or killing cells
CC   expressing STEAP in a patient, comprises administering a vaccine that
CC   composition to the patient. Treating a patient with a cancer that

CC expresses STEAP, or inhibiting growth or killing cells expressing STEAP,
CC comprises administering to the patient a vector encoding single chain
CC monoclonal antibody that comprises the variable domains of the heavy and
CC light chains of the monoclonal antibody that specifically binds to STEAP,
CC such that the vector delivers the single chain monoclonal antibody coding
CC sequence to the cancer cells and the encoded single chain monoclonal
CC antibody is expressed intracellularly. Note: The present sequence is also
CC shown in sequence listing of the specification, but it lacks nucleotides
CC at its 5' end
XX
SQ Sequence 1193 BP; 382 A; 219 C; 233 G; 359 T; 0 U; 0 Other;

Query Match   100.0%; Score 1017; DB 5; Length 1193;
Best Local Similarity   100.0%; Pred. No. 2.6e-276;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ATGGAAAAGCAGAAAAAGACAATCACAAAACCAAGAGAGAACTTTGGAAAATGAAGCCTAGGAGA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   64 ATGGAAAAGCAGAAAAAGACAATCACAAAACCAAGAGAGAACTTTGGAAAATGAAGCCTAGGAGA 123

Qy   61 AATTTAGAAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGAGACCAGCATGCTAAAAAGA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   124 AATTTAGAAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGAGACCAGCATGCTAAAAAGA 183

Qy   121 CCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGTGATGAAATTTGACTGCGCCCTTCAGAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   184 CCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGTGATGAAATTTGACTGCGCCCTTCAGAA 243

Qy   181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCCACTTGCCCAATTAAAATTAGCTGCTATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   244 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCCACTTGCCCAATTAAAATTAGCTGCTATT 303

Qy   241 ATAGCATCTCTGACTTTTCTTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   304 ATAGCATCTCTGACTTTTCTTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 363

Qy   301 TCCCATCAACAAATATTTTTTATAAAAATTCCAATCCTGGTCATCAACAAAAGTCTTGCCAATG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   364 TCCCATCAACAAATATTTTTTATAAAAATTCCAATCCTGGTCATCAACAAAAGTCTTGCCAATG 423

Qy   361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   424 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 483

Qy   421 CTTCATAATGGAACCAAGTATAAGAAGTTCCCACATTGGTTGGATAAGTGGATGTTAACA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   484 CTTCATAATGGAACCAAGTATAAGAAGTTCCCACATTGGTTGGATAAGTGGATGTTAACA 543

Qy   481 AGAAAGCAGTTGGGCCTTCTCAGTTCTTTTTTGCTGCTATGCATGCAATTATAGTCTG 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   544 AGAAAGCAGTTGGGCCTTCTCAGTTCTTTTTTGCTGCTATGCATGCAATTATAGTCTG 603

Qy   541 TCTTACCCAAATGAGGCGATCCTACAGTAGCATCAAAGTTGCTAAAACTGGGCATTCAACAGGTC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   604 TCTTACCCAAATGAGGCGATCCTACAGTAGCATCAAAGTTGCTAAAACTGGGCATTCAACAGGTC 663

Qy   601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGAGTGTTGGAGAATGGAGAATTATGTG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   664 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGAGTGTTGGAGAATGGAGAATTATGTG 723

Qy   661 TCTCTGGGAATTGTGGGAATTGGGCAATACTGGCGCTCTGTTGCTGGCAATCTATTCCATCT 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   724 TCTCTGGGAATTGTGGGAATTGGGCAATACTGGCGCTCTGTTGCTGGCAATCTATTCCATCT 783

Qy   721 GTGAGTGACTCTTTGACATGGAGAATTTCACTATTATTCAGACGCAAGCTAGGAATTGTT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   784 GTGAGTGACTCTTTGACATGGAGAATTTCACTATTATTCAGACGCAAGCTAGGAATTGTT 843

Qy   781 TCCCTTCTACTGGGCACCATGGAATTAGGAATTAAGTTGGATAGATATA 840
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   844 TCCCTTCTACTGGGCACCATGGAATTAGGAATTAAGTTGGATAGATATA 903

Qy   841 AAACAATTTGTATGTATACACCTCCAACTTTTATGATGACTGTGTTTTCCTTCCAATTGTT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   844 AAACAATTTGTATGTATACACCTCCAACTTTTATGATGACTGTGTTTTCCTTCCAATTGTT 903

Db   904 AAACAATTTGTATGTATACACCTCCAACTTTTATGATGACTGTGTTTTCCTTCCAATTGTT 963
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   901 GTCCTGATATTTAAAAGCATACTAATTCCTGCCATGCCTTGAGGAGGAAGAAGTACTGAGAGATT 960

Qy   904 GTCCTGATATTTAAAAGCATACTAATTCCTGCCATGCCTTGAGGAGGAAGAAGTACTGAGAGATT 1023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   964 GTCCTGATATTTAAAAGCATACTAATTCCTGCCATGCCTTGAGGAGGAAGAAGTACTGAGAGATT 1023

Qy   961 AGACATGGTTGGGAGGAAGACGTCACCAAAAATTAACAAAACTGAGATATGGTTCCCAGTTG 1017
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1024 AGACATGGTTGGGAGGAAGACGTCACCAAAAATTAACAAAACTGAGATATGGTTCCCAGTTG 1080

RESULT 4
ACD02597
ID   ACD02597 standard; cDNA; 1193 BP.
XX
AC   ACD02597;
XX
DT   31-JUL-2003 (first entry)
XX
DE   cDNA encoding novel human gene STEAP-1 variant 1.
XX
KW   STEAP-1; six transmembrane epithelial antigen of the prostate; cancer;
KW   cancer vaccine; delineation; cytogenetic abnormality; cytostatic;
KW   vaccine; gene; ss.
OS   Homo sapiens.
XX
PN   WO200302995-A2.
XX
PD   20-MAR-2003.
XX
PF   06-SEP-2002; 2002WO-US028371.
XX
PR   06-SEP-2001; 2001US-0317840P.
PR   05-APR-2002; 2002US-0370387P.
XX
PA   (AGEN-) AGENSYS INC.
XX
PI   Faris M, Ge W, Raitano AB, Challita-Eid PM, Jakobovits A;
XX
DR   WPI; 2003-313240/30.
DR   P-PSDB; ABU98383.
XX
PT   New composition comprising a substance that modulates the status of a
PT   STEAP-1-related protein, useful for treating and detecting cancer.
XX
PS   Example 2; Fig 2A; 248pp; English.
XX
CC   The invention describes a composition comprising a substance that
CC   modulates the status of a protein (I) of 340 or 283 amino acids, or of
CC   any of the 15 sequences of 259 amino acids, given in the specification,
CC   or a molecule that is modulated by the protein, where the status of the
CC   cell that expresses the protein is modulated. The compositions, proteins,
CC   polynucleotides and methods are useful for treating and detecting cancer.
CC   The STEAP-1-related proteins are useful for generating cancer vaccines.
CC   The polynucleotides are useful as tools for delineating, with greater
CC   precision, cytogenetic abnormalities in the chromosomal region that
CC   encodes STEAP-1 that may contribute to the malignant phenotype. This
CC   sequence encodes a variant of human six transmembrane epithelial antigen
CC   of the prostate or STEAP-1
XX
SQ   Sequence 1193 BP; 382 A; 221 C; 233 G; 357 T; 0 U; 0 Other;

Query Match   100.0%; Score 1017; DB 8; Length 1193;
Best Local Similarity   100.0%; Pred. No. 2.6e-276;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ATGGAAAAGCAGAAAAAGACAATCACAAAACCAAGAGAGAACTTTGGAAAATGAAGCCTAGGAGA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   66 ATGGAAAAGCAGAAAAAGACAATCACAAAACCAAGAGAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy   61 AATTTAGAAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGAGACCAGCATGCTAAAAAGA 120

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Qy  126 AATTTAGAAGAAGACAGGATTATTTGCATAAGGACACGGGAGGAGAGACCAGCATGTAAAAAGA
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  126 AATTTAGAAGAAGACAGGATTATTTGCATAAGGACACGGGAGGAGAGACCAGCATGTAAAAAGA 185

Qy  121 CCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAAATTTGACTGCCTTCAGAA
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  186 CCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAAATTTGACTGCCTTCAGAA 245

Qy  181 CTTCAGCACACACAGGAAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  246 CTTCAGCACACACAGGAAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy  241 ATAGGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  306 ATAGGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy  301 TCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGGTCATCAACAAAAGTCTTGCCAATG
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  366 TCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGGTCATCAACAAAAGTCTTGCCAATG 425

Qy  361 GTTTCCATCATCACTCTCTTGGCATTGGTTTTACCTGGGTGTGATAGCAGCAAATTGTCCAA
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  426 GTTTCCATCATCACTCTCTTGGCATTGGTTTTACCTGGGTGTGATAGCAGCAAATTGTCCAA 485

Qy  421 CTTCATAATGGACACCAAGTATAAGAGTTTCCACATTGGTTGGATAAGTGGATTGTTAACA
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  486 CTTCATAATGGACACCAAGTATAAGAGTTTCCACATTGGTTGGATAAGTGGATTGTTAACA 545

Qy  481 AGAAAGCAGTTTGGGGCTTCTCAGTTTCTTTTTTGCTGTATCTGCAATTTATAGTCTG
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  546 AGAAAGCAGTTTGGGGCTTCTCAGTTTCTTTTTTGCTGTATCTGCAATTTATAGTCTG 605

Qy  541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAAACTGGCATATCAACACAGGTC
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAAACTGGCATATCAACACAGGTC 665

Qy  601 CAACAAAATAAAGAAGAGAATGCCTGGAATGAGCATGAATGGAGAAATTCAGTTATGTG
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  666 CAACAAAATAAAGAAGAGAATGCCTGGAATGAGCATGAATGGAGAAATTCAGTTATGTG 725

Qy  661 TCTTCTGGGAATTGTGGGCAATTGGCAATACTGGCTCTGTTGTGTGACACTCTATTCCATCT
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  726 TCTTCTGGGAATTGTGGGCAATTGGCAATACTGGCTCTGTTGTGTGACACTCTATTCCATCT 785

Qy  721 GTGAGTGACTCTTTGACATGGAGAGAATTCACTATATTATTCAGTAGGAATTGTT
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  786 GTGAGTGACTCTTTGACATGGAGAGAATTCACTATATTATTCAGTAGGAATTGTT 845

Qy  781 TCCCTTCTACTGGGCACAATACACGCATTGAATTGGATAAGTGGATAGAGATATA
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  846 TCCCTTCTACTGGGCACAATACACGCATTGAATTGGATAAGTGGATAGAGATATA 905

Qy  841 AAACAATTTGTATGGTATACACCCCAACTTTATGAAGCTGTTTTTCCTTCAAATTGTT
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  906 AAACAATTTGTATGGTATACACCCCAACTTTATGAAGCTGTTTTTCCTTCAAATTGTT 965

Qy  901 GTCCTGATATTTAAAAGCATAACTAYTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  966 GTCCTGATATTTAAAAGCATAACTAYTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy  961 AGACATGGTTGGGAAGAGCGTCACCAAAATTAACAAAACTGAGATATAGTTCCCAGTTG
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Db 1026 AGACATGGTTGGGAAGAGCGTCACCAAAATTAACAAAACTGAGATATAGTTCCCAGTTG 1082
```

XX
KW   Vaccine; antibody therapy; immune stimulation; gene amplification;
KW   prostate tumor; cytostatic; andrology; genitourinary disease; neoplasm;
KW   cancer; six transmembrane epithelial antigen of prostate 1; STEAP-1;
KW   chromosome 7; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FH
FT   CDS   64..1191
FT   /tag= b
FT   /product= "Human STEAP-1 protein #2"
FT   /transl_except= (pos:1078..1086, aa:Leu-Asn)
FT   /partial
FT   /note= "No stop codon"
FT   CDS   64..1083
FT   /tag= a
FT   /product= "Human STEAP-1 protein #1"
XX
PN   US2005063975-A1.
XX
PD   24-MAR-2005.
XX
PF   05-JAN-2004; 2004US-00752421.
XX
PR   01-JUN-1999; 99US-00323873.
PR   06-DEC-1999; 99US-00455486.
XX
PA   (AFAR/) AFAR D E H.
PA   (HUBE/) HUBERT R S.
PA   (RAIT/) RAITANO A B.
PA   (SAFF/) SAFFRAN D.
PA   (MITC/) MITCHELL S C.
XX
PI   Afar DEH, Hubert RS, Raitano AB, Saffran D, Mitchell SC;
XX
PS   Example 1; SEQ ID NO 1; 80pp; English.
XX
PT   Novel isolated polynucleotide that encodes six transmembrane epithelial
PT   antigen of prostate polypeptide, useful for diagnosing or treating
PT   prostate cancer.
XX
PR   Novel isolated polynucleotide that encodes six transmembrane antigens
CC   predominantly expressed in the prostate termed as six transmembrane
CC   epithelial antigen of prostate (STEAP-2) and their corresponding nucleic
CC   acid sequences. STEAP-2 DNA is useful for diagnosing or treating prostate
CC   cancer; it can be used as a primer or probe for the amplification and/or
CC   detection of STEAP genes and as a tool for modulating or inhibiting the
CC   expression of the STEAP genes. STEAP-2 DNA is also useful in cancer
CC   vaccines for the generation of therapeutic or prophylactic immunity
CC   against prostate cancer. STEAP antibodies are useful in antibody therapy.
CC   The present sequence is the human STEAP-1 cDNA. Human STEAP-1 gene maps
CC   within chromosome 7p22 (7p2.3).
XX
SQ   Sequence 1193 BP; 382 A; 219 C; 233 G; 359 T; 0 U; 0 Other;

DR   WPI; 2005-252610/26.
DR   P-PSDB; ADY92699, ADY92744.
XX

Query Match   100.0%; Score 1017; DB 14; Length 1193;
Best Local Similarity   100.0%;
Matches 1017; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy    1 ATGGAAAGCGAGAAAAGACATCACAAACACAAGAGAGAACTTTGGAAAATGAAGGCCTAGGAGA 60
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Db   64 ATGGAAAGCGAGAAAAGACATCACAAACACAAGAGAGAACTTTGGAAAATGAAGGCCTAGGAGA 123

Qy   61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGGAGAGACCAGCATGTAAAAAGA 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  124 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGGAGAGACCAGCATGTAAAAAGA 183

Qy  121 CCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAAATTTGACTGCCTTCAGAA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   184  CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA  243
Qy   181  CTTCAGCACACACAGAGAACTCTTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGTATT  240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   244  CTTCAGCACACACAGAGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT  303
Qy   241  ATAGCACATCTCTGACTTTTCTTTACACTCTTCTGAGGGAGAAGTAATTCACCCTTTAGCAACT  300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   304  ATAGCACATCTCTGACTTTTCTTTACACTCTTCTGAGGGAGAAGTAATTCACCCTTTAGCAACT  363
Qy   301  TCCCATCAACAAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG  360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   364  TCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG  423
Qy   361  GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA  420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   424  GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA  483
Qy   421  CTTCATATAATGGAACCAAGTAATAAGAAGTTTCCACATTGGTTGGGATAAGTGGATGTTAACA  480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   484  CTTCATATAATGGAACCAAGTAATAAGAAGTTTCCACATTGGTTGGGATAAGTGGATGTTAACA  543
Qy   481  AGAAAGCAGTTTGGGCTTCCAGTTTCTTTTTGTGTACTGCATCGCAATTTATAGTCTG  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   544  AGAAAGCAGTTTGGGCTTCCAGTTTCTTTTTGCTGTACTGCATCGCAATTTATAGTCTG  603
Qy   541  TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAAACTGGGCATATCAACAGTC  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   604  TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAAACTGGGCATATCAACAGTC  663
Qy   601  CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   664  CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG  723
Qy   661  TCTCTGGGAATTGTGGGATTGGCAATACTGGCCTCGTTGCGTGTGACATCTATTCCATCT  720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   724  TCTCTGGGAATTGTGGGATTGGCAATACTGGCCTCGTTGCGTGTGACATCTATTCCATCT  783
Qy   721  GTGAGTGACTCTCTTTGACATGGAGAATTCACTATATATTCAGAGCAAGCTAGGAATTGTT  780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   784  GTGAGTGACTCTCTTTGACATGGAGAATTCACTATATATTCAGAGCAAGCTAGGAATTGTT  843
Qy   781  TCCCTTCTACTCGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGAATATA  840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   844  TCCCTTCTACTCGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGAATATA  903
Qy   841  AAACAATTTGTATGGTATACACCTCCCAACTTTTATGATAGCTGTTTTCCTTCCAAATTGTT  900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   904  AAACAATTTGTATGGTATACACCTCCCAACTTTTATGATAGCTGTTTTCCTTCCAAATTGTT  963
Qy   901  GTCCTGATATTTTAAAAGCATACTATTCCTGCCATGCTTGAGGAGAAGAAGATACTGAAGATT  960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   964  GTCCTGATATTTTAAAAGCATACTATTCCTGCCATGCTTGAGGAGAAGAAGATACTGAAGATT  1023
Qy   961  AGACATGGTTGGGAGGAGAGGTCACCAAAAAATTAACAAAAACTGAGAATATGTTCCCAGTTG  1017
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1024  AGACATGGTTGGGAGGAGAGGTCACCAAAAAATTAACAAAAACTGAGAATATGTTCCCAGTTG  1080
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RESULT 6
AAH93924
ID   AAH93924 standard; cDNA; 1195 BP.
XX
AC   AAH93924;
XX
DT   04-OCT-2001 (first entry)
XX
DE   P789P full length cDNA sequence.
XX
KW   Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW   cytostatic; gene therapy; metastasis; ss.
OS   Homo sapiens.

XX
PN   WO20015163-A2.
XX
PD   19-JUL-2001.
XX
PF   16-JAN-2001; 2001WO-US001574.
XX
PR   14-JAN-2000; 2000US-00483672.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI   Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI   Wang A, Meagher MJ;
XX
DR   WPI; 2001-425873/45.
XX
PT   New polynucleotide encoding a prostate-specific protein, for diagnosing,
PT   monitoring and treating prostate cancer in a patient and for use in
PT   vaccines.
XX
PS   Claim 1; Page 510; 543pp; English.
XX
CC   The present invention describes polynucleotide sequences (I) which encode
CC   prostate-specific proteins (III). (I) and (II) have cytostatic activity,
CC   and can be used in vaccine production and gene therapy. (I), (II),
CC   antibodies to (II), fusion proteins comprising (III), and isolated T cells
CC   prepared using (I) or (II) are used to treat cancer in a patient. (I) and
CC   the antibodies are also used in the detection of cancer in a patient. The
CC   cancer that is diagnosed or treated is particularly prostate cancer. (I)
CC   and (II) can be used in vaccines. The antibodies or (II) can be used for
CC   monitoring the progression of cancer in a patient. (I) and (II) can also
CC   be used to improve diagnostic and therapeutic methods for prostate
CC   cancer. They can indicate the level of metastasis as well as the prostate
CC   volume. AAH93357 to AAH93944 and AAM01115 to AAM01318 represent
CC   polynucleotide and amino acid sequences used in the exemplification of
CC   the present invention
XX
SQ   Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

Query Match   100.0%; Score 1017; DB 4; Length 1195;
Best Local Similarity 100.0%; Pred. No. 2.6e-276;
Matches 1017; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy     1  ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAGAACTTTGGAAAATGAAGCCTAGGAGA  60
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Db    66  ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAGAACTTTGGAAAATGAAGCCTAGGAGA  125
Qy    61  AATTTAGAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCGATGTGCTAAAAAGA  120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   126  AATTTAGAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCGATGTGCTAAAAAGA  185
Qy   121  CCCTGTGCTTTTGCAATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA  180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   186  CCCTGTGCTTTTGCAATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA  245
Qy   181  CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT  240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   246  CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT  305
Qy   241  ATAGCACATCTCTGACTTTTCTTTACACTCTTCTGAGGGAGAAGTAATTCACCCTTTAGCAACT  300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   306  ATAGCACATCTCTGACTTTTCTTTACACTCTTCTGAGGGAGAAGTAATTCACCCTTTAGCAACT  365
Qy   301  TCCCATCAACAAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG  360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   366  TCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG  425
Qy   361  GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTTGATAGCAGCACAAATTGTCCAA  420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   426  GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTTGATAGCAGCACAAATTGTCCAA  485
Qy   421  CTTCATATAATGGAACCAAGTAATAAGAAGTTCCACATTGGTTGGGATAAGTGGATGTTAACA  480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGAATAAGTTGTAACA
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTTTGCTGTACTGCATGCAATTTATAGTTCTG 540

Qy  481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTTTGCTGTACTGCATGCAATTTATAGTTCTG 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTTTGCTGTACTGCATGCAATTTATAGTTCTG 605

Qy  541 TCTTACCCAATGAGGCGGATCCTACAGATACAAGTTGCTAAACTGGCCATATCAACACAGGTC 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  606 TCTTACCCAATGAGGCGGATCCTACAGATACAAGTTGCTAAACTGGCCATATCAACACAGGTC 665
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RESULT 7

AAS64160
ID   AAS64160 standard; cDNA; 1195 BP.
XX
AC   AAS64160;
XX
DT   29-JAN-2002 (first entry)
XX
DE   Human prostate cDNA sequence #590.
XX
KW   Human; prostate cancer; ssi cytostatic; immunostimulant; tumour.
OS   Homo sapiens.
XX
PN   WO20017303-A2.
XX
PD   04-OCT-2001.
XX
PF   27-MAR-2001; 2001WO-US009919.
XX
PR   27-MAR-2000; 2000US-00336857.
PR   09-MAY-2000; 2000US-00558100.
PR   12-MAY-2000; 2000US-00570737.
PR   13-JUN-2000; 2000US-00593793.
PR   27-JUN-2000; 2000US-00605783.
PR   09-AUG-2000; 2000US-00635215.
PR   29-AUG-2000; 2000US-00651236.
PR   06-SEP-2000; 2000US-00657279.
PR   02-OCT-2000; 2000US-00679426.
PR   10-OCT-2000; 2000US-00685166.
PR   09-NOV-2000; 2000US-00709729.
XX
PA   (CORI-) CORIXA CORP.

XX
PI   Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI   Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI   Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
DR   WPI; 2001-639232/73.
DR   P-PSDB; AAU69927.
XX
PT   New human prostate-specific polypeptides and polynucleotides useful for
PT   the diagnosis and treatment of cancer, especially prostate cancer.
XX
PS   Claim 1; Page 548; 579pp; English.
XX
CC   The invention relates to isolated prostate-specific polynucleotides,
CC   polypeptides, fusion proteins of the polypeptides, antibodies raised
CC   against the polypeptides (or antigenic epitopes derived from them) and
CC   antigen-presenting cells expressing the polypeptides. The antibodies are
CC   useful for detecting the presence of cancer, especially prostate cancer.
CC   The polypeptides, polynucleotides and the antigen-presenting cells are
CC   useful for stimulating and/or expanding T cells specific for a tumour
CC   protein, and for inhibiting the development of cancer especially prostate
CC   cancer. Compositions comprising the polynucleotide and/or polypeptide are
CC   useful for stimulating an immune response, and for treating cancer. The
CC   oligonucleotide is useful for detecting cancer. The present sequence is a
CC   prostate specific polynucleotide of the invention
SQ   Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

Query Match   100.0%; Score 1017; DB 4; Length 1195;
Best Local Similarity   100.0%;
Matches 1017; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy    1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy   61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACACGGGAGAGAGAGCAGCAGCATGTA 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACACGGGAGAGAGAGCAGCAGCATGTA 185

Qy  121 CCTGTGCTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  186 CCTGTGCTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy  181 CTTCAGCGACACACAGGAGAACTCTTTCCACAGTGGCACTTGCCAATTAAAAATAGCTGCTATT 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  246 CTTCAGCGACACACAGGAGAACTCTTTCCACAGTGGCACTTGCCAATTAAAAATAGCTGCTATT 305

Qy  241 ATAGCATCTCTGACTTTTCTTTACTCTTCTCTGAGGGAAGTAAATCACCCTTTAGCAACT 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  306 ATAGCATCTCTGACTTTTCTTTACTCTTCTCTGAGGGAAGTAAATCACCCTTTAGCAACT 365

Qy  301 TCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  366 TCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy  361 GTTTCCATCACTCTCTTGGGCATTGGTTTACCTGCCAGTGTGAATAGCAGCAATTGTCCAA 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  426 GTTTCCATCACTCTCTTGGGCATTGGTTTACCTGCCAGTGTGAATAGCAGCAATTGTCCAA 485

Qy  421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGAATAAGTTGTAACA 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGAATAAGTTGTAACA 545

Qy  481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTTTGCTGTACTGCATGCAATTTATAGTTCTG 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTTTGCTGTACTGCATGCAATTTATAGTTCTG 605

Qy  541 TCTTACCCAATGAGGCGGATCCTACAGATACAAGTTGCTAAACTGGCCATATCAACACAGGTC 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  606 TCTTACCCAATGAGGCGGATCCTACAGATACAAGTTGCTAAACTGGGCCATATCAACACAGGTC 665

Qy  601 CAACAAAATAAAGAAGAATGCCTGGATTGAGCATGATGATGTTTGGGAGAAATGAGGAGATTTATGTG 660
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Db  601 CAACAAAATAAAGAAGAATGCCTGGATTGAGCATGATGATGTTTGGGAGAAATGAGGAGATTTATGTG
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  606 TCTTACCCAATGAGGCGGATCCTACAGATACAAGTTGCTAAACTGGGCCATATCAACACAGGTC 665

Db  666 CAACAAAATAAAGAAGAATGCCTGGATTGAGCATGATGATGTTTGGGAGAAATGAGGAGATTTATGTG 725

Db  661 TCTCTGGGAATTGTGGGCGATTGGGCATTGGCCTCGTTGTGTGACATCTTATTCCATCT 720

Db  726 TCTCTGGGAATTGTGGGCGATTGGGCAATACTGGCCTCGTTGTGGCTGTGACATCTTATTCCATCT 785

Db  721 GTGAGTGACTCTTTGGACATGGAGAGAAATTTCACTATAATTCAGAGAGCAAGCTAGGAATTGTT 780

Db  786 GTGAGTGACTCTTTGGACATGGAGAGAAATTTCACTATAATTCAGAGAGCAAGCTAGGAATTGTT 845

Db  781 TCCCTTCTACTGGGCACAATACACGGCATTGATTTTTGCCTGGAATAAGTAAGTAGATAGATATA 840

Db  846 TCCCTTCTACTGGGCACAATACACGGCATTGATTTTTTGCCTGGAATAAGTAAGTAGATAGATATA 905

Db  841 AAACAAATTTGTATGGTATACACCCTCCAACTTTTATGTATGTAGCTGTTTTCCTTCTTTCCCAAATTGTT 900

Db  906 AAACAAATTTGTATGGTTATACACCCTCCAACTTTTATGTATGTAGCTGTTTTCCTTCTTTCCCAAATTGTT 965

Db  901 GTCCTGATATTTAAAAGCATACTAATTCCTGCCATGCTTGAGGAAGAAGAGAGAAGAATACTGAAGATT 960

Db  966 GTCCTGATATTTAAAAGCATACTAATTCCTGCCATGCTTGAGGAAGAAGAGAGAAGAATACTGAAGATT 1025

Db  961 AGACATGGTTGGGAAGAGACGTCACCAAAAATTAACAAAAATTGAGATATGTTTCCCAGTTG 1017

Db 1026 AGACATGGTTGGGAAGAGACGTCACCAAAAATTAACAAAAAACTGAGAATATGTTTCCCAGTTG 1082
```

Qy   666 TCTCTCGGGAATTGTGGGAATTGGGAATACTGGGCTCTGTTGCTGTGACATCTATTCCATCT 725
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 TCTCTCGGGAATTGTGGGAATTGGGAATACTGGGCTCTGTTGCTGTGACATCTATTCCATCT 720

Qy   726 TCTCTCGGAATTGTGGGAATTGGGAATACTGGGCTCTGTTGCTGTGACATCTATTCCATC 785
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GTGAGTGACTCTTTTGACATGGAGAGAATTTCACTATTCAGAGCAACGCTAGGAATTGTT 780

Qy   786 GTGAGTGACTCTTTTGACATGGAGAGAATTTCACTATTCAGAGACCAAGCTAGGAATTGTT 845
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TCCCTTCTACTGGGCACAAATACACGCATTGATTTTTTGCCTGGAATAAGTGGATAGATATA 840

Qy   846 TCCCTTCTACTGGGCACAAATACACGCATTGATTTTTTGCCTGGAATAAGTGGATAGATATA 905
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 AAACAAATTTGTATGTATACACCTCCACACTTTATGATAGACTGTTTTCCTTCCAAATTGTT 900

Qy   906 AAACAAATTTGTATGTATACACCTCCACACTTTATGATAGACTGTTTTCCTTCCAAATTGTT 965
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 GTTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGAGATAGTGAAGATT 960

Qy   966 GTTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGAGATAGTGAAGATT 1025
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 AGACATGGTTGGGGAAGAGCGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017

Qy   1026 AGACATGGTTGGGGAAGAGCGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1026 AGACATGGTTGGGGAAGAGCGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082

RESULT 8
ACA59968
ID   ACA59968 standard; cDNA; 1195 BP.
XX
AC   ACA59968;
XX
DT   10-JUN-2003 (first entry)
XX
DE   Prostate cancer therapy associated cDNA #655.
XX
KW   Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
KW   immunogen; cancer; prostate specific antigen; PSA;
KW   prostatic acid phosphatase; PAP; prostate specific membrane antigen;
KW   PSMA; gene; ss.
XX
OS   Homo sapiens.
XX
PN   US20021927763-A1.
XX
PD   19-DEC-2002.
XX
PF   29-JUN-2001; 2001US-00895793.
XX
PR   04-OCT-1999; 99US-0157455P.
PR   04-OCT-2000; 2000US-00679272.
PR   28-MAR-2001; 2001US-00822827.
XX
PA   (XUJJ/) XU J.
PA   (DILL/) DILLON D C.
PA   (MITC/) MITCHAM J L.
PA   (HARL/) HARLOCKER S L.
PA   (JIAN/) JIANG Y.
PA   (KALO/) KALOS M D.
PA   (FANG/) FANGER G R.
PA   (RETT/) RETTER M W.
PA   (STOL/) STOLK J A.
PA   (DAYC/) DAY C H.
PA   (VEDV/) VEDVICK T S.
PA   (CART/) CARTER D.
PA   (LISX/) LI S X.
PA   (WANG/) WANG A.
PA   (SKEI/) SKEIKY Y A W.
PA   (HEPL/) HEPLER W T.
PA   (HEND/) HENDERSON R A.
PA   (HURA/) HURAL J.

PA   (MCNE/) MCNEILL P D.
PA   (HOUG/) HOUGHTON R L.
PA   (DBAS/) Y DE BASSOLS C V.
PA   (FOYT/) FOY T M.
XX
PI   Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI   Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI   Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;
PI   Mcneill PD, Houghton RL, Y De BassolsCV, Foy TM;
XX
DR   WPI; 2001-245062/25.
DR   P-PSDB; ABU71821.
XX
PT   Prostate specific protein and its encoding polynucleotide, useful for the
PT   treatment and diagnosis of prostate cancer.
XX
PS   Example 5; SEQ ID NO 878; 85pp; English.
XX
CC   The invention describes a fusion protein comprising at least one amino
CC   acid sequence of immunogenic portions of any of the 3 sequences not
CC   defined in the specification, or sequences having at least 70 or 90 %
CC   sequence identity to any one of the 35 sequences defined in the USPTO web
CC   site, which is encoded by any of the 4 nucleotide sequences not defined
CC   in the specification. The fusion protein, composition and methods are
CC   useful for diagnosing, preventing and/or treating cancer, particularly
CC   prostate cancer. The proteins are useful as markers to indicate the
CC   presence or absence of cancer. Note: The sequence represents a prostate
CC   therapy associated cDNA. This sequence data for this patent did not
CC   form part of the printed specification, but was obtained in electronic
CC   format directly from the US patent office at
CC   seqdata.uspto.gov/sequence.html?DocId=US20020192763
XX
SQ   Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

Query Match   100.0%; Score 1017; DB 5; Length 1195;
Best Local Similarity   100.0%;   Pred. No. 2.6e-276;
Matches 1017; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ATGGAAAAGCAGAAAAAGACACATCACAAAACCAAGAAGAACTTTGAAAATGAAGCCTAGGAGA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   66 ATGGAAAAGCAGAAAAAGACATCACAAAACCAAGAAGAACTTTGAAAATGAAGCCTAGGAGA 125

Qy   61 AAATTTAGAAGAAGAACGAGATTATTTGCATAAGGAACACAGCGGGAGAGACCAGCATGCTAAAAAGA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   126 AAATTTAGAAGAAGAACGAGATTATTTGCATAAGGAACACAGCGGGAGAGACCAGCATGCTAAAAAGA 185

Qy   121 CCTCTGCTTTTGCATTTGCACCAAACAGCCCATCTTGATGAATTTGACTGCCCTTCAGAA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   186 CCTCTGCTTTTGCATTTGCACCAAACAGCCCATCTTGATGAATTTGACTGCCCTTCAGAA 245

Qy   181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTTGCTATT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy   241 ATAGACATCTCTGACTTTTCTTTACACTCTTCTCTGAGGGAGTAATTCACCCTTAGCAACT 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   306 ATAGACATCTCTGACTTTTCTTTACACTCTTCTCTGAGGGAGTAATTCACCCTTAGCAACT 365

Qy   301 TCCCATCACACAATATTTTTTATAAAAATTCCAAATCCTGGTCATCAACAAACTCTTGCCAATG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   366 TCCCATCACACAATATTTTTTATAAAAATTCCAAATCCTGGTCATCAACAAACTCTTGCCAATG 425

Qy   361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCGAATTGTCCAA 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAGAATTGTCCAA 485

Qy   421 CTTCATAATGGAACCAAGTATATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   486 CTTCATAATGGAACCAAGTATATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy   481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

```
Qy    541 TCTTACCCAATGAGGCGGATCCTACAGATACACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    606 TCTTACCCAATGAGGCGGATCCTACAGATACACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy    601 CAACAAAATAAAGAAGAATGCCTGGATTGAGCATGATCAAGTGTTTGGAGAATGGAGAATTATTAGTG 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    666 CAACAAAATAAAGAAGAATGCCTGGATTGAGCATGATCAAGTGTTTGGAGAATGGAGAATTATTAGTG 725

Qy    661 TCTCTGGGAATTGTGGGATTGGCAAATACTGGCTCTCGTTGGCGTGTGACATCTATTCATCT 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    726 TCTCTGGGAATTGTGGGATTGGCAAATACTGGCTCTCGTTGGCGTGTGACATCTATTCATCT 785

Qy    721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATATTCAGAGCAAGCTAGGAATTGTT 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATATTCAGAGCAAGCTAGGAATTGTT 845

Qy    781 TCCCTTCTACTGGGGCACAATACACGCCATTGATTGATTTTTTGCCTGGAATTAAGTGGAATTGT 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    846 TCCCTTCTACTGGGGCACAATACACGCCATTGATTGATTTTTTGCCTGGAATTAAGTGGAATTGT 905

Qy    841 AAACAAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    906 AAACAAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy    901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGACGAAGAAGAACTACTGAAGATT 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGACGAAGAAGAACTACTGAAGATT 1025

Qy    961 AGACATGGTTGGGAGAGACGTCACCAAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1026 AGACATGGTTGGGAGAGACGTCACCAAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082
```

RESULT 9

```
ID   ABL95531 standard; cDNA; 1195 BP.
XX
AC   ABL95531;
XX
DT   19-JUL-2002  (first entry)
XX
DE   Human P78P cDNA sequence SEQ ID NO 878.
XX
KW   Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW   gene therapy; gene; 88.
XX
OS   Homo sapiens.
XX
PN   US2002022248-A1.
XX
PD   21-FEB-2002.
XX
PF   12-JAN-2001; 2001US-00759143.
XX
PR   25-FEB-1997; 97US-00806099.
PR   01-AUG-1997; 97US-00904804.
PR   10-FEB-1998; 98US-00020956.
PR   25-FEB-1998; 98US-00030607.
PR   14-JUL-1998; 98US-00115453.
PR   23-SEP-1998; 98US-00159812.
PR   15-JAN-1999; 99US-00232149.
PR   09-APR-1999; 99US-00288946.
PR   13-JUL-1999; 99US-00352616.
PR   12-NOV-1999; 99US-00439313.
PR   18-NOV-1999; 99US-00443686.
PR   14-JAN-2000; 2000US-00483672.
PR   27-MAR-2000; 2000US-00536857.
PR   09-MAY-2000; 2000US-00568100.
PR   12-MAY-2000; 2000US-00570737.
PR   13-JUN-2000; 2000US-00593793.
PR   27-JUN-2000; 2000US-00605783.
PR   10-AUG-2000; 2000US-00636215.
PR   29-AUG-2000; 2000US-00651236.
PR   06-SEP-2000; 2000US-00652279.
PR   02-OCT-2000; 2000US-00679426.
PR   10-OCT-2000; 2000US-00685166.
XX
PA   (XUJJ/)  XU J.
PA   (DILL/)  DILLON D C.
PA   (MITC/)  MITCHAM J L.
PA   (HARL/)  HARLOCKER S L.
PA   (JIAN/)  JIANG Y.
PA   (KALO/)  KALOS M D.
PA   (FANG/)  FANGER G R.
PA   (RETT/)  RETTER M W.
PA   (STOL/)  STOLK J A.
PA   (DAYC/)  DAY C H.
PA   (VEDV/)  VEDVICK T S.
PA   (CART/)  CARTER D.
PA   (LISX/)  LI S X.
PA   (WANG/)  WANG A.
PA   (SKEI/)  SKEIKY Y A W.
PA   (HEPL/)  HEPLER W T.
PA   (HEND/)  HENDERSON R A.
XX
PI   Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI   Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI   Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
DR   WPI; 2002-255649/30.
XX
SQ   Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;
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PS   Claim 1; SEQ ID NO 878; 87pp; English.
XX
PT   New prostate-specific polynucleotides for diagnosing and treating
PT   diseases, in particular prostate cancer, and as markers for the
PT   progression of cancer.
XX
CC   The present invention provides prostate-specific coding sequences and
CC   their encoded proteins. These can be used in the diagnosis and treatment
CC   of cancers, particularly prostate cancer. The present sequence is a cDNA
CC   described in the invention
XX
```

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Query Match             100.0%;  Score 1017;  DB 6;  Length 1195;
Best Local Similarity   100.0%;  Pred. No. 2.6e-276;
Matches 1017;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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```
Qy     1 ATGGAAAAGCAGAAAAAGACAATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGAGA 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    66 ATGGAAAAGCAGAAAAAGACAATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGAGA 125

Qy    61 AATTTAGAAGAAGACGAATTATTTGCATAAGGACACGGGAGGAGGACCAGCATGCTAAAAGA 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   126 AATTTAGAAGAAGACGAATTATTTGCATAAGGACACGGGAGGAGGACCAGCATGCTAAAAGA 185

Qy   121 CCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   186 CCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy   181 CTTCAGCACACACAGGAGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   246 CTTCAGCACACACAGGAGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy   241 ATAGCATCTCTGACTTTTCTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   306 ATAGCATCTCTGACTTTTCTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy   301 TCCCATCAACAATATATTTTTATAAAATTCCAATCCTCTGGTCATCAACAAAGTCTTGCCAATG 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   366 TCCCATCAACAATATATTTTTATAAAATTCCAATCCTCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy   361 GTTTTCATCACTCTCTTGGCATTGGTTTACCTGCGCCAGGTGTTGATAGCAGCAGAATTGTCCAA 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   426 GTTTTCATCACTCTCTTGGCATTGGTTTACCTGCGCCAGGTGTTGATAGCAGCAGAATTGTCCAA 485
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Qy  421 CTTCATAAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAGTTAAGTGGATGTTAACA 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  486 CTTCATAAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAGTTAAGTGGATGTTAACA 545

Qy  481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTCTTTTTTTTGCTGTGTACTGCATGCAATTTATAGTTCTG 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTCTTTTTTTTGCTGTGTACTGCATGCAATTTATAGTTCTG 605

Qy  541 TCTTACCCAATGAGGCGGATCTTCACAGATTACAAGTTGCTAAAACTGGGCATATCAACAGGTC 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  606 TCTTACCCAATGAGGCGGATCCTTACAGATACAAGTTGCTAAAACTGGGCATATCAACAGGTC 665

Qy  601 CAACAAAATAAAGAAGATGCCTGGATTGAGCGATGTGTTGGAGAATGGGAGATTTATGTG 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  666 CAACAAAATAAAGAAGATGCCTGGATTGAGCGATGTGTTGGAGAATGGGAGATTTATGTG 725

Qy  661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGGCTGTGACATCTATTCCATCT 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGGCTGTGACATCTATTCCATCT 785

Qy  721 GTGGAGTGACTCTTTGACATGGAGGAGAATTCACTATATTCACTATTATTCAGAGCAAGCTAGGAATTGTT 780
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  786 GTGGAGTGACTCTTTGACATGGAGGAGAATTCACTATATTCACTATTATTCAGAGCAAGCTAGGAATTGTT 845

Qy  781 TCCCTTCTACTGGGCACAATACACGGCCATTGAATTTGGCCTGGAATAAGTAGTGGATAGAATATA 840
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  846 TCCCTTCTACTGGGCACAATACACGGCCATTGATTTTGGCCTGGAATAAGTAGTGGATAGAATATA 905

Qy  841 AAACAAATTTGTATCGGTATACACACCTCCACACTTTTTATGATAGCTGTTTTCCTTCCAAATTGTT 900
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  906 AAACAAATTTGTATCGGTATACACACCTCCACACTTTTTATGATAGCTGTTTTCCTTCCAAATTGTT 965

Qy  901 GTCCTGATTATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTACTGAAAGATT 960
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  966 GTCCTGATTATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTACTGAAAGATT 1025

Qy  961 AGACATGGTTGGGAAGACGTCACCAAAAATTAACAAAAAACTGAGATATGTTCCCAGTTG 1017
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1026 AGACATGGTTGGGAAGACGTCACCAAAAATTAACAAAAAACTGAGATATGTTCCCAGTTG 1082
```

RESULT 10
ABK92128
```
ID   ABK92128 standard; DNA; 1195 BP.
XX
AC   ABK92128;
XX
DT   15-AUG-2002  (first entry)
XX
DE   Prostate cancer-associated DNA sequence #14.
XX
KW   Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
KW   gene therapy; gene; ds.
XX
OS   Mammalia.
XX
PN   WO200230268-A2.
XX
PD   18-APR-2002.
XX
PF   12-OCT-2001; 2001WO-US032045.
XX
PR   13-OCT-2000; 2000US-00687576.
PR   08-DEC-2000; 2000US-00733288.
PR   08-DEC-2000; 2000US-00733742.
PR   24-JAN-2001; 2001US-02639557P.
PR   16-MAR-2001; 2001US-02767791P.
PR   16-MAR-2001; 2001US-02768888P.
PR   06-APR-2001; 2001US-02819922P.
PR   24-APR-2001; 2001US-0286214P.
PR   30-APR-2001; 2001US-00847046.
PR   04-MAY-2001; 2001US-0288589P.
```

```
XX
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI   Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
XX
DR   WPI; 2002-471335/50.
DR   P-PSDB; ABG61813.
XX
PT   Detecting a prostate cancer-associated transcript in a cell in a patient,
PT   useful for diagnosing prostate cancer (PC) or screening modulators of PC,
PT   by determining if prostate cancer-associated genes are expressed in a
PT   prostate tissue.
XX
PS   Claim 22; Page 311-312; 436pp; English.
XX
CC   The present invention relates to methods of detecting a prostate cancer-
CC   associated transcript in a cell from a patient. The method comprises
CC   contacting a biological sample from the patient with prostate cancer-
CC   associated polynucleotides (designated PC genes) that selectively
CC   hybridise to a sequence that is at least 80% identical to them. The
CC   prostate cancer-associated polynucleotide sequences are differentially
CC   expressed in prostate tumour tissue or in prostate cancer and are derived
CC   from the tissues of various organisms such as humans or other mammals
CC   (e.g. mice, sheep and dogs). The methods of the invention are useful for
CC   diagnosing and treating prostate cancer in mammals. The prostate cancer-
CC   associated genes are useful for diagnosing or treating prostate cancer,
CC   as well as for identifying modulators of prostate cancer or agents that
CC   inhibit prostate cancer. The nucleic acid sequences are particularly
CC   useful in gene therapy, as a vaccine or in antisense applications.
CC   ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
CC   sequences
XX
SQ   Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;
```

```
Query Match             100.0%;  Score 1017;  DB 6;  Length 1195;
Best Local Similarity   100.0%;  Pred. No. 2.6e-276;
Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy   1 ATGGAAAGCAGAAAAAGACATCACAAACCAAGAAGAGAACTTTGGAAAATGAAAGCCTAGGAGA 60
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  66 ATGGAAAGCAGAAAAAGACATCACAAACCAAGAAGAGAACTTTGGAAAATGAAAGCCTAGGAGA 125

Qy  61 AATTTAGAGAGAAGACGATTATTTCCATAAGGACGACACGGGAGAGACACCGATGCAAAAGA 120
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 126 AATTTAGAGAGAAGACGATTATTTCCATAAGGACGACACGGGAGAGACACCGATGCTAAAAAGA 185

Qy 121 CCTGTGCTTTTGCATTGCACCAAACAGCCCATGCTGATGAATTGACTGCCCTTCAGAA 180
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 186 CCTGTGCTTTTGCATTGCACCAAACAGCCCATGCTGATGAATTGACTGCCCTTCAGAA 245

Qy 181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAAATAGCTGCTATT 240
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAAATAGCTGCTATT 305

Qy 241 ATAGCACTCTCTGACTTTCTTTACACTCTTCTGAGGGAAGTAAATTCACCCTTTAGCAACT 300
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 306 ATAGCACTCTCTGACTTTCTTTACACTCTTCTGAGGGAAGTAAATTCACCCTTTAGCAACT 365

Qy 301 TCCCATCAACAAATAATTTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 366 TCCCATCAACAAATAATTTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy 361 GTTTCCATCACTCTTCTTGGCCATTGGTTTACCTGCCAGGTGTGATAGCAGCGCAATTGTCCAA 420
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 426 GTTTCCATCACTCTTCTTGGCCATTGGTTTACCTGCCAGGTGTGATAGCAGCGCAATTGTCCAA 485

Qy 421 CTTCATAAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAGTTAAGTGGATGTTAACA 480
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 486 CTTCATAAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAGTTAAGTGGATGTTAACA 545

Qy 481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTCTTTTTTTTGCTGTACTGCATGCAATTTATAGTTCTG 540
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTCTTTTTTTTGCTGTACTGCATGCAATTTATAGTTCTG 605
```

```
Qy   541 TCTTACCCAATGAGCGGATCCTTACAGATACAAGTTGCTAAACTGGGCCATATCAACAGGTC 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   606 TCTTACCCAATGAGCGGATCCTTACAGATACAAGTTGCTAAACTGGGCCATATCAACAGGTC 665

Qy   601 CAACAAAAATAAAGAAGAAGATGGCCTGGATTGAGCATGATGTTGGAGAATGGAGATTTATGTG 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   666 CAACAAAAATAAAGAAGAAGATGGCCTGGATTGAGCATGATGTTGGAGAATGGAGATTTATGTG 725

Qy   661 TCTCTGGGAATTGTGGGATTGGCAATAACTGGCCTCTCGTTGGCCTGTGTGACACATCTTATTC 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   726 TCTCTGGGAATTGTGGGATTGGCAATAACTGGCCTCTCGTTGGCCTGTGTGACACATCTTATTC 785

Qy   721 GTGAGTGACTCCTTTGACATGGAGAGAAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   786 GTGAGTGACTCCTTTGACATGGAGAGAAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy   781 TCCCTTCTACTGGGGCACAATACACGCCATTGATTTTTGCCTGGAATAAGTTGGATAGAATA 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   846 TCCCTTCTACTGGGGCACAATACACGCCATTGATTTTTGCCTGGAATAAGTTGGATAGAATA 905

Qy   841 AAACAAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTGTTTTCCTTCCAATTGTT 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   906 AAACAAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTGTTTTCCTTCCAATTGTT 965

Qy   901 GTCCTGATAATTAAAAGCAATACTATTCCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   966 GTCCTGATAATTAAAAGCAATACTATTCCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 1025

Qy   961 AGACATGGTTGGGAGAAGAGCGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1026 AGACATGGTTGGGAGAAGAGCGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082
```

RESULT 11

ACC95695
ID   ACC95695 standard; cDNA; 1195 BP.
XX
AC   ACC95695;
XX
DT   28-AUG-2003 (first entry)
XX
DE   Prostate tumour specific cDNA sequence SEQ ID 878.
XX
KW   Cytostatic; gene therapy; prostate-specific protein; PSP; human;
KW   immune response; prostate cancer; 88.
XX
OS   Homo sapiens.
XX
XX
PN   WO2002089747-A2.
XX
PD   14-NOV-2002.
XX
PF   09-MAY-2002; 2002WO-US014753.
XX
PF   09-MAY-2002; 2002WO-US014753.
PR   09-MAY-2002; 2001US-00852911.
PR   29-JUN-2001; 2001US-0095814.
PR   10-DEC-2001; 2001US-00012896.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
PI   Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
PI   Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
PI   Mcneill PD, Houghton RL, Vinals Y De Bassolsc, Foy TM, Watanabe Y;
PI   Deng T;
XX
DR   WPI; 2003-167130/16.
XX
PT   New prostate-specific proteins and genes, useful in gene therapy,
PT   particularly for stimulating an immune response in a patient, or treating
PT   prostate cancer in a patient, as well as for diagnosing prostate cancer
PT   in a patient.

XX
PS   Example 5; Page 617-618; 691pp; English.
XX
CC   The present invention relates to novel prostate-specific proteins (PSP)
CC   and their coding sequences. The PSPs and their coding sequences are
CC   useful for stimulating an immune response in a patient, or for treating
CC   prostate cancer in a patient and for determining, detecting or diagnosing
CC   the presence of a cancer in a patient. The present sequence was used to
CC   illustrate the invention
XX
SQ   Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

Query Match   100.0%; Score 1017; DB 8; Length 1195;
Best Local Similarity   100.0%; Pred. No. 2.6e-276;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy     1 ATGGAAAAGCAGAAAAAGACATCAAAAACCAAAGAAGAGAACTTTGGAAAATGAAGCCTAGAGA 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   366 ATGGAAAAGCAGAAAAAGACATCAAAAACCAAAGAAGAGAACTTTGGAAAATGAAGCCTAGAGA 425

Qy    61 AATTTAGAAGAAGACGATTATTTGCATAAGGAGGACACGGGAGAGAGCCAGCATGCTAAAAAGA 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   426 AATTTAGAAGAAGACGATTATTTGCATAAGGAGGACACGGGAGAGAGCCAGCATGCTAAAAAGA 485

Qy   121 CCTGTGTCTTTTGCATTTGCACCAAAACAGCCCATGGCTGTGATGAATTTGACTGCCCTTCAGAA 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   486 CCTGTGTCTTTTGCATTTGCACCAAAACAGCCCATGGCTGTGATGAATTTGACTGCCCTTCAGAA 545

Qy   181 CTTCAGCAGCACACAGGAAGAACTCTTTCCACAGTAGGCACTTGCCAAATTAAAAATAGCTGCTATT 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   546 CTTCAGCAGCACACAGGAAGAACTCTTTCCACAGTAGGCACTTGCCAAATTAAAAATAGCTGCTATT 605

Qy   241 ATAGCATCTCTGACTTTTCTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   606 ATAGCATCTCTGACTTTTCTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 665

Qy   301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCACAAAAGTCTTGCCAATG 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   666 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCACAAAAGTCTTGCCAATG 725

Qy   361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAGCAATTGTCCAA 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   726 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAGCAATTGTCCAA 785

Qy   421 CTTCATAATGGAACCAAGTATAAGAAGTTCCACATTGGTTGGGATAAGTGGATGGTTAACA 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   786 CTTCATAATGGAACCAAGTATAAGAAGTTCCACATTGGTTGGGATAAGTGGATGGTTAACA 845

Qy   481 AGAAAGCAGTTTGGGCTTCTCCAGTTTTCTTTTTTTGCTGTACTGCATCGCATGCAATTTTATAGTCTG 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   846 AGAAAGCAGTTTGGGCTTCTCCAGTTTTCTTTTTTTGCTGTACTGCATCGCATGCAATTTTATAGTCTG 905

Qy   541 TCTTACCCAATGAGCGGATCCTTACAGATACAAGTTGCTAAACTGGGCCATATCAACAGGTC 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   906 TCTTACCCAATGAGCGGATCCTTACAGATACAAGTTGCTAAACTGGGCCATATCAACAGGTC 965

Qy   601 CAACAAAAATAAAGAAGAAGATGGCCTGGATTGAGCATGATGTTGGAGAATGGAGATTTATGTG 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   966 CAACAAAAATAAAGAAGAAGATGGCCTGGATTGAGCATGATGTTGGAGAATGGAGATTTATGTG 1025

Qy   661 TCTCTGGGAATTGTGGGATTGGCAATAACTGGCCTCTCGTTGGCCTGTGTGACACATCTTATTC 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1026 TCTCTGGGAATTGTGGGATTGGCAATAACTGGCCTCTCGTTGGCCTGTGTGACACATCTTATTC 1085

Qy   721 GTGAGTGACTCCTTTGACATGGAGAGAAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1086 GTGAGTGACTCCTTTGACATGGAGAGAAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 1145

Qy   781 TCCCTTCTACTGGGGCACAATACACGCCATTGATTTTTGCCTGGAATAAGTTGGATAGAATA 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   846 TCCCTTCTACTGGGGCACAATACACGCCATTGATTTTTGCCTGGAATAAGTTGGATAGAATA 905

Qy   841 AAACAAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTGTTTTCCTTCCAATTGTT 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

RESULT 12
ADB75572

ID   ADB75572 standard; cDNA; 1195 BP.
XX
AC   ADB75572;
XX
DT   04-DEC-2003 (first entry)
XX
PD   06-FEB-2003.
XX
PN   WO2003009814-A2.
XX
OS   Homo sapiens.
XX
KW   Prostate; cancer; cytostatic; gene therapy; marker; ss.
XX
DE   Prostate cancer marker cDNA.
XX
PF   25-JUL-2002; 2002WO-US023913.
XX
PR   25-JUL-2001; 2001US-03079822P.
PR   22-AUG-2001; 2001US-03143567.
PR   25-SEP-2001; 2001US-0325020P.
PR   12-DEC-2001; 2001US-03417746P.
PR   05-MAR-2002; 2002US-0321758P.
XX
PT   New nucleic acid molecule, useful for diagnosing or treating prostate
PT   cancer.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbatcheva B;
PI   Hoersh S, Kamatkar S, Wonsey AM, Glatt K, Zhao X, Anderson D;
XX
DR   WPI; 2003-248033/24.
XX
PS   Disclosure; SEQ ID NO 396; 99pp; English.
XX
CC   The invention relates to newly discovered cancer markers associated with
CC   the cancerous state of prostate cells. Also disclosed is a method of
CC   assessing whether a patient is afflicted with prostate cancer. The method
CC   of the invention involves assessing whether a patient is afflicted with
CC   prostate cancer by comparing the level of expression of a marker in a
CC   patient sample and the normal level of expression of the marker in a
CC   control non-prostate cancer sample, where a significant increase in the
CC   level of expression of the marker in the patient sample and the normal
CC   level indicates that the patient is afflicted with prostate cancer.
CC   Nucleic acids of the invention are useful for diagnosing or treating
CC   prostate cancer, and may be useful in gene therapy. Sequences given in
CC   ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

Qy   901 GTCCTGATATTTAAAAGCATACATTCCTGCCATGCTTGAGGAGAAGAACTGAAGATT 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   906 AAAACAATTTGTATGTARGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCAATTGTT 965

Qy   961 AGACATGGTTGGGAAGACGTCACCAAAAATTACAAAACTGAGATATGTTCCCAGTTG 1017
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1026 AGACATGGTTGGGAAGACGTCACCAAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082

Query Match   100.0%; Score 1017; DB 10; Length 1195;
Best Local Similarity   100.0%;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAGAGAGCATTTTGGAAAATGAAGCCTAGGAGA 60

RESULT 13
ADB14328

ID   ADB14328 standard; cDNA; 1195 BP.
XX
AC   ADB14328;

XX
DT   18-DEC-2003 (first entry)
XX
DE   Human prostate specific full length cDNA P789P.
XX
KW   Human; ss; prostate specific cDNA; cytostatic; immunostimulant;
KW   gene therapy; cell therapy; vaccine; T-cell epitope;
KW   class I major histocompatibility complex allele; MHC; prostate cancer;
KW   tumour; antigen presenting cell.
XX
OS   Homo sapiens.
XX
PN   US2003185830-A1.
XX
PD   02-OCT-2003.
XX
PF   12-NOV-2002; 2002US-00294025.
XX
PR   25-FEB-1997; 97US-00806099.
PR   01-AUG-1997; 97US-00904804.
PR   05-FEB-1998; 98US-00020956.
PR   25-FEB-1998; 98US-00030607.
PR   14-JUL-1998; 98US-00115453.
PR   23-SEP-1998; 98US-00159812.
PR   15-JAN-1999; 99US-00232149.
PR   09-APR-1999; 99US-00289946.
PR   13-JUL-1999; 99US-00352616.
PR   12-NOV-1999; 99US-00439313.
PR   18-NOV-1999; 99US-00443686.
PR   14-JAN-2000; 2000US-00483672.
PR   27-MAR-2000; 2000US-00536857.
PR   09-MAY-2000; 2000US-00568100.
PR   12-MAY-2000; 2000US-00570737.
PR   13-JUN-2000; 2000US-00593793.
PR   27-JUN-2000; 2000US-00605783.
PR   09-AUG-2000; 2000US-00636215.
PR   29-AUG-2000; 2000US-00651236.
PR   06-SEP-2000; 2000US-00657279.
PR   02-OCT-2000; 2000US-00679426.
PR   10-OCT-2000; 2000US-00685166.
PR   09-NOV-2000; 2000US-00709729.
PR   12-JAN-2001; 2001US-00759143.
PR   09-FEB-2001; 2001US-00780669.
PR   09-MAY-2001; 2001US-00852911.
PR   29-JUN-2001; 2001US-00895814.
PR   10-DEC-2001; 2001US-00012896.
PR   09-MAY-2002; 2002US-00144678.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Xu J, Stolk JA, Kalos MD;
XX
DR   WPI; 2003-756193/71.
DR   P-PSDB; ADB14329.
XX
PT   New isolated polypeptide for use in a vaccine for stimulating an immune
PT   response, or for treating or diagnosis cancer, preferably prostate
PT   cancer.
XX
PS   Example 5; Page; 101pp; English.
XX
CC   The invention relates to an isolated polypeptide comprising no more than
CC   11-542 amino acids of ADB13563 comprising a sequence ADB14487. The
CC   peptides comprise a fragment ADB13563 of that contain naturally processed
CC   T-cell epitopes for 3 class I major histocompatibility complex (MHC)
CC   alleles. ADB13563 is a polypeptide encoded by a human prostate specific
CC   cDNA. One of 648 disclosed as new. Also included are nucleic acids
CC   encoding the proteins and peptides, expression vectors, a host cell
CC   transformed with the vector, an isolated antibody (or antigen binding
CC   fragment) that specifically binds to the protein or peptide, detecting
CC   the presence of a cancer in a patient (comprising contacting a patient
CC   sample with a binding agent that binds to the peptides or a polypeptide
CC   appearing as ADB13558, detecting the amount of polypeptide that binds to

CC   the agent and comparing the amount of polypeptide to a predetermined cut-
CC   off value to determine the presence of cancer), a fusion protein
CC   comprising the peptides or proteins, stimulating or expanding T cells
CC   specific for a tumour protein comprising contacting T cells with the
CC   peptides or the isolated T cell population, treating prostate cancer in a
CC   patient comprising administering a composition comprising the peptides,
CC   nucleic acids, antibodies or compounds, determining the presence of a
CC   cancer in a patient and treating prostate cancer in a patient comprising
CC   incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated
CC   from a patient with the peptides or antigen presenting cells that express
CC   (the peptides so that the T cells proliferate, and administering the
CC   proliferated T cells to the patient. The peptides (or an oligonucleotide
CC   that hybridises to nucleic acid encoding them), is used to detect the
CC   presence of cancer in a patient. The peptides, nucleic acids encoding, or
CC   antigen-presenting cells expressing the peptides, nucleic acids, are used to
CC   stimulate or expand T cells specific for a tumour protein. The peptides,
CC   nucleic acids, antibodies, fusion proteins, T cell populations or antigen
CC   presenting cells are used to stimulate an immune response or treat
CC   prostate cancer in a patient. The present sequence is a known cDNA
CC   showing sequence similarity to one of the disclosed human prostate
CC   specific cDNAs. Note: Except where otherwise indicated, the sequence data
CC   for this patent did not form part of the printed specification, but was
CC   obtained in electronic format directly from USPTO at
CC   seqdata.uspto.gov/sequence.html?DocID=20030185830.
XX
SQ   Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

Query Match   100.0%;   Score 1017;   DB 10;   Length 1195;
Best Local Similarity   100.0%;   Pred. No. 2.6e-276;
Matches 1017;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

```
Qy      1 ATGGAAAAGCAGAAAAAGACAATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     66 ATGGAAAAGCAGAAAAAGACAATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy     61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAGA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAGA 185

Qy    121 CCTGTGCCTTTTGCATTTGACCAAAACAGCCCATGCTGATGAAATTTGACTGCCCTTCAGAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    186 CCTGTGCCTTTTGCATTTGACCAAAACAGCCCATGCTGATGAAATTTGACTGCCCTTCAGAA 245

Qy    181 CTTCAGCACACACAGGAAACTCTTTCCACAGTGGCACTTGCCAATTAAAAATAGCTGCTATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    246 CTTCAGCACACACAGGAAACTCTTTCCACAGTGGCACTTGCCAATTAAAAATAGCTGCTATT 305

Qy    241 ATAGCATCTCTGACTTTCTTTCTTTACACTCTTCTGAGGGAGTAATTCACCCCTTTAGCAACT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    306 ATAGCATCTCTGACTTTCTTTCTTTACACTCTTCTGAGGGAGTAATTCACCCCTTTAGCAACT 365

Qy    301 TCCCATCACACAATATTTTTATAAAATTCCAATCCTGGTCATCACAAAAGTCTTGCCAATG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    366 TCCCATCACACAATATTTTTATAAAATTCCAATCCTGGTCATCACAAAAGTCTTGCCAATG 425

Qy    361 GTTTCCATCACTCTCTTGGCATTGGTTTTACCTGCCAGGTGTGATAGCAGCGAATTGTCCAA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    426 GTTTCCATCACTCTCTTGGCATTGGTTTTACCTGCCAGGTGTGATAGCAGCGAATTGTCCAA 485

Qy    421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAGTGGATGTTAACA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAGTGGATGTTAACA 545

Qy    481 AGAAAGCAGTTTGGGCTTCAGTTTCTTTTTGCTGTACTGCAGTTGTCTG 540
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Db    546 AGAAAGCAGTTTGGGCTTCAGTTTCTTTTTGCTGTACTGCAGTTGTCTG 605

Qy    541 TCTTACCCAATGAGGCGGATCCTACAGATACAAGGTTGCTAAAACTGGCCATATCAACAGGTC 600
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Qy    601 CAACAAAATAAAGAAGAATGCCTGGATTGAGCATGATGTTGGAGAATGGAGAGATTTATGTG 660
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Db   666  CAACAAAATAAAGAAGAATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTATGTG   725
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Qy   721  GTGAGTGACTCTTTGACATGGAGAGAATTCACTATATTCAGAGCAAGCTAGGAATTGTT   780
Db   786  GTGAGTGACTCTTTGACATGGAGAGAATTCACTATATTCAGAGCAAGCTAGGAATTGTT   845
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Query Match           100.0%;  Score 1017;  DB 10;  Length 1195;
Best Local Similarity 100.0%;  Pred. No. 2.6e-276;
Matches 1017;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy     1  ATGGAAAAGCAGAAAAGACACTCACAAACCCAAGAAGAAGAACTTTGGAAAAATGAAAGCCTAGGAGA   60
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Db   126  AATTTAGAAGAAGAACGATTATTTGCATAAGGACAACGGGAGACCAGCCAGATGGCTAAAAAGA   185
Qy   121  CCTGTGCTTTTGCATTTGCACCAAAACAGCCCAATGCTGATGAAATTTGACTGACCCCTTCAGAA   180
Db   186  CCTGTGCTTTTGCATTTGCACCAAAACAGCCCAATGCTGATGAAATTTGACTGACCCCTTCAGAA   245
Qy   181  CTTCAGCACACACAGGAACTCTTTCCACAGTGGCCACTTGCCAATTAAAATAGCTGCTATT   240
Db   246  CTTCAGCACACACAGGAACTCTTTCCACAGTGGCCACTTGCCAATTAAAATAGCTGCTATT   305
Qy   241  ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT   300
Db   306  ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT   365
Qy   301  TCCCATCAACAATATTTTTATAAAATTCCAATCCTTGGTCATCAACAAAGTCTTGCCAATG   360
Db   366  TCCCATCAACAATATTTTTATAAAATTCCAATCCTTGGTCATCAACAAAGTCTTGCCAATG   425
Qy   361  GTTTCCATCACTCCTTGGCATTGGTTTACCTGCCAGTGTGATGAGTAGCAGCAATTGTCCAA   420
Db   426  GTTTCCATCACTCCTTGGCATTGGTTTACCTGCCAGTGTGATGAGTAGCAGCAATTGTCCAA   485
Qy   421  CTTCATAATGGAACCAAGTATAAGAAGTTCCACATTGGTTGGAATGGGATGTTAACA   480
Db   486  CTTCATAATGGAACCAAGTATAAGAAGTTCCACATTGGTTGGAATGGGATGTTAACA   545
Qy   481  AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTGTTTTGGCTTGTACTGCAATTTATAGTCTG   540
Db   546  AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTGTTTTGGCTTGTACTGCAATTTATAGTCTG   605
Qy   541  TCTTACCCAATGAGGCGGATCCTACAGATACAGTTGCTAAACTGGGCCATATCAAACAGTC   600
Db   606  TCTTACCCAATGAGGCGGATCCTACAGATACAGTTGCTAAACTGGGCCATATCAAACAGGTC   665
Qy   601  CAACAAAAATAAAGAGAATGCCTGGATTGAGCATGATGAGTGGGAAATGGAGATTTATGTG   660
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Qy   661  TCTCTGGGAATTGTGGGGATTGGCAATACTACTGGCCTCTGTTGGCGTGTGACATCTATTCCATCT   720
Db   726  TCTCTGGGAATTGTGGGGATTGGCAATACTACTGGCCTCTGTTGGCGTGTGACATCTATTCCATCT   785
Qy   721  GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCACTATATTCAGAGCAAGCTAGGAATTGTT   780
Db   786  GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT   845
Qy   781  AAACAAATTTGTATGGTATACACCTCCAACTTTATGATAGCTGTTTTTCCTTCCAATTGTT   840
Db   846  GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT   905
Qy   841  AAACAAATTTGTATGGTATACACCTCCAACTTTATGATAGCTGTTTTTCCTTCCAATTGTT   900
Db   906  AAACAAATTTGTATGGTATACACCTCCAACTTTATGATAGCTGTTTTTCCTTCCAATTGTT   965
Qy   901  GTCCTGATATTTAAAAGCATACACCTCCAACTATTCCTGCCATGCTTGAGGAAGAATACTGAAGGATT   960
Db   966  GTCCTGATATTTAAAAGCATACTAATTCCTGCCATGCTTGAGGAAGAATACTGAAGGATT   1025
Qy   961  AGACATGGTTGGGGAAGAGACCTCACCAAAAATTAACAAAAACTGAGATATGTTCCCAGTTG   1017
Db   1026 AGACATGGTTGGGGAAGAGACGTCACCAAAAATTAACAAAAACTGAGATATGTTCCCAGTTG   1082
```

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RESULT 15
AAD62763
ID    AAD62763  standard; DNA; 1195 BP.
XX
AC    AAD62763;
XX
DT    12-FEB-2004  (first entry)
XX
DE    Human STEAP (six transmembrane epithelial antigen of the prostate) DNA.
XX
KW    Human; cancer; differential modulation; gene expression profile; STEAP;
KW    six transmembrane epithelial antigen of the prostate; ds.
XX
OS    Homo sapiens.
XX
PN    US2003194733-A1.
XX
PD    16-OCT-2003.
XX
PF    21-MAR-2003; 2003US-00393567.
XX
PR    29-MAR-2002; 2002US-0368667P.
XX
PA    (WANG/) WANG Y.
XX
PI    Wang Y;
XX
DR    WPI; 2003-844450/78.
XX
PS    Claim 4; Page 54-55; 0pp; English.
XX
PT    Diagnosing cancer comprises identifying differential modulation of each
PT    gene (relative to the expression of the same genes in a normal
PT    population) in a combination of genes.
XX
CC    The invention relates to a method for diagnosing cancer. The method
CC    comprising identifying differential modulation of each gene (relative to
CC    the expression of the same genes in a normal population) in a combination
CC    of genes. The method, diagnostic portfolio and the kit are useful in
CC    diagnosing cancer. The method may also be used for determining gene
CC    expression profiles. The present sequence is human STEAP (six
CC    transmembrane epithelial antigen of the prostate) DNA used to illustrate
CC    the method of the invention
XX
SQ    Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

Query Match             100.0%;  Score 1017;  DB 10;  Length 1195;
Best Local Similarity   100.0%;
Matches 1017;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;
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Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAGAGAGACTTTGGAAAATGAAGCCTAGGAGA 60
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Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAGAGAGACTTTGGAAAATGAAGCCTAGGAGA 125

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              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCGCCCTTCAGAA 180
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Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTGGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTGGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAGTAATTCACCCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAGTAATTCACCCCTTTAGCAACT 365

Qy        301 TCCCATCAACAAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTTCTTTGGCATTTGTTTACCTGCCAAGGTGTTGATAGCAGCAATTGTCCAA 420
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Db        426 GTTTCCATCACTCTTCTTTGGCATTTGTTTACCTGCCAAGGTGTTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCAATAATGGAACCAAGTATAAGAAGAACTTTCCACATTGGTTGGGATAAGAAGTGGATGGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCAATAATGGAACCAAGTATAAGAAGAACTTTCCACATTGGTTGGGATAAGAAGTGGATGGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATCGCAATTTATAGTCTG 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATCGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGGGCCATCCTACAGATACAAAGTTGCTAAAACTGGGCATATCAACAGGTC 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGGGCCATCCTACAGATACAAAGTTGCTAAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGAATGCCTGGATTGAGCGATGAGATGAGTTTGGAGAATGGAGATTTATGTG 660
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Qy        661 TCTCTGGGAATTGTGGGAATTGGGCAATACTGGCCTCCGTGTGTGACATCTATTCCATCT 720
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Db        726 TCTCTGGGAATTGTGGGAATTGGGCAATACTGGCCTCCGTGTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACATACACGCATTGGATTGTTTGGTTCTGGAATAAGTGGATAGATATA 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACATACACGCATTGGATTGTTTGGTTCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAAATTTGTATGGTATACACCTCCAAACTTTTATGATAAGTTGTTTTCCTTCCAATTGTT 900
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        901 GTCCTGATATTTAAAGCAATACTATTCCTTGACGAGGAGAAGATACTGAAGATT 960
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Qy        961 AGACATGGTTCGGAGAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
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Job time : 685.751 secs
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OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

Run on: December 4, 2005, 20:37:01 ; Search time 5376.03 Seconds
(without alignments)
10753.247 Million cell updates/sec

Title: US-10-750-262-1_COPY_66_1082
Perfect score: 1017
Sequence: 1 atggaaagcagagaaaagacat..........ctgagatatgttcccagttg 1017
Scoring table: IDENTITY_NUC
Gapop 10_0, Gapext 1.0
Searched: 5883141 seqs, 2842172653 residues
Total number of hits satisfying chosen parameters: 11766282
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
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12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: gb_htg:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1017	100.0	1193	6	BD232184	BD232184 Novel ser
2	1017	100.0	1193	6	AR617054	AR617054 Sequence
3	1017	100.0	1193	6	AX155243	AX155243 Sequence
4	1017	100.0	1195	6	CQ776742	CQ776742 Sequence
5	1017	100.0	1195	6	AR366780	AR366780 Sequence
6	1017	100.0	1195	6	AR405830	AR405830 Sequence
7	1017	100.0	1195	6	AR564210	AR564210 Sequence
8	1017	100.0	1195	6	AR589196	AR589196 Sequence
9	1017	100.0	1195	6	AR654075	AR654075 Sequence
10	1017	100.0	1195	6	AX201105	AX201105 Sequence
11	1017	100.0	1195	6	AX267904	AX267904 Sequence
12	1017	100.0	1195	6	AX926483	AX926483 Sequence
13	1017	100.0	1195	6	AX951736	AX951736 Sequence
14	1017	100.0	1195	6	AX960014	AX960014 Sequence
15	1017	100.0	1195	8	AF186249	AF186249 Homo sapi
16	1017	100.0	1240	8	BC011802	BC011802 Homo sapi
17	1017	100.0	1277	6	CQ412839	CQ412839 Sequence
18	1017	100.0	1330	6	CQ981397	CQ981397 Sequence
19	1017	100.0	1330	6	AF319659	AF319659 Sus scrof
20	1017	100.0	1330	6	CS031875	CS031875 Sequence
21	1017	100.0	1330	6	CS036259	CS036259 Sequence
22	1017	100.0	1330	6	CS040827	CS040827 Sequence
23	844.2	83.0	1754	4	CS045211	CS045211 Sequence
24	760.6	74.8	3627	6	BD232188	BD232188 Novel ser
25	760.6	74.8	3627	6	AR366784	AR366784 Sequence
26	760.6	74.8	3627	6	AR617056	AR617056 Sequence
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29	738.6	72.6	1234	9	BC061023	BC061023 Mus muscu
30	737	72.5	1175	9	CQ777614	CQ777614 Sequence
31	737	72.5	1211	9	AF297098	AF297098 Mus muscu
32	719.4	70.7	1198	9	BD192004	BD192004 Modulator
33	636.2	62.6	1191	9	AY029584	AY029584 Mus muscu
34	615.6	60.5	1209	8	BC066301	BC066301 Homo sapi
35	517.2	50.9	87401	14	AC021898	AC021898 Homo sapi
36	517.2	50.9	105247	14	AC004969	AC004969 Homo sapi
c 37	517.2	50.9	110000	14	AC147308_0	AC147308_0 Pan trogl
c 38	517.2	50.9	157646	14	AC142337	AC142337 Pan trogl
c 39	517.2	50.9	161732	14	AC104475	AC104475 Pan trogl
c 40	517.2	50.9	211383	8	AC161278	AC161278 Pan trogl
c 41	517.2	50.9	219769	14	AC162380	AC162380 Pan trogl
c 42	516	50.7	592	6	BD242240	BD242240 Compounds
c 43	516	50.7	592	6	AR278447	AR278447 Sequence
c 44	516	50.7	592	6	AR367143	AR367143 Sequence
c 45	516	50.7	592	6	AR371039	AR371039 Sequence

ALIGNMENTS

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LOCUS       BD232184                1193 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Novel serpiginous transmembrane antigen expressed in human cancer
            and utilization thereof.
ACCESSION   BD232184
VERSION     BD232184.1  GI:33041954
KEYWORDS    JP 2002517184-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1193)
  AUTHORS   Afar,D.E., Hubert,R.S., Leong,K., Raitano,A.B., Saffran,D.C. and
            Mitchell,S.C.
  TITLE     Novel serpiginous transmembrane antigen expressed in human cancer
            and utilization thereof
  JOURNAL   Patent: JP 2002517184-A 1 18-JUN-2002;
            UROGENSYS INC
COMMENT     Homo sapiens (human)
OS          Homo sapiens (human)
PN          JP 2002517184-A/1
PD          18-JUN-2002
PF          01-JUN-1999 JP 2000552151
PR          01-JUN-1998 US 60/087520,30-JUN-1998 US 60/091183 PI
DANIEL E AFAR, RENE S HUBERT, KAHAN LEONG, ARTHUR B RAITANO PI
,DOUGLAS C SAFFRAN
PI          STEPHEN CHAPPELL MITCHELL
PC          C12N15/09,A61K38/00,A61K39/395,A61P35/00,C07K14/47,C07K16/18,
PC          C12N15/10,
PC          C12P21/00,C12P21/08,G01N33/574,C12N15/00,A61K37/02,
PC          C12N5/00
PC          C12N5/00
CC          Novel serpiginous transmembrane antigen expressed in human CC
            cancer and
CC          utilization thereof
FH          Key            Location/Qualifiers
FT          source         1..1193
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FEATURES             Location/Qualifiers
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ORIGIN

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/db_xref="taxon:9606"

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Query Match       100.0%;   Score 1017;   DB 6;   Length 1193;
Best Local Similarity  100.0%;   Pred. No. 2.6e-231;
Matches 1017;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     61 AAATTTAGAGAGAAGACGATTATTTGCATAAGGACACACGGGAGAGACCATGCTAAAAAGA 120
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    304 ATAGCATCTCTGACTTTTCTTTACACTCTTCTCTGAGGGAAGTAATTCACCCTTTAGCAACT 363

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Qy    601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
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Db    664 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 723

Qy    661 TCTCTGGGAATTGTGGGAATTGGCAATACTCGGCTCTGTGTTGGCGTGTGACATCTATTCCATCT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    724 TCTCTGGGAATTGTGGGAATTGGCAATACTCGGCTCTGTGTTGGCGTGTGACATCTATTCCATCT 783

Qy    721 GTGAGTGACTCTTTGACATGGAGAGAATTCACTATATTATTCAGAGACGAAGTGTTCCAA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    784 GTGAGTGACTCTTTGACATGGAGAGAATTCACTATATTATTCAGAGACGAAGTGTTCCAA 843

Qy    781 TCCCTTCTACTGGGCACAATACACGGCATTGAGTTTGGCGGATAGAGTAGA 840
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Db    844 TCCCTTCTACTGGGCACAATACACGGCATTGAGTTTGGCGGATAGAGTAGA 903

Qy    841 AAACAATTTGTATGGTATACACCTCCAACTTTATGATAGCTGTTTTCCTTCCAAATTGTT 900
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Db    904 AAACAATTTGTATGGTATACACCTCCAACTTTATGATAGCTGTTTTCCTTCCAAATTGTT 963

Qy    901 GTCCTGATATTTAAAAGCATACTATTCCTCGCCATGCTTCAGGAAGAAGATACTGAAGATT 960
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Db    964 GTCCTGATATTTAAAAGCATACTATTCCTCGCCATGCTTCAGGAAGAAGATACTGAAGATT 1023

Qy    961 AGACATGGTTGGGAAGACGTCACCAAAAATTAACAAAACTGAGATAATGTTCCCAGTTG 1017
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Db   1024 AGACATGGTTGGGAAGACGTCACCAAAAATTAACAAAACTGAGATAATGTTCCCAGTTG 1080
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RESULT 2
LOCUS           AR617054                     1193 bp      DNA       linear   PAT 14-FEB-2005
DEFINITION      Sequence 1 from patent US 6833438.
ACCESSION       AR617054
VERSION         AR617054.1   GI:59720558
KEYWORDS        .
SOURCE          Unknown.
  ORGANISM      Unknown.
                Unclassified.
REFERENCE       1 (bases 1 to 1193)
  AUTHORS       Afar,D.E., Hubert,R.S., Raitano,A.B., Saffran,D.C. and
                Mitchell,S.C.
  TITLE         Serpentine transmembrane antigens expressed in human cancers and
                uses thereof
  JOURNAL       Patent: US 6833438-A 1 21-DEC-2004;
                Agensys, Inc.; Santa Monica, CA
FEATURES             Location/Qualifiers
     source          1..1193
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN
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Query Match       100.0%;   Score 1017;   DB 6;   Length 1193;
Best Local Similarity  100.0%;   Pred. No. 2.6e-231;
Matches 1017;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Qy      1 ATGGAAAGCAGAAAAAGACATCACAAAACCAAGAAGAACTTTGGGAAAATGAAGCCTAGGAGA 60
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Db     64 ATGGAAAGCAGAAAAAGACATCACAAAACCAAGAAGAACTTTGGGAAAATGAAGCCTAGGAGA 123

Qy     61 AAATTTAGAGAGAAGACGATTATTTGCATAAGGACACACGGGAGAGACCATGCTAAAAAGA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    124 AAATTTAGAGAGAAGACGATTATTTGCATAAGGACACACGGGAGAGACCATGCTAAAAAGA 183

Qy    121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    184 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 243

Qy    181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCCAATTAAAAATAGCTGCTATT 240
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Db    244 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCCAATTAAAAATAGCTGCTATT 303

Qy    241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    304 ATAGCATCTCTGACTTTTCTTTACACTCTTCTCTGAGGGAAGTAATTCACCCTTTAGCAACT 363

Qy    301 TCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    364 TCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 423

Qy    361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAGAATTGTCCAA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    424 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAGAATTGTCCAA 483

Qy    421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATGGATGTTAACA 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    484 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATGGATGTTAACA 543

Qy    481 AGAAAGCAGTTTGGGCCTTCTCAGTTTCTTTTTTGCTGTACTGCAATTTATAGTCTG 540
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Db    544 AGAAAGCAGTTTGGGCCTTCTCAGTTTCTTTTTTGCTGTACTGCAATTTATAGTCTG 603

Qy    541 TCTTACCCAATGAGGCGACCTCTACAGATACAAGTTGCTAAACTGCAGTCATCACAGGTC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    604 TCTTACCCAATGAGGCGACCTCTACAGATACAAGTTGCTAAACTGCAGTCATCACAGGTC 663

Qy    601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
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Db    664 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 723
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RESULT 3

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LOCUS       AX155243                1193 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1 from Patent WO0140276.
ACCESSION   AX155243
VERSION     AX155243.1  GI:14536707
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Afar,D.E., Hubert,R.S., Raitano,A.B., Saffran,D.C., Mitchell,S.C.,
            Faris,M. and Jakobovits,A.
  TITLE     Serpentine transmembrane antigens expressed in human prostate
            cancers and uses thereof
  JOURNAL   Patent: WO 040276-A 1 07-JUN-2001;
            Urogenesys, Inc. (US)
FEATURES             Location/Qualifiers
     source          1..1193
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     CDS             64..1083
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                     /codon_start=1
                     /protein_id="CAC42677.1"
                     /db_xref="GI:14536708"
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                     RKQFGLLSFFFAVLHAIYSLSYPMRRSYRYKLLWAYQQVQQNKEDAWIEHDVWRMEI
                     YVSLGIVGLAILALLAVTSIPSVSDSLTWREFHYIQSKLGIVSLLLGTIHALIPAWNK
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                     ICSQL"
ORIGIN
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Qy          664 CAACAAAATAAAGAAGAATGATGCCTGGATTGATGATGTTTGAGAGATTTATGTG 723
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Db          661 TCTCTGGGAATTGTGGGATTGGGCAATACTGGCTCTCGTTGGCTGTGACATCTAT 720

Qy          724 TCTCTGGGAATTGTGGGATTGGGCAATACTGGCTCTCGTTGGCTGTGACATCTATCCATCT 783
Qy          721 GTGAGTGACTCTTTGACATGGAGGAGAATTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
Db          724 TCTCTGGGAATTGTGGGATTGGGCAATACTGGCTCTCGTTGGCTGTGACATCTATTCCATCT 783
Qy          784 GTGAGTGACTCTTTGACATGGAGGAGAATTCACTATATTCAGAGCAAGCTAGGAATTGTT 843
Qy          781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTTGCCTGGAATAAGTGGATAGATATA 840
Db          784 GTGAGTGACTCTTTGACATGGAGGAGAATTCACTATATTCAGAGCAAGCTAGGAATTGTT 843
Qy          844 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTTGCCTGGAATAAGTGGATAGATATA 903
Qy          841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
Db          844 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTTGCCTGGAATAAGTGGATAGATATA 903
Qy          904 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 963
Qy          901 GTCCTGATATTTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAGAGATATGTTCAA 960
Db          904 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 963
Qy          964 GTCCTGATATTTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAGAGATATGTTCCA 1023
Qy          961 AGACATGGTTGGGAAGAGACGTCACCAAAAATTAACAAAAACTGAGATATGTTCCCAGTTG 1017
Db          964 GTCCTGATATTTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAGAGATATGTTCAA 1023
Qy         1024 AGACATGGTTGGGAAGACGTCACCAAAAATTAACAAAAACTGAGATATGTTCCCAGTTG 1080
Db          961 AGACATGGTTGGGAAGAGACGTCACCAAAAATTAACAAAAACTGAGATATGTTCCCAGTTG 1017
Db         1024 AGACATGGTTGGGAAGACGTCACCAAAAATTAACAAAAACTGAGATATGTTCCCAGTTG 1080
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Query Match   100.0%; Score 1017; DB 6; Length 1193;
Best Local Similarity 100.0%; Pred. No. 2.6e-231;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy            1 ATGGAAAGCAGAAAAGACATCACAAAACCAAGAAGAGAACTTTGAAAAATGAAGCCTAGGAGA 60
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Db           64 ATGGAAAGCAGAAAAGACATCACAAAACCAAGAAGAGAACTTTGGAAAATGAAGCCTAGGAGA 123
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RESULT 4

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LOCUS       CQ776742                1195 bp    DNA     linear   PAT 11-MAR-2004
DEFINITION  Sequence 428 from Patent EP1394274.
ACCESSION   CQ776742
VERSION     CQ776742.1  GI:45380132
KEYWORDS    .
SOURCE      Homo sapiens (human)
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Qy           61 AATTTAGAAGAAGACGATTATTTGCATAAGGACGGGGAGGAGAGACCAGCATGCTAAAAAGA 120
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Db          124 AATTTAGAAGAAGACGATTATTTGCATAAGGACGGGGAGGAGAGACCAGCATGCTAAAAAGA 183

Qy          121 CCTGTGCTTTTGCATTTGCATTGCACAGCCCATGCTGATGAATTTGACTGGGCAGAA 180
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Qy          181 CTTCAGCACACACAGGAGAACTCTTTCCACAGTGGGCACTTGCCAATTAAAATAACTGCTATT 240
Db          244 CTTCAGCACACACAGGAGAACTCTTTCCACAGTGGGCACTTGCCAATTAAAATAACTGCTATT 303

Qy          241 ATAGCACTCTGACTTTCTTTACACTCTTCTGAGGATGGGCACCCCTTTAGCAACT 300
Db          304 ATAGCACTCTGACTTTCTTTTACACTCTTCTGAGGATGGGCACCCCTTTAGCAACT 363

Qy          301 TCCCATCAACACATATTTTTATTAAAATTCCAATACCTGGTCATCACAACAGTCTTGGTG 360
Db          364 TCCCATCAACACATATTTTTATTAAAATTCCAATACCTGGTCATCACAACAGTCTTGGTG 423

Qy          361 GTTTCCATCACTCTCTTGGGCATTGGTTTACCTGCCAGTGCAATTGTCCAA 420
Db          424 GTTTCCATCACTCTCTTGGGCATTGGTTTACCTGCCAGTGCAATTGTCCAA 483

Qy          421 CTTCATAATGGAACCAAGTAATAAGAAGTTCCACAATGGTTGGGATAAGTGGCTAACA 480
Db          484 CTTCATAATGGAACCAAGTAATAAGAAGTTCCACAATGGTTGGGATAAGTGGCTAACA 543

Qy          481 AGAAAGCAGTTTGGGCTTCAGTTTCTTCTTTTTTTGCATGATGCATGCAATTTATAGTCTG 540
Db          544 AGAAAGCAGTTTGGGCTTCAGTTTCTTCTTTTTTTGCATGATGCATGCAATTTATAGTCTG 603

Qy          541 TCTTACCCAATGAGGGCGATCCTACAGATACAAGATGTTGCTAAAACTGGGCATATCCAGTC 600
Db          604 TCTTACCCAATGAGGGCGATCCTACAGATACAAGATGTTGCTAAAACTGGGCATATCAACAGTC 663

Qy          601 CAACAAAATAAAGAAGAATGCCTGGATTGATGATGTTTGAGAGATTTATGTG 660
Db          664 CAACAAAATAAAGAAGAATGCCTGGATTGATGATGTTTGAGAGATTTATGTG 723

Qy          661 TCTCTGGGAATTGTGGGATTGGGCAATACTGGCTCTCGTTGGCTGTGACATCTATTCCATCT 720
Db          724 TCTCTGGGAATTGTGGGATTGGGCAATACTGGCTCTCGTTGGCTGTGACATCTATTCCATCT 783

Qy          721 GTGAGTGACTCTTTGACATGGAGGAGAATTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
Db          784 GTGAGTGACTCTTTGACATGGAGGAGAATTCACTATATTCAGAGCAAGCTAGGAATTGTT 843

Qy          781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTTGCCTGGAATAAGTGGATAGATATA 840
Db          844 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTTGCCTGGAATAAGTGGATAGATATA 903

Qy          841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
Db          904 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 963

Qy          901 GTCCTGATATTTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAGAGATATGTTCAA 960
Db          964 GTCCTGATATTTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAGAGATATGTTCAA 1023

Qy          961 AGACATGGTTGGGAAGAGACGTCACCAAAAATTAACAAAAACTGAGATATGTTCCCAGTTG 1017
Db         1024 AGACATGGTTGGGAAGAGACGTCACCAAAAATTAACAAAAACTGAGATATGTTCCCAGTTG 1080
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ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
REFERENCE 1
AUTHORS   Ohtani,N., Sugita,Y., Yamaya,M., Kubo,H., Nagai,H. and Izuhara,K.
TITLE   Methods of testing for bronchial asthma or chronic obstructive
          pulmonary disease
JOURNAL   Patent: EP 1394274-A 428 03-MAR-2004;
          Genox Research, Inc. (JP)
FEATURES   Location/Qualifiers
     source   1..1195
                   /organism="Homo sapiens"
                   /mol_type="unassigned DNA"
                   /db_xref="taxon:9606"
ORIGIN

Query Match   100.0%;   Score 1017; DB 6; Length 1195;
Best Local Similarity 100.0%; Pred. No. 2.6e-231;
Matches 1017; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy     1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAAGAACTTTGGAAAAATGAAGCCTAGGAGA 60
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Db    66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAAGAACTTTGGAAAAATGAAGCCTAGGAGA 125

Qy    61 AATTTAGAAGAAGAGACGGATTATTTGCATAAGGACACACGGGAGAGACCAGCCATGCTAAAAAGA 120
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Db   126 AATTTAGAAGAAGAGACGATTATTTGCATAAGGACACACGGGAGAGACCAGCCATGCTAAAAAGA 185

Qy   121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
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Db   186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy   181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAAAATAGCTATT 240
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Db   246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAAAATAGCTATT 305

Qy   241 ATAGCACATCTCTGACTTTCTTTCTTTACACTCTTCTGAGGGAGAAGTAAATTCACCCCTTTAGCAAACT 300
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Db   306 ATAGCACATCTCTGACTTTCTTTCTTTACACTCTTCTGAGGGAGAAGTAAATTCACCCCTTTAGCAAACT 365

Qy   301 TCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAGTCTTGCCAATG 360
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Db   366 TCCCATCAACAATATTTTTTATAAAAATTCCAATCCTGGTCATCAACAAGTCTTGCCAATG 425

Qy   361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAGCAATTGTCCAA 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAGCAATTGTCCAA 485

Qy   421 CTTCATAATGGAACCAAGTATAAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
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Db   486 CTTCATAATGGAACCAAGTATAAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy   481 AGAAAGCAGTTTGGGCCTTCTTCAGTTCTTTTTGCTGTGATGCATCAATTTATATGTCTG 540
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Db   546 AGAAAGCAGTTTGGGCCTTCTTCAGTTTCTTTTTGCTGTGATGCATCAATTTATATGTCTG 605

Qy   541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
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Db   606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy   601 CAACAAAATAAAGAAGATGCCTGGATTGACGCATGACGTGCTATCACAAGTTATGTG 660
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Db   666 CAACAAAATAAAGAAGATGCCTGGATTGACGCATGACGTGCTATCACAAGTTATGTG 725

Qy   661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTCGCTGTGACATCTATTCCATCT 720
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Db   726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTCGCTGTGACATCTATTCCATCT 785

Qy   721 GTGAGTGACTCTTTGACTATGGAGAGAATTTCAGTAGGAATTCAGAGCAAGCTAGGAATTGTT 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   786 GTGAGTGACTCTTTGACTATGGAGAGAATTTCAGTAGGAATTCAGAGCAAGCTAGGAATTGTT 845
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RESULT 5

LOCUS   AR366780   1195 bp   DNA   linear   PAT 12-SEP-2003
DEFINITION Sequence 1 from patent US 6329503.
ACCESSION   AR366780
VERSION   AR366780.1 GI:34599746
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1195)
  AUTHORS   Afar,D.E., Hubert,R.S., Leong,K., Raitano,A.B., Saffran,D.C. and
            Mitchell,S.C.
  TITLE   Serpentine transmembrane antigens expressed in human cancers and
            uses thereof
  JOURNAL   Patent: US 6329503-A 1 11-DEC-2001;
            Agensys, Inc.; Santa Monica, CA;
WOX;
FEATURES   Location/Qualifiers
     source   1..1195
                   /organism="unknown"
                   /mol_type="genomic DNA"
ORIGIN

Query Match   100.0%;   Score 1017; DB 6; Length 1195;
Best Local Similarity 100.0%; Pred. No. 2.6e-231;
Matches 1017; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy     1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAAGAACTTTGGAAAAATGAAGCCTAGGAGA 60
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Db    66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAAGAACTTTGGAAAAATGAAGCCTAGGAGA 125

Qy    61 AATTTAGAAGAAGAGACGATTATTTGCATAAGGACACACGGGAGAGACCAGCCATGCTAAAAAGA 120
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Db   126 AATTTAGAAGAAGAGACGATTATTTGCATAAGGACACACGGGAGAGACCAGCCATGCTAAAAAGA 185

Qy   121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
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Db   186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy   181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAAAATAGCTATT 240
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Db   246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAAAATAGCTATT 305

Qy   241 ATAGCACATCTCTGACTTTCTTTCTTTACACTCTTCTGAGGGAGAAGTAAATTCACCCCTTTAGCAAACT 300
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Db   306 ATAGCACATCTCTGACTTTCTTTCTTTACACTCTTCTGAGGGAGAAGTAAATTCACCCCTTTAGCAAACT 365

Qy   301 TCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAGTCTTGCCAATG 360
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Db   366 TCCCATCAACAATATTTTTTATAAAAATTCCAATCCTGGTCATCAACAAGTCTTGCCAATG 425

Qy   361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAGCAATTGTCCAA 420
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Db   426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAGCAATTGTCCAA 485
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Right continuation:

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Qy   781 TCCCTTCTACTGGGCACAAATACACGCAGCCATTGATTTTTGCCTGGAATGAAGTGGATAGAGATATA 840
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Db   846 TCCCTTCTACTGGGCACAAATACACGCAGCCATTGATTTTTGCCTGGAATGAAGTGGATAGAGATATA 905

Qy   841 AAACAAATTGTATGGTATACAACCTCCAACTTTTATGATAAGTCTGTTTTCCTTCCAAATGTT 900
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Db   906 AAACAAATTGTATGGTATACAACCTCCAACTTTTATGATAAGTCTGTTTTCCTTCCAAATGTT 965

Qy   901 GTCCTGATTATTTAAAAGCATAACTAATTCCTGCCATGCTTGAGGAAGAAGAAGATTGAAGATT 960
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Db   966 GTCCTGATTATTTAAAAGCATAACTAATTCCTGCCATGCTTGAGGAAGAAGAAGATTGAAGATT 1025

Qy   961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAAACTGAGATATGTTCCCAGTTG 1017
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RESULT 6

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LOCUS       AR405830                1195 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 878 from patent US 6630305.
ACCESSION   AR405830
VERSION     AR405830.1  GI:40154667
KEYWORDS
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1195)
  AUTHORS   Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
            Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
            Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
            Hepler,W.T. and Henderson,R.A.
  TITLE     Compositions and methods for the therapy and diagnosis of prostate
            cancer
  JOURNAL   Patent: US 6630305-A 878 07-OCT-2003;
            Corixa Corporation; Seattle, WA;
            WOX;
FEATURES             Location/Qualifiers
     source          1..1195
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN
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Query Match           100.0%;  Score 1017;  DB 6;  Length 1195;
Best Local Similarity 100.0%;  Pred. No. 2.6e-231;
Matches  1017;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Qy      1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
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(sequence alignment block — Qy/Db paired lines, positions 421–1082)

RESULT 7

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LOCUS       AR564210                1195 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 878 from patent US 6759515.
ACCESSION   AR564210
VERSION     AR564210.1  GI:53979261
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(sequence alignment block — Qy/Db paired lines, positions 66–1082)

Left column

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KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1  (bases 1 to 1195)
AUTHORS      Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
             Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
             Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
             Hepler,W.T. and Henderson,R.A.
TITLE        Compositions and methods for the therapy and diagnosis of prostate
             cancer
JOURNAL      Patent: US 6759515-A 878 06-JUL-2004;
             Corixa Corporation; Seattle, WA
FEATURES             Location/Qualifiers
     source          1..1195
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match     100.0%;  Score 1017;  DB 6;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-231;
  Matches 1017;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     1 ATGGAAAAGCAGAAAAAGACATCACAAAACCAAGAAGAGAACTTTGGAAAAATGAAGCCTAGGAGA    60
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Db    66 ATGGAAAAGCAGAAAAAGACATCACAAAACCAAGAAGAGAACTTTGGAAAAATGAAGCCTAGGAGA   125

Qy    61 AATTTAGAAGAAGAACGAGATTATTTGCATAAGGACACGGGAGAGAGACCAGCATGCTAAAAAGA   120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   126 AATTTAGAAGAAGAACGAGATTATTTGCATAAGGACACGGGAGAGAGACCAGCATGCTAAAAAGA   185

Qy   121 CCTGTGCTTTTGCATTGCACCAAACAGCCCATGCCCTTCAGAA   180
         |||||||||||||||||||||||||||||||||||||||||||
Db   186 CCTGTGCTTTTGCATTGCACCAAACAGCCCATGCCCTTCAGAA   245

Qy   181 CTTCAGCACACACAGGACACTCTTTCCACAGTGGCACTTGCCCAATTAAAATAGCTGCTATT   240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   246 CTTCAGCACACACAGGACACTCTTTCCACAGTGGCACTTGCCCAATTAAAATAGCTGCTATT   305

Qy   241 ATAGCATCTCTGACTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT   300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   306 ATAGCATCTCTGACTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT   365

Qy   301 TCCCATCAACAAATATTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG   360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   366 TCCCATCAACAAATATTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG   425

Qy   361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCGCAGGCAAATTGTCCAA    420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCGCAGGCAAATTGTCCAA   485

Qy   421 CTTCATAATGGAACCAAGTAATATAAGGAAGTTCCACATTGGTTGGATAAGGATGTTAACA   480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   486 CTTCATAATGGAACCAAGTAATATAAGGAAGTTCCACATTGGTTGGATAAGGATGTTAACA   545

Qy   481 AGAAAGCAGTTGGGCTTCAGTTTCTTCAGTTTTGCTGTACTGCATGCAAATTTATAGTCTG   540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   546 AGAAAGCAGTTGGGCTTCAGTTTCTTCAGTTTTGCTGTACTGCATGCAAATTTATAGTCTG   605

Qy   541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGTC   600
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db   606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGTC   665

Qy   601 CAACAAAATAAAGAAGAATGCCTGGAATTGAGCAATGATGTTTGGAGCAAGATTATGTG   660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   666 CAACAAAATAAAGAAGAATGCCTGGAATTGAGCAATGATGTTTGGAGCAAGATTATGTG   725

Qy   661 TCCTCTGGGAATTGTGGGAATTGGGCAATACTCGGCTCTGTTGGCTGTGAGACTATTCCATCT   720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   726 TCCTCTGGGAATTGTGGGAATTGGGCAATACTCGGCTCTGTTGGCTGTGAGACTATTCCATCT   785

Qy   721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATTATTCAGAGAGCAAGCTAGGAATTGTT   780
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Right column

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RESULT 8
LOCUS       AR589196                1195 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 878 from patent US 6800746.
ACCESSION   AR589196
VERSION     AR589196.1  GI:56636093
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1  (bases 1 to 1195)
AUTHORS     Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
            Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
            Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
            Hepler,W.T. and Henderson,R.A.
TITLE       Compositions and methods for the therapy and diagnosis of prostate
            cancer
JOURNAL     Patent: US 6800746-A 878 05-OCT-2004;
            Corixa Corporation; Seattle, WA
FEATURES             Location/Qualifiers
     source          1..1195
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match     100.0%;  Score 1017;  DB 6;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-231;
  Matches 1017;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     1 ATGGAAAAGCAGAAAAAGACATCACAAAACCAAGAAGAGAACTTTGGAAAAATGAAGCCTAGGAGA    60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    66 ATGGAAAAGCAGAAAAAGACATCACAAAACCAAGAAGAGAACTTTGGAAAAATGAAGCCTAGGAGA   125

Qy    61 AATTTAGAAGAAGAACGAGATTATTTGCATAAGGACACGGGAGAGAGACCAGCATGCTAAAAAGA   120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   126 AATTTAGAAGAAGAACGAGATTATTTGCATAAGGACACGGGAGAGAGACCAGCATGCTAAAAAGA   185

Qy   121 CCTGTGCTTTTGCATTGCACCAAACAGCCCATGCCCTTCAGAA   180
         |||||||||||||||||||||||||||||||||||||||||||
Db   186 CCTGTGCTTTTGCATTGCACCAAACAGCCCATGCCCTTCAGAA   245

Qy   181 CTTCAGCACACACAGGACACTCTTTCCACAGTGGCACTTGCCCAATTAAAATAGCTGCTATT   240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   246 CTTCAGCACACACAGGACACTCTTTCCACAGTGGCACTTGCCCAATTAAAATAGCTGCTATT   305

Qy   241 ATAGCATCTCTGACTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT   300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   306 ATAGCATCTCTGACTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT   365

Qy   301 TCCCATCAACAAATATTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG   360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   366 TCCCATCAACAAATATTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG   425

Qy   361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCGCAGGCAAATTGTCCAA   420
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RESULT 9
LOCUS   AR654075   1195 bp   DNA   linear   PAT 13-JUN-2005
DEFINITION Sequence 1 from patent US 6887975.
ACCESSION   AR654075
VERSION   AR654075.1 GI:67584962
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1195)
  AUTHORS   Afar,D.E., Hubert,R.S., Leong,K., Raitano,A.B., Saffran,D.C. and
            Mitchell,S.C.
  TITLE   Peptides derived from STEAP1
  JOURNAL   Patent: US 6887975-A 1 03-MAY-2005;
            Agensys, Inc.; Santa Monica, CA
FEATURES   Location/Qualifiers
     source   1..1195
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Query Match   100.0%; Score 1017; DB 6; Length 1195;
Best Local Similarity 100.0%;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ATGGAAAGCAGAAAAGRCATCACAAAACCAAGAGAAGAACTTTGGAAAAATGAAGCCTAGGAGA 60
              ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db   66 ATGGAAAGCAGAAAAGACATCACAAAACCAAGAGAAGAACTTTGGAAAAATGAAGCCTAGGAGA 125

[Sequence alignment continues — Qy/Db paired lines from positions 61–1082 / 126–1195, with matching bars between each pair, representing the full-length alignment of Query against Db AR654075.]

RESULT 10
LOCUS   AX201105   1195 bp   DNA   linear   PAT 29-AUG-2001
DEFINITION Sequence 735 from Patent WO0151633.
ACCESSION   AX201105
VERSION   AX201105.1 GI:15390890
KEYWORDS   .

[Sequence alignment block for RESULT 10 — Qy/Db paired lines from positions 61–1082 / 126–1195 against Db AX201105, with matching bars between each pair.]

SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
            Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
            Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
  TITLE   Compositions and methods for the therapy and diagnosis of prostate
            cancer
  JOURNAL   Patent: WO 0151633-A 735 19-JUL-2001;
            CORIXA CORPORATION (US)
FEATURES   Location/Qualifiers
     source   1..1195
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match   100.0%; Score 1017; DB 6; Length 1195;
Best Local Similarity   100.0%;
Matches 1017; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ATGGAAAGCAGAAAAGACATCACAAACACCAAGAGAGAGAGAACTTTGGAAAAATGAAGCCTAGGAGA 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   66 ATGGAAAGCAGAAAAGACATCACAAACACCAAGAGAGAGAGAACTTTGGAAAAATGAAGCCTAGGAGA 125

Qy   61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGGAGAACCAGCTACTTAAAAGA 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGGAGAACCAGCTACTTAAAAGA 185

Qy   121 CCTGTGCTTTTGCATTTGACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   186 CCTGTGCTTTTGCATTTGACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy   181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy   241 ATAGCATCTCTGACTTTTCTTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   306 ATAGCATCTCTGACTTTTCTTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy   301 TCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
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Db   366 TCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy   361 GTTTCCATCACTCTTCTTGGCATTGGTTTTACCTGCACGTGATAGCAGCAATTGTCAA 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   426 GTTTCCATCACTCTTCTTGGCATTGGTTTTACCTGCACGTGATAGCAGCAATTGTCAA 485

Qy   421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy   481 AGAAAGCAGTTTGGGCCTTCTCTCAGTTTCTTTTTTGCTGTACTGCATGCATATCAAGTTG 540
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Db   546 AGAAAGCAGTTTGGGCCTTCTCTCAGTTTCTTTTTTGCTGTACTGCATGCATATCAAGTTG 605

Qy   541 TCTTACCCCAATGAGGCGATCCTACAGATACAACAGTTGCTAAACTGGGCATATCAAACAGGTC 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   606 TCTTACCCCAATGAGGCGATCCTACAGATACAACAGTTGCTAAACTGGGCATATCAAACAGGTC 665

Qy   601 CAACAAAATAAAGAAGATGCCTGGAATTGAGCAGCATAGAGAATGAGAGATTTATGTG 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   666 CAACAAAATAAAGAAGATGCCTGGAATTGAGCAGCATAGAGAATGAGAGATTTATGTG 725

Qy   661 TCTCTGGGAATTGTGGCAATAACTGGCCTCGTGTTGGCTGTGACATCTATTCCATCT 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   726 TCTCTGGGAATTGTGGCAATAACTGGCCTCGTGTTGGCTGTGACATCTATTCCATCT 785

Qy   721 GTGAGTGACTCTTTGACATGGAGGAGAATTCACTATATTCAGAGAGCCAAGCTAGGAATTGTT 780

RESULT 11
LOCUS   AX267904   1195 bp   DNA   linear   PAT 26-OCT-2001
DEFINITION Sequence 878 from Patent WO0173032.
ACCESSION   AX267904
VERSION   AX267904.1 GI:16516522
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
            Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
            Vedvik,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
            and Henderson,R.A.
  TITLE   Compositions and methods for the therapy and diagnosis of prostate
            cancer
  JOURNAL   Patent: WO 0173032-A 878 04-OCT-2001;
            CORIXA CORPORATION (US)
FEATURES   Location/Qualifiers
     source   1..1195
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match   100.0%; Score 1017; DB 6; Length 1195;
Best Local Similarity   100.0%;
Matches 1017; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ATGGAAAGCAGAAAAGACATCACAAACACCAAGAGAGAGAGAACTTTGGAAAAATGAAGCCTAGGAGA 60
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Db   66 ATGGAAAGCAGAAAAGACATCACAAACACCAAGAGAGAGAGAACTTTGGAAAAATGAAGCCTAGGAGA 125

Qy   61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGGAGAACCAGCTACTTAAAAGA 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGGAGAACCAGCTACTTAAAAGA 185

Qy   121 CCTGTGCTTTTGCATTTGACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   186 CCTGTGCTTTTGCATTTGACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy   181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy   241 ATAGCATCTCTGACTTTTCTTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   306 ATAGCATCTCTGACTTTTCTTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy   301 TCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360

RESULT 12

LOCUS   AX926483   1195 bp   DNA   linear   PAT 19-DEC-2003
DEFINITION Sequence 35 from Patent EP1355150.
ACCESSION   AX926483
VERSION   AX926483.1 GI:40246089
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Wang,Y.
  TITLE   Panel of nucleic acid sequences for cancer diagnosis
  JOURNAL   Patent: EP 1355150-A 35 22-OCT-2003;
            Ortho-Clinical Diagnostics, Inc. (US)
FEATURES   Location/Qualifiers
     source   1..1195
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match   100.0%; Score 1017; DB 6; Length 1195;
                        Best Local Similarity   100.0%;
  Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 13

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AX951736
LOCUS           AX951736                1195 bp    DNA     linear   PAT 08-JAN-2004
DEFINITION      Sequence 35 from Patent EP1367138.
ACCESSION       AX951736
VERSION         AX951736.1  GI:40782084
KEYWORDS        .
SOURCE          Homo sapiens (human)
  ORGANISM      Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Hominidae; Homo.
REFERENCE       1
  AUTHORS       Wang,Y.
  TITLE         Markers for breast cancer prognosis
  JOURNAL       Patent: EP 1367138-A 35 03-DEC-2003;
                Ortho Clinical Diagnostics Inc. (US)
FEATURES             Location/Qualifiers
     source          1..1195
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match             100.0%;  Score 1017;  DB 6;  Length 1195;
Best Local Similarity   100.0%;
Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATGGAAAAGCAGAAAAAGACAATCACAAAACCAAGAAGAGAACTTTGGAAAAATGAAAGCCTAGGAGA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     66 ATGGAAAAGCAGAAAAAGACAATCACAAAACCAAGAAGAGAACTTTGGAAAAATGAAAGCCTAGGAGA 125

Qy     61 AATTTAGAAGAAGACGAATTATTTGCATAAGGACACGGGAGAGAGACCAGCATGCTAAAAAGA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    126 AATTTAGAAGAAGACGAATTATTTGCATAAGGACACGGGAGAGAGACCAGCATGCTAAAAAGA 185

Qy    121 CCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCGCCCTTCAGAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    186 CCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCGCCCTTCAGAA 245

Qy    181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCCACTTGCCAATTAAAATAGCTGCTATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCCACTTGCCAATTAAAATAGCTGCTATT 305

Qy    241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAGTAATTCACCCTTTAGCAACT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAGTAATTCACCCTTTAGCAACT 365

Qy    301 TCCCATCAACAATATTTTTTATAAAATTCAAATCCTGGTCATCAACAACAAAGTCTTGCCAATG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    366 TCCCATCAACAATATTTTTTATAAAATTCAAATCCTGGTCATCAACAACAAAGTCTTGCCAATG 425

Qy    361 GTTTCCATCACTCTCTTGGCATTGGTTTTACCTGCCAGGTGTGTGATAGCGCAGCAATTGTCCAA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    426 GTTTCCATCACTCTCTTGGCATTGGTTTTACCTGCCAGGTGTGTGATAGCGCAGCAATTGTCCAA 485

Qy    421 CTTCATAATGGAACCAAGTTATAAGGAGTTCCACATTGGATTGGATTGAAGTTAACA 480
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Db    486 CTTCATAATGGAACCAAGTTATAAGGAGTTCCACATTGGATTGGATTGAAGTTAACA 545

Qy    481 AGAAAGCAGTTTGGGCTTCTCAGTTTTCTTTTTTGCTGTACTGCATGCATTTATAGTCTG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    546 AGAAAGCAGTTTGGGCTTCTCAGTTTTCTTTTTTGCTGTACTGCATGCATTTATAGTCTG 605

Qy    541 TCTTACCCAAATGAGGCGATCCTACAGATACAAGTTGCTAAACTCGGGCATATCAAACAGTC 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    606 TCTTACCCAAATGAGGCGATCCTACAGATACAAGTTGCTAAACTCGGGCATATCAAACAGTC 665

Qy    601 CAACAAAATAAAGAAGAAGATGCCTGGATTGAGCATGATGTTTGGGAGAATGGAGATTTATGTG 660
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Db    666 CAACAAAATAAAGAAGAAGATGCCTGGATTGAGCATGATGTTTGGGAGAATGGAGATTTATGTG 725

Qy    661 TCTCTGGGAATTGTGGGAATTGGCAATACTGGCTCTGTTGGCGTGTGCACATCTTATTCCATCT 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    726 TCTCTGGGAATTGTGGGAATTGGCAATACTGGCTCTGTTGGCGTGTGCACATCTTATTCCATCT 785

Qy    721 GTGAGTGACTCTTTGACATGGAGAGAATTCACTATATTCAGAGCAGCAAGCTAGGAATTGTT 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    786 GTGAGTGACTCTTTGACATGGAGAGAATTCACTATATTCAGAGCAGCAAGCTAGGAATTGTT 845

Qy    781 TCCCTTCTTACTGGGCCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
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Db    846 TCCCTTCTTACTGGGCCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy    841 AAACAAATTTGTATGGTAATACACCTCCAACTTTTTATGATAGCTGTGTTTTCCTTCCAATTGTT 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    906 AAACAAATTTGTATGGTAATACACCTCCAACTTTTTATGATAGCTGTGTTTTCCTTCCAATTGTT 965

Qy    901 GTCCTGATATTTAAAAGCATAATACACTATTCCTGCCATGCTTTGAGGAAGAAGACTACTGAAGATT 960
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Db    966 GTCCTGATATTTAAAAGCATAATACACTATTCCTGCCATGCTTTGAGGAAGAAGACTACTGAAGATT 1025

Qy    961 AGACATGGTTGGGGAAGACGTCACCAAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
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Db   1026 AGACATGGTTGGGGAAGACGTCACCAAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082
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RESULT 14
AX960014
LOCUS           AX960014                1195 bp    DNA     linear   PAT 14-JAN-2004
DEFINITION      Sequence 35 from Patent EP1349104.
ACCESSION       AX960014
VERSION         AX960014.1  GI:40880240
KEYWORDS        .
SOURCE          Homo sapiens (human)
  ORGANISM      Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Hominidae; Homo.
REFERENCE       1
  AUTHORS       Jatkoe,T.
  TITLE         Method of selecting a portfolio of markers for use in a diagnostic
                application
  JOURNAL       Patent: EP 1349104-A 35 01-OCT-2003;
                Ortho-Clinical Diagnostics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1..1195
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match             100.0%;  Score 1017;  DB 6;  Length 1195;
Best Local Similarity   100.0%;
Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db     66 ATGGAAAAGCAGAAAAAGACAATCACAAAACCAAGAAGAGAACTTTGGAAAAATGAAAGCCTAGGAGA 125

Qy     61 AATTTAGAAGAAGACGAATTATTTGCATAAGGACACGGGAGAGAGACCAGCATGCTAAAAAGA 120
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Db    126 AATTTAGAAGAAGACGAATTATTTGCATAAGGACACGGGAGAGAGACCAGCATGCTAAAAAGA 185

Qy    121 CCTGTGCTTTTGCATTTGACCAAAACAGCCCATGCTGATGAATTTGACTGCGCCCTTCAGAA 180
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Db    186 CCTGTGCTTTTGCATTTGACCAAAACAGCCCATGCTGATGAATTTGACTGCGCCCTTCAGAA 245

Qy    181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCCACTTGCCAATTAAAATAGCTGCTATT 240
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Qy    241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAGTAATTCACCCTTTAGCAACT 300
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Qy    301 TCCCATCAACAATATTTTTTATAAAATTCAAATCCTGGTCATCAACAACAAAGTCTTGCCAATG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    366 TCCCATCAACAATATTTTTTATAAAATTCAAATCCTGGTCATCAACAACAAAGTCTTGCCAATG 360
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RESULT 15
AF186249

LOCUS   AF186249   1195 bp   mRNA   linear   PRI 14-DEC-1999
DEFINITION Homo sapiens six transmembrane epithelial antigen of prostate
            (STEAP1) mRNA, complete cds.
ACCESSION   AF186249
VERSION   AF186249.1 GI:6572947
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 1195)
  AUTHORS   Hubert,R.S., Vivanco,I., Chen,E., Rastegar,S., Leong,K.,
            Mitchell,S.C., Madraswala,R., Zhou,Y., Kuo,J., Raitano,A.B.,
            Jakobovits,A., Saffran,D.C. and Afar,D.E.
  TITLE   STEAP: a prostate-specific cell-surface antigen highly expressed in
            human prostate tumors
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (25), 14523-14528 (1999)
  PUBMED   10588738
REFERENCE   2 (bases 1 to 1195)
  AUTHORS   Hubert,R.S., Vivanco,I., Chen,E., Rastegar,S., Leong,K.,
            Mitchell,S.C., Madraswala,R., Zhou,Y., Kuo,J., Raitano,A.B.,
            Jakobovits,A., Saffran,D.C. and Afar,D.E.H.
  TITLE   Direct Submission
  JOURNAL   Submitted (14-SEP-1999) UroGenesys Inc., 1701 Colorado Ave., Santa
            Monica, CA 90404, USA
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                     /db_xref="GI:6572948"
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                     WIDIKQFVWYTPPFMIAVFLPIVVLIFKSILFLPCLRKKILKIRHGWEDVTKINKTE
                     ICSQL"

ORIGIN

Query Match   100.0%; Score 1017; DB 8; Length 1195;
Best Local Similarity   100.0%;
Matches 1017; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ATGGAAAGCAGAAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   66 ATGGAAAGCAGAAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy   61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACAGGGGAGACAAGCATGCTAAAAAGA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACAGGGGAGACAAGCATGCTAAAAAGA 185

Qy   121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAAATTTGACTGCCCTTCAGAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAAATTTGACTGCCCTTCAGAA 245

Qy   181 CTTCAGCACACACAGGAACTCTTCCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   246 CTTCAGCACACACAGGAACTCTTCCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy   241 ATAGCATCTCTGACTTTTCTTTACACTCTCTTGAGGGAAGTAAATCCACCCTTTAGCAACT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   306 ATAGCATCTCTGACTTTTCTTTACACTCTCTTGAGGGAAGTAAATCCACCCTTTAGCAACT 365

Qy   301 TCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
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Db   366 TCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy   361 GTTTCCATCACTCTCTTGGCATTGGTTTTACCTGCCAGGGTGTGATAGCCAGCAAATTGTCCAA 420
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Db   426 GTTTCCATCACTCTCTTGGCATTGGTTTTACCTGCCAGGGTGTGATAGCCAGCAAATTGTCCAA 485

Qy   421 CTTCATAATGGAACCAAGTATATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTGTTAACA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   486 CTTCATAATGGAACCAAGTATATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTGTTAACA 545

Qy   481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy   541 TCTTACCCAATGAGGCGATCCTACAGATACAAAGTTGCTAAAACTGGGCCATATCAACAGGTC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   606 TCTTACCCAATGAGGCGATCCTACAGATACAAAGTTGCTAAAACTGGGCCATATCAACAGGTC 665

Db   366 TCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   361 ...

Db   426 GTTTCCATCACTCTCTTGGCATTGGTTTTACCTGCCAGGGTGTGATAGCCAGCAAATTGTCCAA 485

Db   486 CTTCATAATGGAACCAAGTATATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTGTTAACA 545

Db   546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy   541 TCTTACCCAATGAGGCGATCCTACAGATACAAAGTTGCTAAAACTGGGCCATATCAACAGGTC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
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Qy   661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGTGACATCTATTCCATCT 720
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Qy   721 GTGAGTGACTCCTTTGACATGGAGAGAATTCACTATATTCAGAGCAAGCTAGGGAATTGTT 780
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Db   786 GTGAGTGACTCCTTTGACATGGAGAGAATTCACTATATTCAGAGCAAGCTAGGGAATTGTT 845

Qy   781 TCCCTTCTACTGGGGCACAATACACACCCATTGATTTGATTTTGCTTGGAATAAGTGGATAGATATA 840
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Qy   841 AAACAAATTGTATGGTATACACCTCCAACTTTATGATAGCTGTGTTTCCTCCAATTGTT 900
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Db   906 AAACAAATTGTATGGTATACACCTCCAACTTTATGATAGCTGTGTTTCCTCCAATTGTT 965

Qy   901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCCTTGAGGAAGAAGATACTGAAAGATT 960
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Qy   961 AGACATGGTTGGGGAAGACGTCACCAAAAATTAACAAAACTGAGAATATGTTCCCAGTTG 1017
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Db   1026 AGACATGGTTGGGGAAGACGTCACCAAAAATTAACAAAACTGAGAATATGTTCCCAGTTG 1082

```
Qy    601 CAACAAAATAAAGAAGAAGATGCCTGGAATGAGCAATGAACTGATGTGTTGGAGAATGGGAGATTTATGTG 660
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Db    666 CAACAAAATAAAGAAGAATGCCTGGAATTGAGCAATGAATGTTTGGAGAATTTATGTG 725

Qy    661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTCGTTGGGCGTGTGACATCTATTCCATCT 720
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Db    726 TCTCTGGGAATTGTGGGAATTGGCAAATACTGGCTCTCGTTGGGCGTGTGACATCTATTCCATCT 785

Qy    721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGACGAAGCTAGGAAATTGTT 780
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Db    786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAAATTGTT 845

Qy    781 TCCCTTCTTACTCGGGCACAAATACACGCATTGATTTTTGCCTGGAATAAGTGGATTAGAGATATA 840
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Db    846 TCCCTTCTTACTCGGGCACAAATACACGCATTGATTTTTTGCCTGGAATAAGTGGATTAGAGATATA 905

Qy    841 AAACAAATTTGTATGGGTATACACCTCCAACTTTTATGATAGCTGTTTCCTTCCAAATTGTT 900
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Job time : 5380.03 secs

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: December 4, 2005, 20:37:26 ; Search time 4645.46 Seconds
(without alignments)
10242.778 Million cell updates/sec

Title: US-10-750-262-1_COPY_66_1082
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0
Searched: 41078325 seqs, 23393541228 residues
Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :   EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_htc1:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1015.4	99.8	1050	10	AY403218	AY403218 Homo sapi
2	904.6	88.9	1045	10	AY403219	AY403219 Pan trogl
3	776	76.3	884	6	CA488012	CA488012 AGENCOURT
4	738.6	72.6	1050	10	AY403220	AY403220 Mus muscu
5	737	72.5	1211	4	AK010437	AK010437 Mus muscu
6	692.8	68.1	881	2	BG565247	BG565247 602582917
7	651	64.0	710	2	BE875216	BE875216 601488516
8	639.2	62.9	827	8	CV983083	CV983083 UMC-bmix
9	623	61.3	961	2	BG762026	BG762026 602718984
c 10	611.4	60.1	796	5	BG182296	BG182296 RST1161 A
c 11	605.4	59.5	720	6	CA446381	CA446381 UI-H-ED1-
c 12	598	58.8	609	6	CD677954	CD677954 ho24h02.Y
c 13	598	58.8	609	6	DN997716	DN997716 TC115356
14	597.8	58.8	920	2	BE881257	BE881257 601492338
15	596	58.6	742	8	CX757709	CX757709 AGENCOURT
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17	590	58.0	783	8	BI552907	BI552907 603197827
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19	589.6	58.0	825	8	BX103101	BX103101 BX103101
c 20	586.2	57.6	788	7	CN153902	CN153902 941069 MA
c 21	569.2	56.0	799	5	BU930271	BU930271 AGENCOURT
22	557	54.8	1071	3	BM920324	BM920324 AGENCOURT
c 23	538	52.9	661	3	BM995067	BM995067 UI-H-ED0-
24	536.6	52.8	1003	3	BI551229	BI551229 603194629
25	522	51.3	684	2	BE439545	BE439545 HTM1-183F
26	521.6	51.3	600	3	BI360480	BI360480 387409 MA
c 27	520	51.1	705	6	CB424830	CB424830 59432 MA
28	511.2	50.3	636	6	CD690450	CD690450 EST6973 h
29	502	49.4	600	1	AI686139	AI686139 tc92e11.x
c 30	501.4	49.3	581	2	BG577403	BG577403 N12 SSH-
31	501.4	49.3	581	2	BF965211	BF965211 602268114
c 32	494.4	48.6	891	2	BG104394	BG104394 602311010
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34	485.2	47.7	779	5	BU929991	BU929991 AGENCOURT
35	474.4	46.6	661	5	BX506262	BX506262 DKP2P686E
36	464.8	45.7	1020	3	BM811413	BM811413 AGENCOURT
37	462	45.4	584	3	BM675259	BM675259 AGENCOURT
38	461	45.3	513	1	AA032221	AA032221 zf01e06.s
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40	459.4	45.2	581	6	BM714075	BM714075 UI-E-EJO-
41	455.4	44.8	759	6	CA509933	CA509933 UI-R-FSO-
c 42	442.8	43.5	468	2	BF119996	BF119996 K-EST0167
c 43	438.8	43.1	791	2	BF573995	BF573995 602131824
c 44	433.2	42.6	654	7	CO594327	CO594327 D2-93n7
c 45	429	42.2	696	3	BQ205543	BQ205543 UI-R-EP0-

ALIGNMENTS

RESULT 1
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LOCUS   AY403218   1050 bp   DNA   linear   GSS 15-DEC-2003
DEFINITION Homo sapiens STEAP gene, VIRTUAL TRANSCRIPT, partial sequence,
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ACCESSION   AY403218
VERSION   AY403218.1 GI:39759201
KEYWORDS   GSS.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 1050)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M..
  TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2 (bases 1 to 1050)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M..
  TITLE   Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES   Location/Qualifiers
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     gene   <1..>1050
                     /gene="STEAP"
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ORIGIN

Query Match   99.8%; Score 1015.4; DB 10; Length 1050;
Best Local Similarity   99.9%; Pred. No. 1.3e-259;
Matches 1016; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 2
AY403219    AY403219    1045 bp    DNA    linear    GSS 15-DEC-2003
LOCUS
```

```
DEFINITION  Pan troglodytes STEAP gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY403219
VERSION     AY403219.1  GI:39759202
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1  (bases 1 to 1045)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
  PUBMED    14671302
REFERENCE   2  (bases 1 to 1045)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1..1045
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
     gene            <1..>1045
                     /gene="STEAP"
                     /locus_tag="HCM1484"
ORIGIN

Query Match             88.9%;  Score 904.6;  DB 10;  Length 1045;
Best Local Similarity   89.2%;  Pred. No. 4.8e-230;
Matches  907;  Conservative    0;  Mismatches  110;  Indels    0;  Gaps    0;
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RESULT 3
CA488012

```
LOCUS       CA488012      884 bp    mRNA    linear    EST 14-NOV-2002
DEFINITION  AGENCOURT_1080782 1 MAPcL Homo sapiens cDNA clone IMAGE:6719746 5',
            mRNA sequence.
ACCESSION   CA488012
VERSION     CA488012.1  GI:24948800
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 884)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Kristi A. Egland, Ira Pastan
            cDNA Library Preparation: Invitrogen Corp
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM14278 row: c column: 10
            High quality sequence stop: 758.
FEATURES             Location/Qualifiers
     source          1..884
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6719746"
                     /cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,
                     hTERT-HME1, LNCaP"
                     /lab_host="EMDH10B"
                     /clone_lib="MAPcL"
                     /note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
                     Directionally cloned. Priming method: oligo-dT. Average
                     insert size: 1800 bp. Library amplification: 26,000 fold.
                     Subtracted with brain, liver, lung, kidney and muscle.
                     Kristi A. Egland, James J. Vincent, Robert Strausberg,
                     Bungkook Lee & Ira Pastan: Discovery of new breast
                     cancer genes encoding membrane and secreted proteins.
                     Manuscript submitted."
```

ORIGIN

```
Query Match             76.3%;  Score 776;  DB 6;  Length 884;
Best Local Similarity   99.4%;  Pred. No. 9.9e-196;
Matches  779;  Conservative 0;  Mismatches 5;  Indels 0;  Gaps 0;

Qy    1 ATGGAAAGCAGAAAAAGACATCACAAACCAAGAAGAAGAACTTGGAAAATGAAGCCTAGGAGA 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   82 ATGGAAAGCAGAAAAAGACATCACAAACCAAGAAGAAGAACTTGGAAAATGAAGCCTAGGAGA 141

Qy   61 AATTTAGAAGAAGAAGCGATTATTTGCATAAGGACACCAGGACCATGTGCTTAAAAAAAGA 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  142 AATTTAGAAGAAGAAGCGATTATTTGCATAAGGACACCAGGACCATGTGCTTAAAAAAAGA 201

Qy  121 CCTGTGCTTTTGCAATTTGCACCAAAACAGCCCATGCTGATGAATTGACTGCCCTTCAGAA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  202 CCTGTGCTTTTGCAATTTGCACCAAAACAGCCCATGCTGATGAATTGACTGCCCTTCAGAA 261

Qy  181 CTTCAGCACACAGCAGGAACTCTTTCCACAGTGCCACTTGCCAATTAAATAGCTGCTATT 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  262 CTTCAGCACACAGCAGGAACTCTTTCCACAGTGCCACTTGCCAATTAAATAGCTGCTATT 321

Qy  241 ATAGCATCTCTGACTTTTCTTCTTACACTCTTCTGAGGGAAGTAAATTCACCCTTTAGCAACT 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  322 ATAGCATCTCTGACTTTTCTTCTTACACTCTTCTGAGGGAAGTAAATTCACCCTTTAGCAACT 381

Qy  301 TCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  382 TCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 441

Qy  361 GTTTCATCACTCTCTTGGCATTGGTTTACTTGCCCAGGTGTGATAGCAGCAAATTGTCCAA 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  442 GTTTCATCACTCTCTTGGCATTGGTTTACTTGCCCAGGTGTGATAGCAGCAAATTGTCCAA 501

Qy  421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAGTTAACA 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  502 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAGTTAACA 561

Qy  481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTTGCGTGTACTGCATGCATGCCAATTTATAGTCTG 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  562 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTTGCGTGTACTGCATGCATGCCAATTTATAGTCTG 621

Qy  541 TCTTACCCAATGAGGCGGATCCTTACAGATACAGAGTTGCTAAAACTGGGCCATATCAACAGGTC 600
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  622 TCTTACCCAATGAGGCGGATCCTTACAGATACAGAGTTGCTAAAACTGGGCCATATCAACAGGTC 681

Qy  601 CAACAAAAATAAAGAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATTGGAGATTTATGTG 660
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  682 CAACAAAAATAAAGAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATTGGAGATTTATGTG 741

Qy  661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCCTCGTTGGCTGTGACATCTATTCCAATCT 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  742 TCTCTGGGAATTGTGGGATTGGCAATACTGGCCTCGTTGGCTGTGACATCTATTCCAATCT 801

Qy  721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAAGCAAGCTAGGAAATTGTT 780
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  802 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAAGCAAGCTAGGAAATTGT 861

Qy  781 TCCC 784
        ||||
Db  862 TTCC 865
```

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RESULT 4
AY403220
LOCUS       AY403220              1050 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  Mus musculus STEAP gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY403220
VERSION     AY403220.1  GI:39752903
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1050)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
  PUBMED    14671302
REFERENCE   2  (bases 1 to 1050)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1..1050
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
     gene            <1..>1050
                     /gene="STEAP"
                     /locus_tag="HCM1484"
ORIGIN

Query Match             72.6%;  Score 738.6;  DB 10;  Length 1050;
Best Local Similarity   82.9%;  Pred. No. 9.9e-186;
Matches  843;  Conservative   0;  Mismatches 174;  Indels   0;  Gaps   0;

Qy         1 ATGGAAAGGCAGAAAAAGACATCACAAAACCAAGAAGAACTTGGAAAATGAAGCCTAGGAGA 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        31 ATGGAAGATCAGTGACGAGCGATGTTACAAAACCCAGAACAACTTTGGAAAATGAAGCCAAAAGGGA 90

Qy        61 AATTTAGAAGAAGAGGAGAGATTATTTCCGATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        91 AACCTGGAAGATGAGCAGTTACTCGACTAAGGAGAAGACGCGAGCATGCTGAAAAAGA 150

Qy       121 CCTGTGCTTTTGCATTTGCACCAAAACAGCCCATGCCTGATGAAATTTGACTGCGTTCAGA 180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       151 CCGGGGCTCTCGCACTTGCACGCGGTTCCACGTGATGCGCTTTTGACTGCCCTTCCGAG 210

Qy       181 CTTCAGCAGCACACAGGAACTCTTTCCACAGTGGGCACTTGCCAATTAAAATAGCTGCTATT 240
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       211 CTTCAGCACGACAGGAATTCTTTTCCAAACTGGCGGCGTTGCCAGTGAAAGTCGCTGCCATC 270

Qy       241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCCAACT 300
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       271 ATACAACATCCCTGACTTTCCTGTACACACTTCTGAGGGGAAATCAACTACCCGTTAGTAACT 330

Qy       301 TCCCATCAACAACAATATTTTTTATAAAAATTCCAATCCTGGTATTCAACAAAGTCTTCGCCAATG 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       331 TCCCGTGAACAATAATTTTTATAAAATTCCAATCCTGGTTATTAACAAAGTCTTGCCAATG 390

Qy       361 GTTTCCATCACTCTTCTTGGCATTGGTTTACCTGCCAGGGTGTGATAGCAGCAAATTGTCCAA 420
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       391 GTCGCCATTACCCTCTTGGCACTGGTTGGCACTGCTAATTTGCCAGGAGAGAGAGTTGAGCGGCGAGGTTAGCTGCGAGTTGTACAG 450

Qy       421 CTTCATAAATGGAACCAAGTATAAGAAGTTCCACATTGGTATTGGAGTTGGATAAGGGTGGAATAACA 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       451 CTTCGCAATGGAACCAAGTACAAGAAGTTCCACCCCTGGTTAGATAGGATGGAATGGCC 510

Qy       481 AGAAAGCAGTTTGGCTTCTCCAGTTTCTTCTTTTTTTTGCTGTTACTGCATGCAATTTATAGTCTG 540
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       511 AGGAAGCAGTTTGGTTCTCCTCAGCTTCTTCTTTTTTGCTGTCGTCGCACGGCTGTTTACAGTCTC 570

Qy       541 TCTTACCCAATGAGCGGATCCTTACAGATACAGATACAGAAGTTGCTAAAACTGGGCATATCACAGGTC 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       571 TCATACCCAATGAGCAGGATCCTTACAGATACAAGCTACTCAACCTGGTAGACAGGTT 630

Qy       601 CAACAAAAATAAAGAAGAGATGGCCTGGATTGAGCATGATGATTGGAGAAGATGGAGAAGTTAGTGTG 660
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       631 CAACAAAACAAAAGAGGATGCCCTGGGTTAGCATGATGTTCTCTGGAGAAGATGGGAATTTATGTG 690

Qy       661 TCTCTCGGGAATTGTGGGATTGGCAATAACTGGGCTCCTGTTGGTTGACACTCTTATTCCATCT 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       691 TCCCTCGGGAGTTGTGGGGCGGCCATCCTCTGCTCGTGGCATCATCTATTTGGGG 750

Qy       721 GTGGAGTGACTCTTTTGACATGGGAGGAGAATTTCACTATTATCAGAGACCAAGCTAGGAAATTGTT 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       751 GTGACGGACTCTTTTAACCTGGAGAGAATTTCACTATATTATTCAGAGACCAAACTAGGAAATTGTC 810

Qy       781 TCCCTTCTACTGGGGCACAATACACCGCATTGGATTTTTGCCTGGAATAAGTGGATAGGATATA 840
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       811 TCTCTTCTTCTCTGGGGCACAGCTTTGGTTTTGGCCTGGGAATAAGTGGAATTTGGGGATGTC 870

Qy       841 AAACAAATTGTATGGTATACACCTCCAACTTTTATGATGAGCTGTGTTTCCTTCAAATTGTT 900
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       871 AGTCAATTTGTATGGTACACGCCCCGACACTTTTATGATGAGCCTGTTTTCCTTCACACTCTT 930

Qy       901 GTCCTGATATTTAAAAGCATACTATTCCTGCCCATGCTTGAGGAAGAAGTAACTGAAAGATT 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       931 GTCCTGATAGTTAAAATCGCCCCTGCCCATGCTTCTGAGGGAAGAGATACTGAAGAATT 990

Qy       961 AGACATGGGTGGGGAAGACGTCACCAAAAATTAACAAAACTGAAGATATGTTCCCAGTTG 1017
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       991 AGATGTGGTTGGGGAGAGATGTCAGCAAAAATTAACAGGGACTGAAGATGGCCTCCAGGTTG 1047
```

```
RESULT 5
AK010437
LOCUS       AK010437              1211 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus ES cells cDNA, RIKEN full-length enriched library,
            clone:2410007B19 product:six transmembrane epithelial antigen of
            the prostate, full insert sequence.
ACCESSION   AK010437
VERSION     AK010437.1  GI:12845880
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  PUBMED    10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  PUBMED    11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
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REFERENCE   4
  AUTHORS   Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
   PUBMED   11076861
REFERENCE   5
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   6  (bases 1 to 1211)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            [...]
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
            Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
            Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,
            Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,
            Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,
            Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,
            Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
            Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,
            Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,
            Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,
            Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Project of Genome Exploration Research Group, RIKEN
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     Please visit our web site (http://genome.gsc.riken.jp/) for further
            details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory (GSC),
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. First strand cDNA was primed with a primer
            [5' GAGAGAGAGAGAGAGAGATCGACAGGCTCTGTTTTTTTTTTTTTTTVN 3'], cDNA was
            prepared by using trehalose thermo-activated reverse transcriptase
            and subsequently enriched for full-length using by cap-trapper. Second
            strand cDNA was prepared with the primer adapter of sequence [5'
            GAGAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCC 3'], cDNA was cleaved
            with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.
            Host: SOLR.
FEATURES             Location/Qualifiers
     source          1..1211
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="FANTOM"
                     /db_xref="taxon:10090"
                     /clone="2410007B19"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /cell_type="ES cells"
     CDS             98..1117
                     /note="unnamed protein product; putative
                     six transmembrane epithelial antigen of the prostate
                     98..1117"
                     /codon_start=1
                     /protein_id="BAB26938.1"
                     /db_xref="GI:12845881"
                     /db_xref="MGI:1917608, GB|AK010437, evidence: BLASTN, 100%,
                     match=1211]"
                     /db_xref="MGD|MGI:1917608, GB|AK010437, evidence: BLASTN, 100%,
     polyA_signal    1186..1191
                     /note="putative"
     polyA_site      1211
                     /note="putative"
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```
ORIGIN
     Query Match    72.5%;  Score 737;  DB 4;  Length 1211;
     Best Local Similarity  82.8%;  Pred. No. 2.7e-185;
     Matches  842;  Conservative  0;  Mismatches 175;  Indels  0;  Gaps  0;

Qy          1 ATGGAAAGCAGAAAAAGACATCAAAACCAAGAAGAGAAGAACTTTGGAAAATGAAGCCTAG   60
              ||||||||||||||||||||||||||||||||| |||||||||||||||||||||| |||
Db         98 ATGGAGAGATCAGTGACGATGTTACAAAACCCAGAACAACTTTGGAAAATGAAGCCAAGGA  157

Qy         61 AATTTAGAAGAAGAGGAATTATTTGCATAAGGACACGGGAGGAGAGACCATGCCTAAAAGA  120
              ||||| |||||||||| ||||||||||||||||| |||||||||||||||| ||||||||
Db        158 AACCTGGAAGAATGACAGTTACTGACTAGGAACTCGGGAGGAGAGACATGCTGAAAAGA    217

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTTGATGAATTTGACTGCCCTTCAGAA  180
              || ||||||||| ||||||||||||||||| |||||| || |||||||||||||| ||||
Db        218 CCGGGGCTCTCGCACTTGCAGCACGCGGGTCCACGTGCCTTTGACTGCCCTCCGAG    277

Qy        181 CTTCAGCACCACAGGAACTCTTCCACAGTGGCACTTGCCAATTAAAATAGTCTGCTATT   240
              ||||||||||||||||||||||||| |||||||| |||||||||   ||| ||||||||
Db        278 CTTCAGCACACGCAGGAATTCTTTCCAAACTGGGCACTTGCCAGTGAAAGTCGCTGCCATC  337

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTCTTCTGAGGGAGTAAATTCACCCTTTAGCAAT  300
              |||||||||||||||||||||||||| |||||||||||| |||||||||| |||||| ||
Db        338 ATATCATCCCTGACTTTCCCTGTACACACTTCTGAGGGAAATCATCTACCCGTTAGTAACT  397

Qy        301 TCCCATCAACAATATTTTTATAAAAATTCCAATCCTCGGTCATCAACAAAGTCTTGCCAATG  360
              |||||||||||||| |||||||||||||||||||||||| |||||||||| |||||||||
Db        398 TCCCGTGAACAATATTTTTTATAAAAATTCCAATCCTGGTTATTAACAAAGTCTTGCCAATG  457

Qy        361 GTTTCCATCACTCTCTTCTGGCCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA  420
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Db        458 GTCCGCCATTACCCTCTTGGCACTGGTCTCTATTTGCCAGGAGAGTTAGGCGGCAGTTGTACAG  517

Qy        421 CTTCATPAATGGAACCAAGTATAAGAAGGTTTCCACATTGGTTGGATAAGTGGATGTTAACA  480
              |||||||||||||||| |||||||||||||||||||||||||||||||||| |||||||
Db        518 CTTCGCAATGGAACCAAGTTACAAGAAGTTCCCACCCGGTTAGATGAATGGCATG    577

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTCTTTTTTGCTGTAGCTGCACATGCAATTTATAGTCTG  540
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        578 AAGAAGCAGTTTGGTCTCCTTCAGCTTCTTTTTTTTCGTGCTGCACGCTGTTTACAGTCTC  637

Qy        541 TCTTACCCAATGAGGCGGCGATCCTACAGATACAGAAGTTGCTAAACAGGGGCATCAACAGGTC  600
              |||| |||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db        638 TCATACCCAATGAGGAGGAGGAATCCTACAGAGAAGAACTGGCTTCAAACTCAACAAACAGGTT  697

Qy        601 CAACAAAAATAAAGAGAAGAGATCCCTGGATTGGAGCACTGATGTTTGGGAGAAATGAAGATTTATGTG  660
              |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db        698 CAACAAAAACAAAAGAGAGGAATGGCCTCGGGCTAGGAGCATGAATGCCTGGGAGAAATGGAGATTTATGTG  757

Qy        661 TCTCTGGGGAATTGTGTGGGATTGGCAATGCTTGGCTCTCGTTGGCTGTGACAATCTAATTCCATCT  720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        758 TCCCTGGGGATTGTGTGGGGCTGGCCATCTGGTGCCTCTGGCTCTCTGGCTGTGACATCTACTCATTCCAT  817

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAGAATTGTT  780
              ||||||||||||||||||||||||||||||||||||| |||||||||||||||| |||||||
Db        818 GTGAGCGGACTCTTTAACCTGGAGGAGAATTCACATATATTCAGAGCAAACTAGGAATTTATATGTC  877

Qy        781 TCCCTTCTACTGGGCGCACAATACACGGCCAATTGATTTTTGCCTGGATATAAGTGGGATAGATATA  840
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Qy   841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATATAGCTGTTTTCCTTCCAATTGTT 900
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Db   938 AGTCAATTTGTATGGTATACACCTCCAACTTTTATGATATAGCTGTTTTCCTTCCAATTGTT 997

Qy   901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
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Db   998 GTCCTGATATGTAAAAATCGCCCCTGTCGCTGCCCCTGTGAGGAAGAAGATACTGAAGATT 1057

Qy   961 AGACANTGGTTGGGAAGAGAGAGCGTCACCAAAAATTAACAAAATTGAGATATGTTCCCAGTTG 1017
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Db   1058 AGATGTGGTTGGGAAGAGTGCACCCAAAAATTAACAGGACTGAGATGGGCCTTCCAGTTG 1114

RESULT 6
BG565247
LOCUS   BG565247   881 bp   mRNA   linear   EST 10-APR-2001
DEFINITION 602582917F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4710436 5',
            mRNA sequence.
ACCESSION   BG565247
VERSION   BG565247.1 GI:13572900
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 881)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONETECH Laboratories, Inc.
            cDNA Library Preparation: CLONETECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LiCM1549 row: b column: 05
            High quality sequence stop: 704.
FEATURES   Location/Qualifiers
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                     /clone_lib="NIH_MGC_76"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: liver; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence: 5'-CACGGCCATTATGGCC-3', and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGCCCAACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C, G, or T). Average insert size 1.85
                     kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."

ORIGIN
Query Match   68.1%; Score 692.8; DB 2; Length 881;
Best Local Similarity 93.6%; Conservative 0; Pred. No. 1.6e-173;
Matches 777; Conservative 0; Mismatches 47; Indels 6; Gaps 5;

Qy   186 GCACACACAGGGAACTCTTTTCCACCAGTGGCCACTTGCCCAATTAAAATAGCTGCTTATTATAGC 245
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Db   1 GCACACAGGGAACTCTTTCCACCAGTGGCCACTTGCCAATTAAAATAGCTGCTTATTATAGC 60

Qy   246 ATCTCTGACTTTTTCTTTACACTCTTCGAGGGGAAGTAATTCACCCTTTAGCAACTTCCCA 305
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Db   61 ATCTCTGACTTTTTCTTTACACTCTTCTGAGGGGAAGTAATTCACCCTTTAGCAACTTCCCA 120

Qy   306 TCAACACATATTTTTATAAAATTCCAATCCTTCATCAACAAGTCTTGGCCAAATGGTTTC 365
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Db   121 TCAACACATATTTTTATAAAATTCCAATCCTTCATCAACAAGTCTTGGCCAAATGGTTTC 180

Qy   366 CATCACTCCTTTGGCATGTTGGTTTACCTGCCTCAGGAATCAACAGGTGTGATAGCAGCAACTTCA 425
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CATCACTCCTTTGGCATGTTGGTTTACCTGCCCAGGTGTGATAGCAGCAACTTCA 240

Qy   426 TAATGGAACCAACTATAAGAAGAGTTTCCACATTCGGTTGGATAAGTTAACAAGAAA 485
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TAATGGAACCAACTATAAGAAGAGTTTCCACAGTGGTTGGATAAGTTAACAAGAAA 300

Qy   486 GCAGTTTGGGCTTTCTCAGTTTCTTTTTTTTGTTTTGCTGTACTGACAATTTATTAGTTCTTA 545
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GCAGTTTGGGCTTCTCAGTTTCTTTTTTTTGCTGTACTGACAATTTATTAGTTCTTA 360

Qy   546 CCCAATGAGGCGGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTTCCAACA 605
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CCCAATGAGGCGGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTTCCAACA 420

Qy   606 AAATAAAGAAGAGATGCCCTGGATTCGACATGATGTTGGAGAATGGATTTATGTGTCTCCT 665
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AAATAAAGAAGAGATGCCCTGGATTCGACATGATGTTGGAGAATGGATTTATGTGTCTCT 480

Qy   666 GGGAAATTGTGGGATTGGCAATACTACTGGCTCTCGTGTTGGCTCTGGACATCTATTCCAATCTCACTGTGAG 725
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GGGAAATTGTGGGATTGG-AATACTGGCTCTCGTGTTGGCTCTGGACATCTATTCCACTGTGAG 539

Qy   726 TGACTCTTTGACATGGAGAGAATTCACTATATCAGACAAGCAGCTAGGAATTGTTTCCCT 785
           |||||||||||||||||||||||||||||||-|||||||||||||||||-||||||||||
Db   540 TGACTCTTTGACATGGAGAGAATTCACTATATTCAGACAAGCAGCTAGGAATTGTTTCCT 599

Qy   786 TCTACTCGGGCCACAATACACGCACATTGATTTTTGCCTGGAATAACTGG--ATAGATATAAAA 843
           |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db   600 TCTACTCGGGCCACAATACACGCACATTGATTTTTGGCTGGATAGATCATAAAC 659

Qy   844 CAATTTGTATGGTATACACCTCCCAACTCTTATGTAGCTGTTTTTCCTTCCAATTGTTGTC 903
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   660 ACAATTGTATGGTATACACCTCCAACTCTTATGTAGCTGTTTTTCCTTCCAATTGTTAGTCC 719

Qy   904 CTGATATTT-AAAAGCATACTATT-CCTGCCATGCTTGAGGAAGAAGAGATACT-GAAGATT 960
           ||||||||| |||||||||| ||||||||||||||||||||||||||||| ||||||
Db   720 CTGATATTTCAAAAGCGATACTACTTGCCCATGCTTGAGGAAGAAGAGATACTGGACGGATT 779

Qy   961 AGACATGTGTTGGGAAGAGAGAGCGTCACCAAAAATTAACAAAAACTGAGATATGTTCC 1010
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   780 AGACTTGGTTGGGAAGAAGAAGGTCACCAAAAATCAAAAAACTGAGATTTGTCC 829

RESULT 7
BB875216
LOCUS   BB875216   710 bp   mRNA   linear   EST 20-OCT-2000
DEFINITION 601488516F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3890930 5',
            mRNA sequence.
ACCESSION   BB875216
VERSION   BB875216.1 GI:10323992
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 710)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/gazdar
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be

RESULT 8

Left column:

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found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9674 row: p column: 03
Site_2 stop: 701.
High quality sequence stop: 701.

FEATURES          Location/Qualifiers
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                  /db_xref="taxon:9606"
                  /clone="IMAGE:9606"
                  /tissue_type="large cell carcinoma, undifferentiated"
                  /lab_host="DH10B (phage-resistant)"
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                  /note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
                  Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                  Average insert size 1.1 kb. Library constructed by Life
                  Technologies."

ORIGIN
Query Match      64.0%;  Score 651; DB 2; Length 710;
Best Local Similarity  99.0%;  
Matches   676;  Conservative   0;  Mismatches   5;  Indels   2;  Gaps   2;
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Qy         1 ATGGAAAGACAGAAAAGACAATCACAAAACCAAGAAGAGAAGAACTTTGGAAAAATGAAGCCTAGGAGA   60
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Db        22 ATGGAAAGACAGAAAAGACAATCACAAAACCAAGAAGAGAAC-TTGGAAAAATGAAGCCTAGGAGA    80

Qy        61 AAATTAGAAGAAGACGAATATTTTGCATAAGGACACGGGAGGAGACCAGCAATGCTAAAAAGA   120
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Db        81 AAATTAGAAGAAGACGAATATTTTGCATAAGGACACGGGAGGAGACCAGCATGCTAAAAGAGA   140

Qy       121 CCTGTGCTTTTGCATTTTGCACCAAACAGCCCATCATCTGATGAAATTGAGTCGCCCTTCAGAA   180
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Db       141 CCTGTGCTTTTGCATTTGCACCAAAACAGCCCATCGTCGATGAAATTTGACTGCCCTTCAGAA   200

Qy       181 CTTCAGCACACAGCAGGAGACTCTTTCCACAGTGGCGCACTTGCCCAATTAAAATAGCTCTATT   240
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Db       201 CTTCAGCACACAGCAGGAGACTCTTTCCACAGTGGCCACTTGCCCAATTAAAATAGCTGCTATT   260

Qy       241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTCGAGGAGAGTAATTCACCCTTTAGCAACT   300
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Db       261 ATAGCATCTCTGACTTTTCTTTACACTCTTCTCGAGGAGAGTAATTCACCCTTTAGCAACT   320

Qy       301 TCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAAGTCTTGCCAATG   360
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Db       321 TCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAAGTCTTGCCAATG   380

Qy       361 GTTTCCATCACTCTCTTGGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAAATTGTCCAA   420
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Db       381 GTTTCCATCACTCTTGGGTTTTACCTGCCAGGTGTGATAGCAGCAAATTGTCCAA   440

Qy       421 CTTCATAATGGAACCAAGTATAAGAGAAGTTTCCACATTGGTTGGATAAGTGGGATGTTAACA   480
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Db       441 CTTCATAATGGAACCAAGTATAAGAGAAGTTTCCACATTGGTTGGATAAGTGGGATGTTAACA   500

Qy       481 AGAAAGCAGTTTGGGCTTCAGTTGTTTTTGCTGTTGTACTGCAATTTATAGTCTG   540
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Db       501 AGAAAGCAGTTTGGGCTTCAGTTGTTTTTGCTGTTGTACTGCAATTTATAGTCTG   560

Qy       541 TCTTACCCAATGAGGCCGATCCTACAGATACAAGTTGCTAAACTGGGCTATATCAACACAGTC   600
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Db       561 TCTTACCCAATGAGGCCGATCCTACAGATACAAGTTGCTAAACTGGGCTATATCAACACAGTC   620

Qy       601 CAACAAAATAAAGAAGATGCCTGGGATTGAGCATGATGTTTGGAGAATCGG-AGATTTATGT   659
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Db       621 CAACAAAATAAAGAAGATGCCTGGGATTGAGCATGATGTTTGGAGAATGGCAGATTTATGT   680

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Right column:

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                  /clone_lib="bmix"
                  /dev_stage="Conceptus-Corpus Luteum(mixed)"
                  /note="Vector: pSportI; Funding: The production of ESTs
                  submitted in this project was funded by USDA Grant
                  NRI-2002-03476 entitled 'Bovine ESTs: Focus on Female
                  Reproduction' to RS Prather (Primary Investigator), E
                  Antoniou, HA Garverick, JA Green, MC Lucy, RM Roberts, MF
                  Smith and RS Youngquist. Genetic Source: Heifers for the
                  project were purchased from Circle A Ranch, Iberia, MO
                  (http://www.circlearanch.com/home.html). These heifers,
                  while not registered have known Angus pedigrees going back
                  at least 4 generations. Samples collected: The samples
                  consisted of the following: germinal vesicle-stage
                  oocytes; in vitro derived embryos (2-cell, morula,
                  blastocyst and nuclear transfer blastocyst); in vivo
                  blastocysts and conceptuses (days 8, 14, 16 and 18);
                  corpora lutea (days 3, 5, 8, 14, 16, 18 and 35); ovarian
                  follicles (days 0, non-recruited, recruited, early
                  selected and preovulatory); oviduct (days 0, 3 and 5);
                  endometrium (days 5, 8, 14, 16, 18 and 35); and
                  placenta/embryo from day 35 conceptuses. Expanded
                  descriptions of how the tissues were collected can be
                  found at the following URL:
                  http://genome.rnet.missouri.edu/Bovine/Methods.html.
                  Library construction (Standard Protocol): All procedures
                  have been described in detail elsewhere (Soares et al.,
                  1994; Bonaldo et al., 1996; Jiang et al., 2001). Total
                  cellular RNA from each sample was isolated by using
                  STAT-60 reagent (Tel-Test, Friendswood, TX) and the
                  poly(A)+ RNA was obtained by two rounds of purification
                  with the Oligotex mRNA isolation kit (Qiagen) according to
                  the manufacturer's instructions. The libraries were
                  constructed essentially as described by the manufacturer's
                  instructions provided with the SuperScript Plasmid System
                  (Invitrogen, cat. no. 18248-013). Briefly, 1mcg of
                  poly(A)+ RNA was annealed at c37 degrees with 10mcg of
                  NotI-tag-dT18 oligonucleotide (GCTGGTTCGCGGCCGC-tag-T18)
                  and reverse transcribed at c37 degrees with SuperScript II
                  (Invitrogen) reverse transcriptase (Jiang et al., 2001).
                  The 'tag' represents a tissue/stage-specific ten-base
                  sequence identifier
                  (http://genome.uiowa.edu/pubsoft/software.html) present in
```

the oligonucleotide used to prime first-strand synthesis.
Second strand synthesis was performed with T4 DNA
polymerase in the presence of DNA ligase and RNase H.
After second strand synthesis, the double-stranded cDNAs
were ligated to SalI adapters (Invitrogen-Life
Technologies) and digested with NotI. The cDNAs were size
selected by passage through cDNA size fractionation
columns (Invitrogen-Life technologies). The cDNAs derived
from each developmental stage of a particular tissue were
mixed on an equimolar basis and ligated directionally into
the NotI and SalI sites of the pCMV-SPORT6 vector
(Invitrogen). After ligation of the inserts, the plasmids
were electroporated into DH10B bacteria. Preliminary
Library Characterization: Randomly chosen clones from each
library were analyzed by restriction digestion to
determine average insert size (96 clones) and by
sequencing (~4 96-well plates) to confirm library quality
[e.g. the presence of short polyA+ tails, genomic DNA
contamination (must be <1%), ribosomal RNA clones (must be
<1%, etc.] and to provide a sequence database
representing the predominant clones in each library. The
clones were sequenced at the University of
Missouri-Columbia DNA Core Facility. After production of
the libraries, equal numbers of recombinants from each
library were pooled to produce a single mixed library
(mega-library) for more extensive sequencing.
Bioinformatics work was performed by GK Springer's
bioinformatics group in Computer Science at the University
of Missouri-Columbia. Clone Requests: Requests for clones
should be made to the Director of the University of
Missouri DNA Core facility at: bovine@rnet.missouri.edu.
Citations: Bonaldo MF, Lennon G, Soares MB. Normalization
and Subtraction: Two approaches to facilitate gene
discovery. Genome Res, 1996; 6:791-806. Jiang H, Bivens
NJ, Ries JE, Whitworth KM, Green JA, Forrester LJ,
Springer GK, Didion BA, Mathialagan N, Prather RS, Lucy MC
(2001) Constructing cDNA libraries with fewer clones that
contain long poly(dA) tails. Biotechniques 31:38-42.
Soares MB, MF Banaldo, P Jelene, L Su, L Lawton, A
Efstantiadis. 1994. Construction and characterization of
a normalized cDNA library. Proc Natl Acad Sci,
91:9228-9232.
TAG_TISSUE=Conceptus-Corpus Luteum (mixed)
TAG_SEQ=Not found"

ORIGIN

Query Match   62.9%;   Score 639.2;   DB 8;   Length 827;
Best Local Similarity   90.2%;   Pred. No. 3.2e-159;
Matches 683;   Conservative   0;   Mismatches 74;   Indels   0;   Gaps   0;

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Qy      1 ATGGAAAAGCAGAAAAGGCATCACAAACCAAGAAGAGAAACTTTGGAAAAATGAAGACGAGA    60
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Db    361 GTTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGGATACAGCAGCAATTGTCCAA 420

Qy     71 ATGGAGACGCAGCAAGACATCACAAAACCAAGAGAGAAACTTTGGAAAAATGAAGCCTAGGAGA   130
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Db    431 GTTTTCCATCACCCCTCTTGGCACTGGTTTATTGCCAGGTGTGATAGCAGCAGTTGTGCAG 490

Qy     61 AATTTAGAGAAGAACGATTATTTGCATAAGGACACGGGAGGACCAGCATGCTAAAAGGA    120
            ||||||||||| |||| ||||||| |||||||||||| ||||||||||||||||
Db    421 CTTCATATAATGGAACCAAGTATAAGAAGTTCCACATTGGTTGGTATAAGTGGATTGTAACA 480

Qy    131 AATCTAGGAGAAGATGATTATTTGAATAAAGAGTCAGAAGAGAGATCGGCATGCGTGAAAAGA   190
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Db    491 CTTCATATAATGGAACTAAGTATAAGAAGTTTCCGCACTGGTTGGATAGCTGGATTGTAACA 550

Qy    121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATCGTCGATGGAATTTGACTGCCCTTCAGAA   180
            |||||||||| |||||||||||||||||||| ||||||||||||||||||
Db    481 AGAAAGCAGGTTTGGGCTTCTCAGTTCTTTTTTGCTGGTACGCATGCAAGTTTATAGTCTG 540

Qy    191 CATGTGCTTTTGCACTTGGACCAAAACAACCCATTTGATGGAATTTGATTGCCCCCCAGAG   250
            ||||||| ||||||||||||||||||||| |||||||| |||
Db    551 AGAAAGCAGTTTGGCTTCTTCCAGTTTTCTTTTTGCTGGTTACCATGCAATTTACAGTTTA 610

Qy    181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCACCCAATTAAAATAGCTGCTATT   240
            ||||||| ||||||||||||| ||||||| ||||| |||||||||||||||
Db    541 TCTTACCCAATGAGGCGAATCCTTACAGATACAGATCAAGTTGCTAAAACTGGGCCATATCAC 600

Qy    251 CTTCAGCACAAAACAGAAACTCTTTCCAAAGTGGGCCCCTTGCCAATTAAAATAGCCCCTATT   310
            ||||| |||||||| ||||||| |||||| |||||| |||||||||||||||
Db    611 TCCTATCCGATGAGGCGAATCCTACAGATTAGGTTGCTCAGTATATAACACAGGTC 670

Qy    241 ATAGCATCTTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCCAACT   300
            |||||||||||||| |||||||| ||||||||||||||||||||||
Db    601 CAACAAAATAAAGAAGATGCCCTGGATTGAGCATGCAGATGATGATGGGAAATGGGAGAATTTATGTG 660

Qy    311 GTATCATCTCTGACTTTTCTTCACTCTTGTGAGGGAAATAATTATTCACCCCTTTTGTGACT   370
            ||||||||||| ||||||||||||||||||||||| ||||||
Db    671 CAACAAAATAACGAAANATGCCTGGATTGAACATGATGTTTGGAAATGGGAGAATTTATGTA 730

Qy    301 TCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAAGTCTTGCCAATG   360
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TCTCTGGGAATTGTGGGATTGGCAATAACTGGCTCTGTGGGGTCGACATCTATTCCATCT 720

Qy    371 TCCCATCAACAGTATTTTTATAAAAATTCCAATCCTGGTCATCAACAAGTCTTGCCAATG    430
            ||||||||||||||||||||||||||||||||||||||||||||
Db    731 TCACTGGGAATCGGTGGCACTTGCAATAACTACTAGCTCTTATTGGCTGTGTGGTGACATCTATTCCATCT 790

Db    721 GTGAGTGGACTCTTTGACATGGCAGGAGAGAATTTCACTATA 757
            ||||||||||||||||||||||||||||||||||||||||||
Db    791 GTGAGTGATTCTCTGACATGGAGGAGAGAATTTCACTATA 827
```

RESULT 9
BG762026
BG762026
LOCUS   BG762026   961 bp   mRNA   linear   EST 15-MAY-2001
DEFINITION 602718984F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4858820 5',
           mRNA sequence.
ACCESSION BG762026
VERSION   BG762026.1 GI:14072679
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominidae; Homo.
REFERENCE 1 (bases 1 to 961)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: ATCC/DCTD/DTP
           cDNA Library Preparation: Ling Hong/Rubin Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCM1713 row: h column: 21

FEATURES   Location/Qualifiers
     source   1..961
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4858820"
                     /tissue_type="melanotic melanoma, high MDR (cell line)"
                     /clone_lib="NIH_MGC_49"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
                     EcoRI; cDNA made by oligo-dT priming Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)"
                     /note="High quality sequence stop: 750."

RESULT 10

LOCUS   BG182296   796 bp   mRNA   linear   EST 21-APR-2001
DEFINITION   RST1161 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG182296
VERSION   BG182296.1 GI:13703983
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Hominidae; Homo.
REFERENCE   1 (bases 1 to 796)
  AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
              Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
              Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S.,
              Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,
              Offenbacher,J., Danzig,J. and Ducar,M.
  TITLE   Creation of genome-wide protein expression libraries using random
              activation of gene expression
  JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
  PUBMED   11329013
COMMENT   Contact: Scott J. Cain
              Athersys, Inc.
              3201 Carnegie Ave, Cleveland, OH 44115, USA
              Tel: 216 431 9900
              Fax: 216 361 9596
              Email: scaina@athersys.com
              High quality sequence stop: 505.
FEATURES   Location/Qualifiers
     source   1..796
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Athersys RAGE Library"
                     /cell_line="HT1080"
                     /note="See 'Creation of Genome-wide Protein Expression
                     Libraries using Random Activation of Gene Expression',
                     Nature Biotechnology, in press. Note that even though the
                     cell type indicated is HT1080, since a random activation
                     method was used, these sequence tags are not necessarily
                     expressed in HT1080 under normal circumstances."

ORIGIN

Query Match   60.1%; Score 611.4; DB 2; Length 796;
Best Local Similarity 97.2%; Pred. No. 8.3e-152;
Matches 632; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

Qy   541 TCTTACCCAATGAGGCGATCCTACAGATCAAGTTGCTAAACTGGGCCATATCAACAGGTC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   687 TCTTACCCAATGAGGCGATCCTACAGATCAAGTTGCTAAACTGGGCCATATCAACAGGTC 746

Qy   601 CAACAAAAATAAAGAAGAGATGCCTGGATTGAGCATGAGTTGCTAAACTGGGAAAATGGA 650
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   747 CAAC-AAATAAAGAAGAGATGCCTGGATTGAGCCATGAGTTGGGAAAATGGA 795

RESULT 11
CA446381/c
LOCUS   CA446381   720 bp   mRNA   linear   EST 08-NOV-2002
DEFINITION UI-H-ED1-axr-o-23-0-UI.s1 NCI_CGAP_ED1 Homo sapiens cDNA clone
            UI-H-ED1-axr-o-23-0-UI 3', mRNA sequence.
ACCESSION   CA446381
VERSION   CA446381.1 GI:24810801
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 720)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jose Mercunde
            cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES   Location/Qualifiers
     source   1..720
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-ED1-axr-o-23-0-UI"
                     /tissue_type="Chondrosarcoma"
                     /dev_stage="Adult"
                     /clone_lib="NCI_CGAP_ED1"
                     /note="Organ: Left Public Bone; Vector: pT7T3-Pac
                     (Pharmacia) with a modified polylinker; Site 1: EcoR I;
                     Site 2: Not I; NCI_CGAP_ED1 is a normalized cDNA library
                     containing the following tissue(s): Chondrosarcoma cell
                     line CS5. The library was constructed according to
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. First strand cDNA synthesis was primed with an
                     oligo-dT primer containing a Not I site. Double stranded
                     cDNA was ligated to an EcoR I adaptor, digested with Not
                     I and cloned directionally into pT7T3-Pac vector. The
                     oligonucleotide used to prime the synthesis of the
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tag for this library is GCTCAAGGCT.
                     TAG_TISSUE=chondrosarcoma
                     TAG_LIB=UI-H-ED1
                     TAG_SEQ=CGTCAAGGCT"

ORIGIN

Qy   411 AATTGTCCAACTTCATAATGGAACCAAGTATATAAGAAGAGTTTCCACATTGGTTGGATAAGTG 470
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   720 AATTGTCCAACTTCATAATGGAACCAAGTATATAAGAAGAGTTTCCACATTGGTTGGATAAGTG 661

Query Match   59.5%; Score 605.4; DB 6; Length 720;
Best Local Similarity   99.8%; Pred. No. 3.3e-150;
Matches   606; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   471 GATGTTAACAGAGAAAGCAGTTTGGGCTTCTCTCAGTTTCTTTTTTTTGCTGTACTGCATGCAAT 530
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   660 GATGTTAACAGAGAAAGCAGTTCGGGCTTCTCTCAGTTTCTTTTTTTTGCTGTACTGCATGCAAT 601

RESULT 12
CD677954
LOCUS   CD677954   609 bp   mRNA   linear   EST 24-JUN-2003
DEFINITION ho24h02.y1 Human Trabecular meshwork cDNA: hohphq Homo sapiens cDNA
            clone ho24h02 5', mRNA sequence.
ACCESSION   CD677954
VERSION   CD677954.1 GI:32179685
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 609)
  AUTHORS   Tomarev,S.I., Wistow,G., Raymond,V., Dubois,S. and Malyukova,I.
  TITLE   Gene expression profile of the human trabecular meshwork: NEIBank
            sequence tag analysis
  JOURNAL   Invest. Ophthalmol. Vis. Sci. 44 (6), 2588-2596 (2003)
  PUBMED   12766061
COMMENT   Contact: Wistow G
            Section on Molecular Structure and Function
            National Eye Institute
            6/331, NIH, Bethesda, MD 20892-2740, USA
            Tel: 301 402 3452
            Fax: 301 496 0078
            Email: graeme@helix.nih.gov
            Plate: 24 row: h column: 02
            Seq primer: M13R21 reverse primer (ABI).
FEATURES   Location/Qualifiers
     source   1..609
                     /organism="Homo sapiens"

Qy   531 TTATAGTCTGTCTTACCCAATGAGCGCGATCCTCACAGATACAAGTTTCTTTTTTGCTAAACTGGGCATA 590
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TTATAGTCTGTCTTACCCAATGAGGCGGATTGGCAATGAGTTGTTGGCTGGGCATC 541

Qy   591 TCAACAGGTCCAACAAAAATAAAGAAGAGATGCCTGGATTGAGCATGAGTTGGGAAATGGA 650
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   540 TCAACAGGTCCCACAAAAATAAAGAAGAGATGCCTGGATTGAGCCATGAGTTGGGAATGGA 481

Qy   651 GATTTATGTGTCTCTGGGAAATTGTGGGATTGGGCAATACTGGGCTCGTTGGCCTGTGGGCATC 710
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   480 GATTTATGTGTCTCTGGGAATTGTGGGATTGGGCAATACTGGGCTCGTTGGCCTGTGGGCATC 421

Qy   711 TATTCCATCTGTGAGTGACTCTTTTGACATGGAGAGAAATTTCACTATATTCAGAGCAAGCT 770
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   420 TATTCCATCTGTGAGTGACTCTTTTGACATGGAGAGAAATTTCACTATATTCAGAGCAAGCT 361

Qy   771 AGGAATTGTTTCCCTTCTTACTGGGGCACAATACACGGCATTGATTGTTTTTGCCTGGGATAAGTG 830
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   360 AGGAATTGTTTCCCTTCTTACTGGGGCACAATACACGGCATTGATTGTTTTTGCCTGGGATAAGTG 301

Qy   831 GATAGATATATAAAACAAATTTGTATGGTATACACCTCCAACTTTATGATAGCTGTTTTTCCT 890
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   300 GATAGATATATAAAACAAATTTGTATGGTATACACCTCCAACTTTATGATAGCTGTTTTTCCT 241

Qy   891 TCCAATTGTTGTTCCTGATATTTAAAAGCATACTAATTCCTGCCCATGCTTGAGGAGAAGAT 950
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   240 TCCAATTGTTGTTCCTGATATTTAAAAGCATACTAATTCCTGCCCATGCTTGAGGAGAGAT 181

Qy   951 ACTGAAGATTAGACATGGTTGGGGAGACGTCACCAAAAATTAACAAAACTGAGAGATATGTTC 1010
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   180 ACTGAAGATTAGACATGGTTGGGGAGACGTCACCAAAAATTAACAAAACTGAGAGATATGTTC 121

Qy   1011 CCAGTTG 1017
          |||||||
Db   120 CCAGTTG 114

RESULT 13

LOCUS   DN997716   697 bp   mRNA   linear   EST 17-MAY-2005
DEFINITION TC115356 Human breast cancer tissue, large insert, pCMV expression
            library Homo sapiens cDNA clone TC115356 5' similar to Homo sapiens
            six transmembrane epithelial antigen of the prostate 1 (STEAP1),
            mRNA sequence.
ACCESSION   DN997716
VERSION   DN997716.1 GI:66257543
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 697)
  AUTHORS   Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L.,
            Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M.,
            Zhang,X., Jay,G. and He,W.
  TITLE   High-throughput cloning of full-length human cDNAs directly from
            cDNA libraries optimized for large and rare transcripts
  JOURNAL   Unpublished (2005)
COMMENT   Contact: Kovacs, KF
            High Throughput cDNA Cloning
            OriGene Technologies, Inc. (www.origene.com)
            6 Taft Court, Suite 100, Rockville, MD 20850, USA
            Tel: 301 340 3188
            Fax: 301 340 8606
            Email: cDNA@origene.com
            This EST submission is part of an on-going human full-length
            cloning project at OriGene Technologies, Inc.
            Please contact OriGene for access.
            OriGene Technologies, Inc.
            6 Taft Ct. Suite 100
            Rockville, MD 20850
            Tel: (301) 340-3188
            http://www.origene.com
            Seq primer: pCMV6 5prime forward vector primer, OriGene
            Technologies Inc.
FEATURES   Location/Qualifiers
     source   1..697
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="TC115356"
                     /tissue_type="Breast cancer"
                     /clone_lib="Human breast cancer tissue, large insert, pCMV
                     expression library"
                     /note="Organ: Mammary gland (cancer tissue); Vector:
                     pCMV6-XL5; Site_1: EcoRI; Site_2: XhoI/SalI compatible end
                     ligatio; Oligo-dT primed reverse transcription optimized
                     for large and GC rich mRNA transcripts; cDNA size
                     selection, optimized ligation for large inserts into
                     mammalian expression vector, random clones selected for
                     end sequence verification of full-length genes"
ORIGIN

Query Match   58.8%; Score 598; DB 8; Length 697;
Best Local Similarity 100.0%; Pred. No. 3.1e-148;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ATGGAAAAGCAGAAAAAGAACATCACAAAACCAAGAAGAACATTTGGAAAATGAAGCCTAGGAGA 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 100 ATGGAAAAGCAGAAAAAGAACATCACAAAACCAAGAAGAACATTTGGAAAATGAAGCCTAGGAGA 159

Qy   61 AAATTTAGAAGAAGAAGACGATTATTTTGCATAAGGAGGACACAGCGAGGAGACCATGCTAAAAGA 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 160 AAATTTAGAAGAAGAAGACGATTATTTTGCATAAGGAGGACACAGCGAGGAGACCATGCTAAAAGA 219

Qy 121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTGACTGCCCTTCAGAA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 220 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTGACTGCCCTTCAGAA 279

Qy 181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCCACTTGCCAATTAAAATAGCTGCTATT 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 280 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCCACTTGCCAATTAAAATAGCTGCTATT 339

                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="ho24h02"
                     /tissue_type="Trabecular meshwork"
                     /dev_stage="Adult"
                     /lab_host="EMDH10B"
                     /clone_lib="Human Trabecular meshwork cDNA; hohphq"
                     /note="Organ: Eye; Vector: pSPORT1; The cDNA,
                     directionally cloned in the pSPORT1 vector (life
                     Technologies, Rockville, MD), was constructed at Bioserve
                     Biotechnology (Laurel, MD) essentially following the
                     protocols of the SuperScript Plasmid System full details
                     of which are contained in the manufacturer's Instruction
                     manual (http://www.lifetech.com/). Sublibraries
                     (designated ho, hp, and hq) were made from the first three
                     35-ul fractions of cDNA from a Sephacryl S-500 HR resin
                     column. EST analysis was performed on the unamplified
                     library at the NIH Intramural Sequencing Center(NISC)."
ORIGIN

Query Match   58.8%; Score 598; DB 6; Length 609;
Best Local Similarity 99.8%; Pred. No. 3e-148;
Matches 609; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 189 CACACAGGAAACTCTTTCCACAGTGGCCACTTGCCAATTAAAATAGCTGCTATTATAGCATC 248
        |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   1 CACACAGGAAACTCTTTCCA-AGTGGCCACTTGCCAATTAAAATAGCTGCTATTATAGCATC 59

Qy 249 TCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACTTCCCATCA 308
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   60 TCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACTTCCCATCA 119

Qy 309 ACAATATTTTATTAAAAATTCCAATCCTGGTTCATCACAAAGTCTTGCCAATGGTTTCCAT 368
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 120 ACAATATTTTATTAAAAATTCCAATCCTGGTTCATCACAAAGTCTTGCCAATGGTTTCCAT 179

Qy 369 CACTCTTCTTGGCCATTGGTTTACCTGCCAGGTGTGATAGCAGCAAATTGTCCAACTTCATAA 428
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 180 CACTCTTCTTGGCCATTGGTTTACCTGCCAGGTGTGATAGCAGCAAATTGTCCAACTTCATAA 239

Qy 429 TGGAACCAAGTATAAGAGAGTTTCCACATTGGTTGGATAAGTGATTGTTAACAGAGAAAGCA 488
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 240 TGGAACCAAGTATAAGAGAGTTTCCACATTGGTTGGATAAGTGATTGTTAACAGAGAAAGCA 299

Qy 489 GTTTGGGCCTTCTCAGTTTCTTTTGCTGTACTGCATGCAAATTTATAGTCTGTCTTACCC 548
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 300 GTTTGGGCCTTCTCAGTTTCTTTTGCTGTACTGCATGCAAATTTATAGTCTGTCTTACCC 359

Qy 549 AATGAGGCGGCCGATCCTACAGATACAAAGTTGCTAAACTGGGCCATATCACAGTCCAACAAA 608
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 360 AATGAGGCGGCCGATCCTACAGATACAAAGTTGCTAAACTGGGCCATATCACAGTCCAACAAA 419

Qy 609 TAAAGAAGAAGATGCCTGGGATTGAGCATGAGCATGATCTTTTGGAGGAAGATTTATGTGTCTCTGGG 668
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 420 TAAAGAAGAAGATGCCTGGGATTGAGCATGAGTGTTTGGAGGAAGATTTATGTGTCTCTGGG 479

Qy 669 AATTGTGGGATTGGCAATACTGGCTCTGTTGGGCTGTGACATCTATTCCATCGTGAGTGA 728
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 480 AATTGTGGGATTGGCAATACTGGCTCTGTTGGGCTGTGACATCTATTCCATCGTGAGTGA 539

Qy 729 CTCTTTGACATGAGAGAATTTTCACTATATTCAGAGCAAGCTAGGAGAGAATTTGTTTCCCTTCT 788
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 540 CTCTTTGACATGAGAGAATTTTCACTATATTCAGAGCAAGCTAGGAGAGAATTTGTTTCCCTTCT 599

Qy 789 ACTGGGGCACA 798
        |||||||||||
Db 600 ACTGGGGCACA 609

Qy   241 ATAGCACTCTGACTTTCTTTCTTTACACTTTTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   340 ATAGCACTCTGACTTTCTTTCTTTACACTTTTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 399

Qy   301 TCCCATCAACAATATTTTATAAAAATTCCAATCGTATTATAGCATCTCTGACTTT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   400 TCCCATCAACAATATTTTATAAAAATTCCAATCGTATTATAGCATCTCTGACTTT 459

Qy   361 GTTTCCATCACTCTTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGACAATTGTCCAA 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   460 GTTTCCATCACTCTTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGACAATTGTCCAA 519

Qy   421 CTTCATAATGGAACCAAGTATATAAGAAGTTTCCACATTGGATTAAGTGGTTTAACA 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   520 CTTCATAATGGAACCAAGTATATAAGAAGTTTCCACATTGGATTAAGTGGTTTAACA 579

Qy   481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTGCTGTACTCGCATGCAATTTATAGTCTG 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   580 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTGCTGTACTCGCATGCAATTTATAGTCTG 639

Qy   541 TCTTACCCAATGAGGGCGATCCTACAGATACAACAAGTTGCTAAAACTGGGCATATCAACAGG 598
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   640 TCTTACCCAATGAGGGCGATCCTACAGATACAACAAGTTGCTAAAACTGGGCATATCAACAGG 697

FEATURES   Location/Qualifiers
source   1..920
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:3894657"
                  /tissue_type="large cell carcinoma, undifferentiated"
                  /lab_host="DH10B (phage-resistant)"
                  /clone_lib="NIH_MGC_69"
                  /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                  Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                  Average insert size 1.1 kb. Library constructed by Life
                  Technologies."

ORIGIN

RESULT 14
LOCUS   BE881257   920 bp   mRNA   linear   EST 20-OCT-2000
DEFINITION 601492338P1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3894657 5',
            mRNA sequence.
ACCESSION   BE881257
VERSION   BE881257.1 GI:10330033
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 920)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9684 row: k column: 10
            High quality sequence stop: 732.

Qy   138 GCACCAAAACAGCCCATGCTGATGAATTGACTGCCCTTCAGACACTTCAGCACACACAGGA 197

Query Match   58.8%; Score 597.8; DB 2; Length 920;
Best Local Similarity 93.4%; Pred. No. 3.7e-148;
Matches 724; Conservative 0; Mismatches 37; Indels 14; Gaps 9;

Db   1 GCACCAAAACAGCCCATGCTGATGAATTGACTGCCCTTCAGACTTCAGCACACACAGGA 60
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Qy   61 ACTCCTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATATAGAGCATCTCTGACTTT 120

Db   61 ACTCCTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATATAGAGCATCTCTGACTTT 120

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Qy   241 GGCATTGGTTTACCTGCCAGGTGTGATAGCAGACAATTGTCCAACTTCATAATGGAACCAA 298
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Db   299 GTATAAGAAGTTTCCACA-TGGTTTGGATTAAGTGGTTTAACAAAAAAGCAG-TTGGGCT 356

Qy   378 GGCATTGGTTTACCTGCCAGGTGTGATAGCAGACAATTGTCCAACTTCATAATGGAACCAA 437
Db   416 ATCCTTACAGATACAAGATGGCTAAAACTGGGCATCACAACAAAACAAAAAAAAAGAAGA 475

Qy   498 TCTCAGTTTCTTTTTGCTGTACTCGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCG 557
Db   357 TCTCAGTTTC-TTTTTGCTGTACTCGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCG 415

Qy   558 ATCCTTACAGATACAAAGTTGCTAAAACTGGGCATCACAACAAAACAAAAAAAAAGAAGA 617
Db   416 ATCCTTACAGATACAAAGTTGCTAAAACTGGGCATCACAACAAAACAAAAAAAAAGAAGA 475

RESULT 15
LOCUS   CX757709   742 bp   mRNA   linear   EST 24-JAN-2005
DEFINITION AGENCOURT_41384224 NIH_MGC_278 Homo sapiens cDNA clone
            IMAGE:7772991 3', mRNA sequence.
ACCESSION   CX757709
VERSION   CX757709.1 GI:58054365
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 742)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Meri Firpo
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM15916 row: h column: 13
High quality sequence start: 6
High quality sequence stop: 726.

FEATURES   Location/Qualifiers
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                  /clone="IMAGE:7772991"
                  /tissue_type="pluripotent cell line derived from
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                  /lab_host="DH10B TonA"
                  /clone_lib="NIH_MGC_278"
                  /note="Organ: Blastocyst; Vector: pExpress-1; Site_1:
                  EcoRV; Site 2: NotI; RNA obtained from pluripotent cell
                  line derived from blastocyst inner cell mass(cell line
                  HSF-1.14, NIH Registry designation UC01. Positive for OCT4
                  expression by rtPCR, Positive for SSEA-3, SSEA-4,
                  Tra-1-81, Tra-1-60 by immunofluorescence. Negative for
                  SSEA-1 by immunofluorescence. Passage 35. This line is a
                  subclone of the parental line; the parental line was
                  subcloned to remove aneuploid cells). cDNA was primed
                  using oligo-dT primer;
                  5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)25-3' and cloned into
                  the EcoRV/NotI sites of pExpress-1. Size-selection >1.25
                  kb resulted in an average insert size of 1.9 kb. This
                  primary library is non-normalized (normalized primary
                  library is NIH_MGC_279) and was constructed by Express
                  Genomics (Frederick, MD). Note: this is a Mammalian Gene
                  collection library."

ORIGIN

Query Match
Best Local Similarity   58.6%;
Matches 605; Conservative   0; Mismatches 15; Indels 0; Gaps 0;

97.6%;   Score 596; DB 8;   Length 742;
Pred. No.1.1e-147;

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Qy    1 ATGGAAAGCAGAGAAAGAGAGACATCACAAAACCAAAGAGAAGAAACTTTGGAAAATGAAAGGCCTAGGAGA  60
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Db  123 ATGGAAAACGAGAAAAGAGACGTCACAAAACCAAGAGAAGAAATTTGGAAAATGAAGCCTAGGAGA 182

Qy   61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGAGACCAGCATGCTAAAAAGA 120
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Db  183 AATTTAGAAGACAACGATTATTTGCATAAGGACACGGAGAGACCAGCATGCTAAAAAGA 242

Qy  121 CCTGTGCTTTTGCATTTTGCACCAAAACAGCCCCATGGTGTTGATGAATTTGACTGCCCTTCAGAA 180
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Qy  181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCCACTTGCCAATTAAAATAGCTGCTATT 240
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Qy  241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGGTTCATCAACAAAGTCTTGCCAACT 300
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Qy  301 TCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTTCATCAACAAAGTCTTGCCAATG 360
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Qy  361 GTTTCCATCACTCTCTGGCATTGGGTTTACCTGCCAGGTGTGTGATTAGCAGCAATTGTCCAA 420
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Qy  421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATTGTTAACA 480
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Qy  481 AGAAAGCAGTTTGGGGCGTTCTTCAGTTTTCTTTTTTTGCTACTGCATGCAATTTATAGTTCTG 540
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Qy  601 CAACAAAAATAAAGAAGAATGC 620
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Db  723 CAACAAAAATGAAGAAGAGAATGC 742
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Search completed: December 5, 2005, 03:12:15
Job time : 4648.46 secs